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(54) Title: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME

(57) Abstract: Newly identified Olfactory G protein-coupled receptors (ORs), and the genes and cDNA encoding said receptors are described. Specifically, G protein-coupled receptors active in olfactory signaling, and the genes and cDNA encoding the same, are described, along with methods for isolating such genes and for isolating and expressing such receptors. Methods for representing olfactory perception of a particular odorant in a mammal are also described, as are methods for generating novel molecules or combinations of molecules that elicit a predetermined odor perception in a mammal, and methods for simulating one or more odors. Further, methods for stimulating or blocking odor perception in a mammal are also disclosed.

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HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAMECross Reference to Related Applications

This application claims priority to the following provisional applications: U.S. Ser. No. 60/188,914, filed March 13, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENES ENCODING SAME," to Zozulya; U.S. Ser. No. 60/192,033, filed March 24, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENES ENCODING SAME," to Zozulya; U.S. Ser. No. 60/198,474, filed April 12, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENE ENCODING THE SAME" to Zozulya; U.S. Ser. No. 60/199,335, filed April 24, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/207,702, filed May 26, 2000, entitled, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/213,849, filed June 23, 2000, entitled, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/226,534, filed August 16, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/230,732, filed September 7, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; and U.S. Ser. No. 60/266,862, filed February 7, 2001, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya. All of these applications are herein incorporated by reference in their entireties.

Field of the Invention

The invention relates to newly identified mammalian chemosensory G protein-coupled receptors, particularly olfactory receptors, fragments thereof, classes of such receptors, genes and cDNAs encoding said receptors, vectors including said receptors, and cells that express said receptors. The invention also relates to methods of using such receptors, fragments, genes, cDNAs, vectors, and cells to identify molecules involved in olfactory perception. The invention therefore has application in the selection and design of odorant compositions, as well as malodor blockers (olfactory receptor antagonists), particularly perfumes and fragrance compositions and components of deodorants and other malodor blocking compositions.

Description of the Related Art

The olfactory system provides sensory information about the chemical composition of the external world. Olfactory sensation is thought to involve distinct
5 signaling pathways. These pathways are believed to be mediated by olfactory receptors (ORs). Cells which express olfactory receptors, when exposed to certain chemical stimuli, elicit olfactory sensation by depolarizing to generate an action potential, which is believed to trigger the sensation.

As such, olfactory receptors specifically recognize molecules that elicit
10 specific olfactory sensation. These molecules are also referred to herein as "odorants." Olfactory receptors belong to the 7-transmembrane receptor superfamily (Buck *et al.*, *Cell* 65:175-87 (1991)), which are also known as G protein-coupled receptors (GPCRs). G protein-coupled receptors control many physiological functions, such as endocrine function, exocrine function, heart rate, lipolysis,
15 carbohydrate metabolism, and transmembrane signaling. The biochemical analysis and molecular cloning of a number of such receptors has revealed many basic principles regarding the function of these receptors.

For example, U. S. Patent No. 5,691,188 describes how upon a ligand binding to a GPCR, the receptor presumably undergoes a conformational change leading to
20 activation of the G protein. G proteins are comprised of three subunits: a guanyl nucleotide binding α subunit, a β subunit, and a γ subunit. G proteins cycle between two forms, depending on whether GDP or GTP is bound to the α subunit. When GDP is bound, the G protein exists as a heterotrimer: the $G\alpha\beta\gamma$ complex. When GTP is bound, the α subunit dissociates from the heterotrimer, leaving a $G\beta\gamma$ complex. When
25 a $G\alpha\beta\gamma$ complex operatively associates with an activated G protein-coupled receptor in a cell membrane, the rate of exchange of GTP for bound GDP is increased and the rate of dissociation of the bound $G\alpha$ subunit from the $G\alpha\beta\gamma$ complex increases. The free $G\alpha$ subunit and $G\beta\gamma$ complex are thus capable of transmitting a signal to downstream elements of a variety of signal transduction pathways. These events form
30 the basis for a multiplicity of different cell signaling phenomena, including for example the signaling phenomena that are identified as neurological sensory perceptions such as taste and/or smell.

Genes encoding the olfactory receptors are active primarily in olfactory neurons (Axel, *Sci. Amer.*, 273:154-59 (1995)). Individual olfactory receptor types are expressed in subsets of cells distributed in distinct zones of the olfactory epithelium (Breer, *Semin. Cell Biol.*, 5:25-32 (1994)). The human genome contains approximately one thousand genes that encode a diverse repertoire of olfactory receptors (Rouquier, *Nat. Genet.*, 18:243-50 (1998); Trask, *Hum. Mol. Genet.*, 7:2007-20 (1998)). It has been demonstrated that members of the OR gene family are distributed on all but a few human chromosomes. Through fluorescence *in situ* hybridization analysis, Rouquier showed that OR sequences reside at more than 25 locations in the human genome. Rouquier also determined that the human genome has accumulated a striking number of dysfunctional OR copies: 72% of the analyzed sequences were found to be pseudogenes. An understanding of an animal's ability to detect and discriminate among the thousands of distinct odorants or tastants, and more particularly to distinguish, for example beneficial tastants or odorants from toxic tastants or odorants, is complicated by the fact that chemosensory receptors belong to a multigene family with over a thousand members. For instance, there are up to 1,000 odorant receptors in mammals.

Moreover, each chemosensory receptor neuron may express only one or a few of these receptors. With respect to odorant receptors, any given olfactory neuron can respond to a small set of odorant ligands. In addition, odorant discrimination for a given neuron may depend on the ligand specificity of the one or few receptors it expresses. To analyze odorant-receptor interactions and their effects on olfactory cells, specific ligands and the olfactory receptors to which they bind are identified. This analysis requires isolation and expression of olfactory polypeptides, followed by binding assays.

Some studies suggest that OR genes can be expressed in tissues other than the olfactory epithelium, indicating potential alternative biological roles for this class of chemosensory receptors. Expression of various ORs has been reported in human and murine erythroid cells (Feingold 1999), developing rat heart (Drutel, *Receptor Channels*, 3(1):33-40 (1995)), avian notochord (Nef, *PNAS*, 94(9):4766-71 (1997)) and lingual epithelium (Abe, *FES Lett.*, 316(3):253-56 (1993)). One experimentally documented case also established the existence of a large subset of mammalian ORs transcribed in testes and expressed on the surface of mature spermatozoa, thereby

suggesting a possible role of ORs in sperm chemotaxis (Parmenthler, *Nature*, 355:453-55 (1992); Walensky, *Mol. Med.*, 1(2):130-41 (1998); Branscomb, *Genetics*, 156(2):785-97 (2000)). It was also hypothesized that olfactory receptors might provide molecular codes for highly specific cell-cell recognition functions in development and embryogenesis (Dreyer, *PNAS*, 95(11):9072-77 (1998)).

Complete or partial sequences of numerous human and other eukaryotic chemosensory receptors are currently known. See, e.g., Pilpel, Y. and Lancet, D., *Protein Science*, 8:969-77 (1999); Mombaerts, P., *Annu. Rev. Neurosci.*, 22:487-50 (1999); see also, EP0867508A2, US 5874243, WO 92/17585, WO 95/18140, WO 97/17444, WO 99/67282. Due to the complexity of ligand-receptor interactions, and more particularly odorant-receptor interactions, information about ligand-receptor recognition is lacking. In part, the present invention addresses the need for better understanding of these interactions. The present invention also provides, among other things, novel chemosensory receptors, and methods for utilizing such novel chemosensory receptors and the genes and cDNAs encoding such receptors, especially for identifying compounds that can be used to module chemosensory transduction, such as olfaction.

Summary of the Invention

Toward that end, it is an object of the invention to provide a new family of G protein-coupled receptors comprising over two hundred fifty olfactory G protein-coupled receptors (OR) active in olfactory perception. It is another object of the invention to provide fragments and variants of such ORs which retain odorant-binding activity.

It is yet another object of the invention to provide nucleic acid sequences or molecules that encode such ORs, fragments, or allelic variants.

It is still another object of the invention to provide expression vectors which include nucleic acid sequences that encode such ORs, or fragments, or variants thereof, which are operably linked to at least one regulatory sequence such as a promoter, enhancer, or other sequences involved in positive or negative gene transcription and/or translation.

It is still another object of the invention to provide human or non-human cells that functionally express at least one of such ORs, or fragments, or variants thereof.

It is still another object of the invention to provide OR fusion proteins or polypeptides which include at least a fragment of at least one of such ORs.

It is another object of the invention to provide an isolated nucleic acid molecule encoding an OR comprising a nucleic acid sequence that is at least 30%,
5 more preferably at least 50%, still more preferably at least 60-70%, and still more preferably 75%, preferably 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to a nucleic acid sequence selected from the group consisting of: SEQ. ID. NO. 2, SEQ. ID. NO. 4, SEQ. ID. NO. 6, SEQ. ID. NO. 8, SEQ. ID. NO. 10, SEQ. ID. NO. 12, SEQ. ID. NO. 14, SEQ. ID. NO. 16, SEQ. ID. NO. 18, SEQ. ID. NO. 20, SEQ. ID.
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NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512.

It is a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a polypeptide having an amino acid sequence which is at least 40%, more preferably at least 50%, still more preferably at least 60-70%, and still more preferably 75%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID.

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ID NO: 509 and SEQ ID NO: 511.

It is still a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a fragment of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO. 243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251, SEQ. ID. NO. 253,

SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ. ID. NO. 259, SEQ. ID. NO. 261, SEQ. ID. NO., 263, SEQ. ID. NO., 265, SEQ. ID. NO. 267, SEQ. ID. NO. 269, SEQ. ID. NO. 271, SEQ. ID. NO. 273, SEQ. ID. NO. 275, SEQ. ID. NO. 277, SEQ. ID. NO. 279, SEQ. ID. NO. 281, SEQ. ID. NO. 283, SEQ. ID. NO. 285, SEQ. ID. NO. 287, 5 SEQ. ID. NO. 289, SEQ. ID. NO. 291, SEQ. ID. NO. 293, SEQ. ID. NO. 295, SEQ. ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID. NO. 301, SEQ. ID. NO. 303, SEQ. ID. NO. 305, SEQ. ID. NO. 307, SEQ. ID. NO. 309, SEQ. ID. NO. 311, SEQ. ID. NO. 313, SEQ. ID. NO. 315, SEQ. ID. NO. 317, SEQ. ID. NO. 319, SEQ. ID. NO. 321, SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ. ID. NO. 327, SEQ. ID. NO. 329, SEQ. 10 ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID. NO. 337, SEQ. ID. NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO. 343, SEQ. ID. NO. 345, SEQ. ID. NO. 347, SEQ. ID. NO. 349, SEQ. ID. NO. 351, SEQ. ID. NO. 353, SEQ. ID. NO. 355, SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ. ID. NO. 361, SEQ. ID. NO. 363, SEQ. ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID. NO. 369, SEQ ID NO: 371, SEQ. ID. NO. 15 373, SEQ. ID. NO. 375, SEQ. ID. NO. 377, SEQ. ID. NO. 379, SEQ. ID. NO. 381, SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ. ID. NO. 389, SEQ. ID. NO. 391, SEQ. ID. NO. 393, SEQ. ID. NO. 395, SEQ. ID. NO. 397, SEQ. ID. NO. 399, SEQ. ID. NO. 401, SEQ. ID. NO. 403, SEQ. ID. NO. 405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413, SEQ. ID. NO. 415, 20 SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ. ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO. 439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447, SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ. 25 ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID. NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO. 473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481, SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ. ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 30 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511, wherein the fragment is at least 10, preferably 20, 30, 50, 70, 100, or 150 amino acids in length.

It is still a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a variant of said fragment, wherein there is a variation in at most 10, preferably 5, 4, 3, 2, or 1 amino acid residues.

5 It is still another object of the invention to provide an isolated polypeptide comprising an amino acid sequence that is at least 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ.
10 ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61,
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5 SEQ. ID. NO. 253, SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ. ID. NO. 259, SEQ.
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10 ID. NO. 295, SEQ. ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID. NO. 301, SEQ. ID.
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SEQ. ID. NO. 355, SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ. ID. NO. 361, SEQ.
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25 ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID.
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ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID.
30 NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO.
473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481,
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499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

It is still a further object of the invention to provide an isolated polypeptide comprising a fragment of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO.

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It is still a further object of the invention to provide an isolated polypeptide comprising a variant of said fragment, especially naturally occurring allelic variants, the expression of which may be significant in the manner by which different persons in the human population perceive odors differently, both on a qualitative and
5 quantitative level, wherein there is a variation in at most 10, preferably 5, 4, 3, 2, or 1 amino acid residues.

It is still another object of the invention to provide agonists, including inverse agonists, or antagonists of such ORs, or fragments or variants thereof.

It is yet another object of the invention to provide methods for representing the
10 perception of odor and/or for predicting the perception of odor in a mammal, including in a human. Preferably, such methods may be performed by using the ORs, or fragments or variants thereof, and genes encoding such ORs, or fragments or variants thereof, disclosed herein.

It is yet another object of the invention to provide novel molecules or combinations of
15 molecules which elicit a predetermined olfactory perception in a mammal. Such molecules or compositions can be generated by determining a value of olfactory perception in a mammal for a known molecule or combinations of molecules; determining a value of olfactory perception in a mammal for one or more unknown molecules or combinations of molecules; comparing the value of olfactory perception
20 in a mammal for one or more unknown compositions to the value of olfactory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal; and combining two or more unknown molecules or combinations of molecules to form a molecule or combination of molecules that elicits a
25 predetermined olfactory perception in a mammal. The combining step yields a single molecule or a combination of molecules that elicits a predetermined olfactory perception in a mammal.

It is still a further object of the invention to provide a method of screening one or more compounds for the presence of an odor detectable by a mammal, comprising:
30 a step of contacting said one or more compounds with the disclosed ORs, fragments or variants thereof, preferably wherein the mammal is a human.

It is another object of the invention to provide a method for simulating a fragrance, comprising: for each of a plurality of ORs, or fragments of variants thereof

disclosed herein, preferably human ORs, ascertaining the extent to which the OR interacts with the fragrance; and combining a plurality of compounds, each having a previously ascertained interaction with one or more of the ORs, in amounts that together provide a receptor-stimulation profile that mimics the profile for the fragrance. Interaction of a fragrance with an OR can be determined using any of the binding or reporter assays described herein. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds substantially stimulate at least 50%, 60%, 70%, 75%, 80% or 90% or all of the receptors that are substantially stimulated by the fragrance.

In yet another aspect of the invention, a method is provided wherein a plurality of standard compounds are tested against a plurality of ORs, or fragments or variants thereof, to ascertain the extent to which the ORs each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on a data storage medium. The method may further comprise providing a desired receptor-stimulation profile for a scent; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the scent.

It is a further object of the invention to provide a method for representing olfactory perception of a particular smell in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n ORs of said vertebrate, where n is greater than or equal to 4, n is greater than or equal to 12; n is greater than or equal to 24, n is greater than or equal to 48; n is greater than or equal to 72; n is greater than or equal to 96; n is greater than or equal to 120; n is greater than or equal to 144; n is greater than or equal to 168; n is greater than or equal to 192; n is greater than or equal to 216, or n is greater than or equal to 256; and generating from said values a quantitative representation of olfactory perception. The ORs may be an olfactory receptor disclosed herein, or fragments or variants thereof, the representation may constitute a point or a volume in n -dimensional space, may constitute a graph or a spectrum, and may constitute a matrix of quantitative representations. Also, the

providing step may comprise contacting a plurality of recombinantly produced ORs, or fragments or variants thereof, with a test composition and quantitatively measuring the interaction of said composition with said receptors.

It is yet another object of the invention to provide a method for predicting the
5 olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n ORs of said vertebrate, where n is greater than or equal to 4 n is greater than or equal to 12; n is greater than or equal to 24, n is greater than or equal to 48; n is
10 greater than or equal to 72; n is greater than or equal to 96; n is greater than or equal to 120; n is greater than or equal to 144; n is greater than or equal to 168; n is greater than or equal to 192; n is greater than or equal to 216, or n is greater than or equal to 256; for one or more molecules or combinations of molecules yielding known olfactory perception in a mammal; and generating from said values a quantitative
15 representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal, providing values X_1 to X_n representative of the quantitative stimulation of each of n ORs of said vertebrate, where n is greater than or equal to 4, n is greater than or equal to 12; n is greater than or equal to 24, n is greater than or equal to 48; n is greater than
20 or equal to 72; n is greater than or equal to 96; n is greater than or equal to 120; n is greater than or equal to 144; n is greater than or equal to 168; n is greater than or equal to 192; n is greater than or equal to 216, or n is greater than or equal to 273; for one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal; and generating from said values a quantitative representation of
25 olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal by comparing the quantitative representation of olfactory perception in a mammal for the
30 one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal to the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known

olfactory perception in a mammal. The ORs used in this method may include an olfactory receptor, or fragment or variant thereof, disclosed herein.

Brief Description of the Drawings

5 Figure 1 illustrates the multiple sequence alignment derived for fifty novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins described herein are designated AOLFR1 through AOLFR52. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences
10 AOLFR2 through AOLFR52 were analyzed for alignment with the AOLFR1 amino acid sequence.

 Figure 2 illustrates the multiple sequence alignment derived for fifty novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins
15 described herein are designated AOLFR54 through AOLFR109. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR55 through AOLFR109 were analyzed for alignment with the AOLFR54 amino acid sequence.

 Figure 3 illustrates the multiple sequence alignment derived for fifty novel
20 ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins described herein are designated AOLFR110 through AOLFR163. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR111 through AOLFR163 were analyzed for alignment with the
25 AOLFR110 amino acid sequence.

 Figure 4 illustrates the multiple sequence alignment derived for fifty-four novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty-four novel human olfactory receptors (hOR) proteins described herein are designated AOLFR165 through AOLFR217. The
30 alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR166 through AOLFR217 were analyzed for alignment with the AOLFR165 amino acid sequence.

Figure 5 illustrates the multiple sequence alignment derived for fifty-two novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty-two novel human olfactory receptors (hOR) proteins described herein, which are designated AOLFR218 through AOLFR328. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR219 through AOLFR328 were analyzed for alignment with the AOLFR218 amino acid sequence.

Detailed Description of the Invention

The invention thus provides isolated nucleic acid molecules encoding olfactory-cell-specific G protein-coupled receptors ("GPCRs"), and the polypeptides they encode. These nucleic acid molecules and the polypeptides that they encode are members of the olfactory receptor family. Other members of the olfactory receptor family are disclosed in Krautwurst, *et al.*, *Cell*, 95:917-26 (1998), and WO 0035274, the contents of which are herein incorporated by reference in their entireties.

According to one aspect of the invention, genes encoding over two hundred fifty distinct, novel human olfactory (odorant) receptors (also herein referred to ORs) have been identified in genome sequence databases. All of these receptor genes have been initially detected by computer DNA sequence analysis of genomic clones (unfinished High Throughput Genomic Sequence database accession numbers AB045359, AP002532, AP002533, AL365440, AC073487, AL359636, AL359955, AP002535, AB045365, AL359218, AC002555, AB045361, AL359512, AC023255, AL358773, AL357767, AL358874, AC068380, AC025283, AP002407, AC018700, AC022289, AC006313, AC002556, AC011571, AL121944, AC007194, AP001112, AC021660, AP000723, AC016856, AC018700, AP000818, AC00596, AP000916, AC011517, AP001112, AP000916, AC021427, AC021427, AC020884, AC019108, AL135841, AL133410, AF186996, AL138834, AC009237, AC025249, AC010930, AC009758, AC009642, AC009758, AC025249, AF101706, AC009642, AC025249, AC021660, AC011647, AC011711, AC09642, AC020597, AC011711, AC019088, AC022882, AC011571, AL121944, AP000435, AC012616, AC010332, AC010766, AP000743, AC021809, AC011879, AC021304, AC023226, AL160314, AC021304, AC020380, AC011904, AC004977, AC021304, AP000868, AP000825, AC023080, AC022207, AC121986, AC010814, AC018700, AC021304, AC008620, AC011537,

AC010760, AC027641, AC017103, AC024729, AC024257, AC025115, AP001524, AP000916, AC010814, AL162254, AC025234, AP001521, AC026090, AC019088, AC016856, AC016787, AC009594, AC026038, AQ628489, AC025942, AL163152, AC026975, AC024654, AP001803, AP001804, AL353767, AP001884, AC026083, 5 AC018793, AP000818, AL353894, AL049734, AL355366, AC011464, AC037472, AC036111, AC019093, AC027239, AC027522, AC009545, AC021333, AC036216, AC021935, AC022762, AL356019, AC055861, AC018375, AC072059, AC068339, AC022891, AL357039, AP002345, AC044810, AC073113, AC024399, AC023564, AL390860, AC074365, AP002826, AL359636, AL391534, AC055731, AC076959, 10 AP002826, AC019088, AC009779, AL445307, AP002512, AP000818, AC079190) by virtue of their sequence homology to some of the known human and other mammalian olfactory receptor genes.

Alternatively, nucleic acids encoding the olfactory receptors (ORs) and polypeptides of the invention can be isolated from a variety of sources, genetically 15 engineered, amplified, synthesized, and/or expressed recombinantly according to the methods disclosed in WO 0035374, which is herein incorporated by reference in its entirety.

These nucleic acids provide valuable probes for the identification of olfactory cells, as the nucleic acids are specifically expressed in olfactory cells. They can also 20 serve as tools for the generation of sensory topographical maps that elucidate the relationship between olfactory cells and olfactory sensory neurons leading to olfactory centers in the brain. Furthermore, the nucleic acids and the polypeptides they encode can be used as probes to elucidate olfactory-induced behaviors.

The invention also provides methods of screening for modulators, *e.g.*, 25 activators, inhibitors, stimulators, enhancers, agonists, inverse agonists and antagonists, of the ORs, or fragments or variants thereof, of the invention. Such modulators of olfactory transduction are useful for pharmacological and genetic modulation of olfactory signaling pathways. These methods of screening can be used to identify high affinity agonists and antagonists of olfactory cell activity. These 30 modulator compounds can then be used in the food, pharmaceutical, and cosmetic industries to customize odors and fragrances.

Thus, the invention provides assays for olfactory modulation, where the ORs, or fragments or variants thereof, of the invention act as direct or indirect reporter

molecules for the effect of modulators on olfactory transduction. The ORs, or fragments or variants thereof, can be used in assays, *e.g.*, to measure changes in ion concentration, membrane potential, current flow, ion flux, transcription, signal transduction, receptor-ligand interaction, second messenger concentrations, *in vitro*, *in vivo* and *ex vivo*. In one embodiment, the ORs, or fragments or variants thereof, can be used as an indirect reporters via attachment to second reporter molecules, such as green fluorescent protein (*see, e.g., Mistili et al., Nature Biotech.*, 15:961-64 (1997)). In another embodiment, the ORs, or fragments or variants thereof, can be expressed in host cells, and modulation of olfactory transduction via OR activity can be assayed by measuring changes in Ca^{2+} levels.

Methods of assaying for modulators of olfactory transduction include *in vitro* ligand binding assays using the ORs of the invention, or fragments or variants thereof. More particularly, such assays can use the ORs; portions thereof such as the extracellular or transmembrane domains; chimeric proteins comprising one or more of such domains; oocyte receptor expression; tissue culture cell receptor expression; transcriptional activation of the receptor; G protein binding to the receptor; ligand binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP and inositol triphosphate; changes in intracellular Ca^{2+} levels; and neurotransmitter release.

The invention also provides for methods of detecting olfactory nucleic acid and protein expression, allowing for the investigation of olfactory transduction regulation and specific identification of olfactory receptor cells. The ORs, fragments, and variants of the invention can also be used to generate monoclonal and polyclonal antibodies useful for identifying olfactory receptor cells. Olfactory receptor cells can be identified using techniques such as reverse transcription and amplification of mRNA, isolation of total RNA or poly A⁺ RNA, northern blotting, dot blotting, *in situ* hybridization, RNase protection, S1 digestion, probing DNA microchip arrays, western blots, and the like.

A. Identification and Characterization of Olfactory Receptors

The amino acid sequences of the ORs and polypeptides of the invention can be identified by putative translation of the coding nucleic acid sequences. These various

amino acid sequences and the coding nucleic acid sequences may be compared to one another or to other sequences according to a number of methods.

For example, in sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, as described below for the BLASTN and BLASTP programs, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window," as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of: from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *PNAS*, 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

A preferred example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1997) and Altschul *et al.*, *J Mol. Biol.* 215:403-410 (1990), respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued

threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J Mol. Biol.* 215:403-410 (1990)). These initial neighborhood word hits act as seeds for initiating
5 searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a
10 scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W , T , and
15 X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) or 10, $M=5$, $N=-4$ and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *PNAS*, 89:10915 (1989))
20 alignments (B) of 50, expectation (E) of 10, $M=5$, $N=-4$, and a comparison of both strands.

Another example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments to show relationship and percent sequence identity. It also plots a so-
25 called "tree" or "dendrogram" showing the clustering relationships used to create the alignment (*see, e.g.*, Figure 2). PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, *J Mol. Evol.* 35:351-60 (1987). The method used is similar to the method described by Higgins & Sharp, *CABIOS* 5:151-153 (1989). The program can align up to 300 sequences, each of a maximum length of
30 5,000 nucleotides or amino acids. The multiple alignment procedure begins with the pairwise alignment of the two most similar sequences, producing a cluster of two aligned sequences. This cluster is then aligned to the next most related sequence or cluster of aligned sequences. Two clusters of sequences are aligned by a simple

extension of the pairwise alignment of two individual sequences. The final alignment is achieved by a series of progressive, pairwise alignments. The program is run by designating specific sequences and their amino acid or nucleotide coordinates for regions of sequence comparison and by designating the program parameters. Using
5 PILEUP, a reference sequence is compared to other test sequences to determine the percent sequence identity relationship using the following parameters: default gap weight (3.00), default gap length weight (0.10), and weighted end gaps. PILEUP can be obtained from the GCG sequence analysis software package, *e.g.*, version 7. 0 (Devereaux *et al.*, *Nuc. Acids Res.* 12:387-395 (1984) encoded by the genes were
10 derived by conceptual translation of the corresponding open reading frames. Comparison of these protein sequences to all known proteins in the public sequence databases using BLASTP algorithm revealed their strong homology to the members of the mammalian olfactory receptor family, each of the odorant receptor sequences having at least 50%, and preferably at least 55%, at least 60%, at least 65%, and most
15 preferably at least 70%, amino acid identity to at least one known member of the family.

The nucleic acid molecules of the present invention are typically intronless and encode putative OR proteins generally having lengths of approximately 290 to approximately 400 amino acid residues that contain seven transmembrane domains, as
20 predicted by hydrophobicity plotting analysis, indicating that they belong to the G protein-coupled receptor 7-transmembrane (7TM) superfamily, which includes the subset of taste and olfactory receptors. In addition to the overall structural similarity, each of the ORs identified herein has a characteristic sequence signature of an olfactory receptor. In particular, all the identified sequences contain very close
25 matches to the following consensus amino acid motifs (Mombaerts, 1999, Pilpel 1999): EFILL (SEQ ID NO: 513) before transmembrane domain 1, LHTPMY (SEQ ID No: 514) in intracellular loop 1, MAYDRYVAIC (SEQ ID NO: 510) at the end of transmembrane domain 3 and the beginning of intracellular loop 2, SY at the end of transmembrane domain 5, FSTCSSH (SEQ ID NO: 516) in the beginning of
30 transmembrane domain 6, and PMLNPF (SEQ ID NO: 517) in transmembrane domain 7. Combination of all the above-mentioned structural features of the identified genes and encoded proteins strongly suggests that they represent novel members of the human olfactory receptor family.

As noted above, complete or partial sequences of numerous human and other eukaryotic olfactory receptors are currently known. The novel human receptors have amino acid sequences distinctly different from the previously known human olfactory receptors, which suggests their different specificity in odorant recognition. Therefore, these novel receptors and their genes can be used, alone or in combination with known olfactory receptors, in developing detection systems and assays for chemically distinct types of odorants not recognized by the known receptors, as well as for diagnostic and research purposes.

B. Definitions

As used herein, the following terms have the meanings ascribed to them unless specified otherwise.

“OR” refers to one or more members of a family of G protein-coupled receptors that are expressed in olfactory cells. Olfactory receptor cells can also be identified on the basis of morphology (*see, e.g., Roper, supra*), or by the expression of proteins specifically expressed in olfactory cells. OR family members may have the ability to act as receptors for olfactory transduction.

“OR” nucleic acids encode a family of GPCRs with seven transmembrane regions that have “G protein-coupled receptor activity,” *e.g.*, they may bind to G proteins in response to extracellular stimuli and promote production of second messengers such as IP₃, cAMP, cGMP, and Ca²⁺ via stimulation of enzymes such as phospholipase C and adenylate cyclase (for a description of the structure and function of GPCRs, *see, e.g., Fong, supra*, and Baldwin, *supra*). A single olfactory cell may contain many distinct OR polypeptides.

Topologically, certain chemosensory GPCRs have an “N-terminal domain;” “extracellular domains;” “transmembrane domains” comprising seven transmembrane regions, and corresponding cytoplasmic, and extracellular loops; “cytoplasmic domains,” and a “C-terminal domain” (*see, e.g., Hoon et al., Cell, 96:541-51 (1999); Buck & Axel, Cell, 65:175-87 (1991)*). These domains can be structurally identified using methods known to those of skill in the art, such as sequence analysis programs that identify hydrophobic and hydrophilic domains (*see, e.g., Stryer, Biochemistry, (3rd ed. 1988); see also* any of a number of Internet based sequence analysis programs, such as those found at dot.imgen.bcm.tmc.edu). Such domains are useful

for making chimeric proteins and for in vitro assays of the invention, *e.g.*, ligand binding assays.

“Extracellular domains” therefore refers to the domains of OR polypeptides that protrude from the cellular membrane and are exposed to the extracellular face of the cell. Such domains generally include the “N terminal domain” that is exposed to
5 the extracellular face of the cell, and optionally can include portions of the extracellular loops of the transmembrane domain that are exposed to the extracellular face of the cell, *i.e.*, the loops between transmembrane regions 2 and 3, between transmembrane regions 4 and 5, and between transmembrane regions 6 and 7.

10 The “N terminal domain” region starts at the N-terminus and extends to a region close to the start of the transmembrane domain. “Transmembrane domain,” which comprises the seven “transmembrane regions,” refers to the domain of OR polypeptides that lies within the plasma membrane, and may also include the corresponding cytoplasmic (intracellular) and extracellular loops. The seven
15 transmembrane regions and extracellular and cytoplasmic loops can be identified using standard methods, as described in Kyte & Doolittle, *J. Mol. Biol.*, 157:105-32 (1982)), or in Stryer, *supra*. The general secondary and tertiary structure of transmembrane domains, in particular the seven transmembrane domains of 7-transmembrane receptors such as olfactory receptors, are well known in the art. Thus,
20 primary structure sequence can be designed or predicted based on known transmembrane domain sequences, as described in detail below. These transmembrane domains are useful for *in vitro* ligand-binding assays, both soluble and solid phase.

“Cytoplasmic domains” refers to the domains of OR polypeptides that face the
25 inside of the cell, *e.g.*, the “C terminal domain” and the intracellular loops of the transmembrane domain, *e.g.*, the intracellular loop between transmembrane regions 1 and 2, the intracellular loop between transmembrane regions 3 and 4, and the intracellular loop between transmembrane regions 5 and 6. “C terminal domain” refers to the region that spans the end of the last transmembrane domain and the C-
30 terminus of the protein, and which is normally located within the cytoplasm.

The term “ligand-binding region” or “ligand-binding domain” refers to sequences derived from a chemosensory receptor, particularly an olfactory receptor,

that substantially incorporates at least transmembrane domains II to VII. The ligand-binding region may be capable of binding a ligand, and more particularly, an odorant.

The phrase "functional effects" in the context of assays for testing compounds that modulate OR family member mediated olfactory transduction includes the determination of any parameter that is indirectly or directly under the influence of the receptor, *e.g.*, functional, physical and chemical effects. It includes ligand binding, changes in ion flux, membrane potential, current flow, transcription, G protein binding, GPCR phosphorylation or dephosphorylation, signal transduction, receptor-ligand interactions, second messenger concentrations (*e.g.*, cAMP, cGMP, IP3, or intracellular Ca^{2+}), *in vitro*, *in vivo*, and *ex vivo* and also includes other physiologic effects such increases or decreases of neurotransmitter or hormone release.

By "determining the functional effect" in the context of assays is meant assays for a compound that increases or decreases a parameter that is indirectly or directly under the influence of an OR family member, *e.g.*, functional, physical and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index), hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties, patch clamping, voltage-sensitive dyes, whole cell currents, radioisotope efflux, inducible markers, oocyte OR gene expression; tissue culture cell OR expression; transcriptional activation of OR genes; ligand-binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP, cGMP, and inositol triphosphate (IP3); changes in intracellular calcium levels; neurotransmitter release, and the like.

"Inhibitors," "activators," and "modulators" of OR genes or proteins are used interchangeably to refer to inhibitory, activating, or modulating molecules identified using *in vitro* and *in vivo* assays for olfactory transduction, *e.g.*, ligands, agonists, antagonists, and their homologs and mimetics. Inhibitors are compounds that, *e.g.*, bind to, partially or totally block stimulation, decrease, prevent, delay activation, inactivate, desensitize, or down regulate olfactory transduction, *e.g.*, antagonists. Activators are compounds that, *e.g.*, bind to, stimulate, increase, open, activate, facilitate, enhance activation, sensitize, or up regulate olfactory transduction, *e.g.*, agonists. Modulators include compounds that, *e.g.*, alter the interaction of a receptor

with: extracellular proteins that bind activators or inhibitor (*e.g.*, ebnerin and other members of the hydrophobic carrier family); G proteins; kinases (*e.g.*, homologs of rhodopsin kinase and beta adrenergic receptor kinases that are involved in deactivation and desensitization of a receptor); and arrestins, which also deactivate
5 and desensitize receptors. Modulators can include genetically modified versions of OR family members, *e.g.*, with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, small chemical molecules and the like. Such assays for inhibitors and activators include, *e.g.*, expressing OR family members in cells or cell membranes, applying putative modulator compounds, in the presence or
10 absence of tastants, *e.g.*, sweet tastants, and then determining the functional effects on olfactory transduction, as described above. Samples or assays comprising OR family members that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of modulation. Control samples (untreated with modulators) are assigned a
15 relative OR activity value of 100%. Inhibition of a OR is achieved when the OR activity value relative to the control is about 80%, optionally 50% or 25-0%. Activation of an OR is achieved when the OR activity value relative to the control is 110%, optionally 150%, optionally 200-500%, or 1000-3000% higher.

The terms "purified," "substantially purified," and "isolated" as used herein
20 refer to the state of being free of other, dissimilar compounds with which the compound of the invention is normally associated in its natural state, so that the "purified," "substantially purified," and "isolated" subject comprises at least 0.5%, 1%, 5%, 10%, or 20%, and most preferably at least 50% or 75% of the mass, by weight, of a given sample. In one preferred embodiment, these terms refer to the
25 compound of the invention comprising at least 95% of the mass, by weight, of a given sample. As used herein, the terms "purified," "substantially purified," and "isolated" "isolated," when referring to a nucleic acid or protein, of nucleic acids or proteins, also refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or
30 concentration greater than that which occurs naturally in the mammalian, especially human, body, including (1) the purification from other associated structures or compounds or (2) the association with structures or compounds to which it is not normally associated in the mammalian, especially human, body, are within the

meaning of "isolated." The nucleic acid or protein or classes of nucleic acids or proteins, described herein, may be isolated, or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the art.

5 As used herein, the term "isolated," when referring to a nucleic acid or polypeptide refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or concentration greater than that which occurs naturally in the body, including (1) the purification from other naturally-occurring associated structures or
10 compounds, or (2) the association with structures or compounds to which it is not normally associated in the body are within the meaning of "isolated" as used herein. The nucleic acids or polypeptides described herein may be isolated or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the
15 art.

As used herein, the terms "amplifying" and "amplification" refer to the use of any suitable amplification methodology for generating or detecting recombinant or naturally expressed nucleic acid, as described in detail, below. For example, the invention provides methods and reagents (*e.g.*, specific degenerate oligonucleotide
20 primer pairs) for amplifying (*e.g.*, by polymerase chain reaction, PCR) naturally expressed (*e.g.*, genomic or mRNA) or recombinant (*e.g.*, cDNA) nucleic acids of the invention (*e.g.*, tastant-binding sequences of the invention) *in vivo* or *in vitro*.

The term "7- transmembrane receptor" means a polypeptide belonging to a superfamily of transmembrane proteins that have seven domains that span the plasma
25 membrane seven times (thus, the seven domains are called "transmembrane" or "TM" domains TM I to TM VII). The families of olfactory and certain taste receptors each belong to this super-family. 7-transmembrane receptor polypeptides have similar and characteristic primary, secondary and tertiary structures, as discussed in further detail below.

30 The term "library" means a preparation that is a mixture of different nucleic acid or polypeptide molecules, such as the library of recombinantly generated chemosensory, particularly olfactory receptor ligand-binding domains generated by amplification of nucleic acid with degenerate primer pairs, or an isolated collection of

vectors that incorporate the amplified ligand-binding domains, or a mixture of cells each randomly transfected with at least one vector encoding an olfactory receptor.

The term "nucleic acid" or "nucleic acid sequence" refers to a deoxy-ribonucleotide or ribonucleotide oligonucleotide in either single- or double-stranded
5 form. The term encompasses nucleic acids, i.e., oligonucleotides, containing known analogs of natural nucleotides. The term also encompasses nucleic-acid-like structures with synthetic backbones (*see e.g., Oligonucleotides and Analogues, a Practical Approach*, ed. F. Eckstein, Oxford Univ. Press (1991); *Antisense Strategies, Annals of the N.Y. Acad. of Sci.*, Vol. 600, Eds. Baserga *et al.* (NYAS 1992); Milligan
10 *J. Med. Chem.* 36:1923-1937 (1993); *Antisense Research and Applications* (1993, CRC Press), WO 97/03211; WO 96/39154; Mata, *Toxicol. Appl. Pharmacol.* 144:189-197 (1997); Strauss-Soukup, *Biochemistry* 36:8692-8698 (1997); Samstag, *Antisense Nucleic Acid Drug Dev.* 6:153-156 (1996)).

Unless otherwise indicated, a particular nucleic acid sequence also implicitly
15 encompasses conservatively modified variants thereof (*e.g., degenerate codon substitutions*) and complementary sequences, as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating, *e.g.,* sequences in which the third position of one or more selected codons is substituted with mixed-base and/or deoxyinosine residues (Batzer *et al., Nucleic*
20 *Acid Res.*, 19:5081 (1991); Ohtsuka *et al., J. Biol. Chem.*, 260:2605-08 (1985); Rossolini *et al., Mol. Cell. Probes*, 8:91-98 (1994)). The term nucleic acid is used interchangeably with gene, cDNA, mRNA, oligonucleotide, and polynucleotide.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid
25 polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymer.

The term "plasma membrane translocation domain" or simply "translocation domain" means a polypeptide domain that, when incorporated into the amino terminus
30 of a polypeptide coding sequence, can with great efficiency "chaperone" or "translocate" the hybrid ("fusion") protein to the cell plasma membrane. For instance, a "translocation domain" may be derived from the amino terminus of the bovine rhodopsin receptor polypeptide. In one embodiment, the translocation domain may be

functionally equivalent to an exemplary translocation domain (5'-MNGTEGPNFYVPFSNKTGVV; SEQ ID NO: 518). However, rhodopsin from any mammal may be used, as can other translocation facilitating sequences. Thus, the translocation domain is particularly efficient in translocating 7-transmembrane fusion proteins to the plasma membrane, and a protein (*e.g.*, an olfactory receptor polypeptide) comprising an amino terminal translocating domain will be transported to the plasma membrane more efficiently than without the domain. However, if the N-terminal domain of the polypeptide is active in binding, the use of other translocation domains may be preferred.

“Functional equivalency” means the domain’s ability and efficiency in translocating newly translated proteins to the plasma membrane as efficiently as exemplary SEQ ID NO: 518 under similar conditions; relative efficiencies can be measured (in quantitative terms) and compared, as described herein. Domains falling within the scope of the invention can be determined by routine screening for their efficiency in translocating newly synthesized polypeptides to the plasma membrane in a cell (mammalian, *Xenopus*, and the like) with the same efficiency as the twenty amino acid long translocation domain SEQ ID NO: 518, as described in detail below.

The “translocation domain,” “ligand-binding domain,” and chimeric receptor compositions described herein also include “analogs,” or “conservative variants” and “mimetics” (“peptidomimetics”) with structures and activity that substantially correspond to the exemplary sequences. Thus, the terms “conservative variant” or “analog” or “mimetic” refer to a polypeptide which has a modified amino acid sequence, such that the change(s) do not substantially alter the polypeptide’s (the conservative variant’s) structure and/or activity, as defined herein. These include conservatively modified variations of an amino acid sequence, *i.e.*, amino acid substitutions, additions or deletions of those residues that are not critical for protein activity, or substitution of amino acids with residues having similar properties (*e.g.*, acidic, basic, positively or negatively charged, polar or non-polar, *etc.*) such that the substitutions of even critical amino acids does not substantially alter structure and/or activity. Conservative substitution tables providing functionally similar amino acids are well known in the art.

More particularly, “conservatively modified variants” applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences,

conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids
5 encode any given protein.

For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide.

10 Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only
15 codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

Conservative substitution tables providing functionally similar amino acids are well known in the art. For example, one exemplary guideline to select conservative
20 substitutions includes (original residue followed by exemplary substitution): ala/gly or ser; arg/lys; asn/gln or his; asp/glu; cys/ser; gln/asn; gly/asp; gly/ala or pro; his/asn or gln; ile/leu or val; leu/ile or val; lys/arg or gln or glu; met/leu or tyr or ile; phe/met or leu or tyr; ser/thr; thr/ser; trp/tyr; tyr/trp or phe; val/ile or leu. An alternative exemplary guideline uses the following six groups, each containing amino acids that
25 are conservative substitutions for one another: 1) Alanine (A), Serine (S), Threonine (T); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (I); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); (*see also, e.g., Creighton, Proteins*, W.H. Freeman and Company (1984); Schultz and Schimer, *Principles of*
30 *Protein Structure*, Springer-Verlag (1979)). One of skill in the art will appreciate that the above-identified substitutions are not the only possible conservative substitutions. For example, for some purposes, one may regard all charged amino acids as conservative substitutions for each other whether they are positive or negative. In

addition, individual substitutions, deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence can also be considered "conservatively modified variations."

The terms "mimetic" and "peptidomimetic" refer to a synthetic chemical
5 compound that has substantially the same structural and/or functional characteristics of the polypeptides, *e.g.*, translocation domains, ligand-binding domains, or chimeric receptors of the invention. The mimetic can be either entirely composed of synthetic, non-natural analogs of amino acids, or may be a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino acids. The mimetic can
10 also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic's structure and/or activity.

As with polypeptides of the invention which are conservative variants, routine experimentation will determine whether a mimetic is within the scope of the
15 invention, *i.e.*, that its structure and/or function is not substantially altered. Polypeptide mimetic compositions can contain any combination of non-natural structural components, which are typically from three structural groups: a) residue linkage groups other than the natural amide bond ("peptide bond") linkages; b) non-natural residues in place of naturally occurring amino acid residues; or c) residues
20 which induce secondary structural mimicry, *i.e.*, to induce or stabilize a secondary structure, *e.g.*, a beta turn, gamma turn, beta sheet, alpha helix conformation, and the like. A polypeptide can be characterized as a mimetic when all or some of its residues are joined by chemical means other than natural peptide bonds. Individual peptidomimetic residues can be joined by peptide bonds, other chemical bonds or
25 coupling means, such as, *e.g.*, glutaraldehyde, N-hydroxysuccinimide esters, bifunctional maleimides, N,N'-dicyclohexylcarbodiimide (DCC) or N,N'-diisopropylcarbodiimide (DIC). Linking groups that can be an alternative to the traditional amide bond ("peptide bond") linkages include, *e.g.*, ketomethylene (*e.g.*, -C(=O)-CH₂- for -C(=O)-NH-), aminomethylene (CH₂-NH), ethylene, olefin
30 (CH=CH), ether (CH₂-O), thioether (CH₂-S), tetrazole (CN₄), thiazole, retroamide, thioamide, or ester (*see, e.g.*, Spatola, *Chemistry and Biochemistry of Amino Acids, Peptides and Proteins*, 7:267-357, "Peptide Backbone Modifications," Marcell Dekker, NY (1983)). A polypeptide can also be characterized as a mimetic by

containing all or some non-natural residues in place of naturally occurring amino acid residues; non-natural residues are well described in the scientific and patent literature.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. For example, useful labels include ^{32}P , fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, for example, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are optionally directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one

source and a coding region from another source. Similarly, a heterologous protein indicates that the protein comprises two or more subsequences that are not found in the same relationship to each other in nature (*e.g.*, a fusion protein).

A “promoter” is defined as an array of nucleic acid sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A “constitutive” promoter is a promoter that is active under most environmental and developmental conditions. An “inducible” promoter is a promoter that is active under environmental or developmental regulation. The term “operably linked” refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

As used herein, “recombinant” refers to a polynucleotide synthesized or otherwise manipulated *in vitro* (*e.g.*, “recombinant polynucleotide”), to methods of using recombinant polynucleotides to produce gene products in cells or other biological systems, or to a polypeptide (“recombinant protein”) encoded by a recombinant polynucleotide. “Recombinant means” also encompass the ligation of nucleic acids having various coding regions or domains or promoter sequences from different sources into an expression cassette or vector for expression of, *e.g.*, inducible or constitutive expression of a fusion protein comprising a translocation domain of the invention and a nucleic acid sequence amplified using a primer of the invention.

The phrase “selectively (or specifically) hybridizes to” refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (*e.g.*, total cellular or library DNA or RNA).

The phrase “stringent hybridization conditions” refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acid, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer

sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology - Hybridisation with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent

5 conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at

10 equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the

15 addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, optionally 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42°C, or, 5x SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1 % SDS at 65°C. Such

20 hybridizations and wash steps can be carried out for, e.g., 1, 2, 5, 10, 15, 30, 60; or more minutes.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially related if the polypeptides that they encode are substantially related. This occurs, for example, when a copy of a nucleic acid is created using the maximum

25 codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1x SSC at 45°C. Such hybridizations and wash steps can be carried out for, e.g., 1, 2, 5, 10, 15, 30, 60, or

30 more minutes. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency.

“Antibody” refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad
5 immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair
10 having one “light” (about 25 kDa) and one “heavy” chain (about 50-70 kDa). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (VL) and variable heavy chain (VH) refer to these light and heavy chains respectively.

A “chimeric antibody” is an antibody molecule in which (a) the constant
15 region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, *e.g.*, an enzyme, toxin, hormone, growth factor, drug, *etc.*; or (b) the variable region, or a portion thereof, is altered, replaced or
20 exchanged with a variable region having a different or altered antigen specificity.

An “anti-OR” antibody is an antibody or antibody fragment that specifically binds a polypeptide encoded by a OR gene, cDNA, or a subsequence thereof.

The term “immunoassay” is an assay that uses an antibody to specifically bind an antigen. The immunoassay is characterized by the use of specific binding
25 properties of a particular antibody to isolate, target, and/or quantify the antigen.

The phrase “specifically (or selectively) binds” to an antibody or, “specifically (or selectively) immunoreactive with,” when referring to a protein or peptide, refers to a binding reaction that is determinative of the presence of the protein in a heterogeneous population of proteins and other biologics. Thus, under designated
30 immunoassay conditions, the specified antibodies bind to a particular protein at least two times the background and do not substantially bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular

protein. For example, polyclonal antibodies raised to an OR family member from specific species such as rat, mouse, or human can be selected to obtain only those polyclonal antibodies that are specifically immunoreactive with the OR polypeptide or an immunogenic portion thereof and not with other proteins, except for orthologs or polymorphic variants and alleles of the OR polypeptide. This selection may be achieved by subtracting out antibodies that cross-react with OR molecules from other species or other OR molecules. Antibodies can also be selected that recognize only OR GPCR family members but not GPCRs from other families. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select antibodies specifically immunoreactive with a protein (*see, e.g., Harlow & Lane, Antibodies, A Laboratory Manual, (1988), for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity*). Typically a specific or selective reaction will be at least twice background signal or noise and more typically more than 10 to 100 times background.

The phrase "selectively associates with" refers to the ability of a nucleic acid to "selectively hybridize" with another as defined above, or the ability of an antibody to "selectively (or specifically) bind to a protein, as defined above.

The term "expression vector" refers to any recombinant expression system for the purpose of expressing a nucleic acid sequence of the invention *in vitro* or *in vivo*, constitutively or inducibly, in any cell, including prokaryotic, yeast, fungal, plant, insect or mammalian cell. The term includes linear or circular expression systems. The term includes expression systems that remain episomal or integrate into the host cell genome. The expression systems can have the ability to self-replicate or not, i.e., drive only transient expression in a cell. The term includes recombinant expression "cassettes which contain only the minimum elements needed for transcription of the recombinant nucleic acid.

By "host cell" is meant a cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, HEK-293, and the like, *e.g.,* cultured cells, explants, and cells *in vivo*.

C. Isolation and Expression of Olfactory Receptors

Isolation and expression of the ORs, or fragments or variants thereof, of the invention can be performed as described below. PCR primers can be used for the amplification of nucleic acids encoding olfactory receptor ligand-binding regions and libraries of these nucleic acids can thereby be generated. Libraries of expression vectors can then be used to infect or transfect host cells for the functional expression of these libraries. These genes and vectors can be made and expressed *in vitro* or *in vivo*. One of skill will recognize that desired phenotypes for altering and controlling nucleic acid expression can be obtained by modulating the expression or activity of the genes and nucleic acids (*e.g.*, promoters, enhancers and the like) within the vectors of the invention. Any of the known methods described for increasing or decreasing expression or activity can be used. The invention can be practiced in conjunction with any method or protocol known in the art, which are well described in the scientific and patent literature.

The nucleic acid sequences of the invention and other nucleic acids used to practice this invention, whether RNA, cDNA, genomic DNA, vectors, viruses or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed recombinantly. Any recombinant expression system can be used, including, in addition to mammalian cells, *e.g.*, bacterial, yeast, insect or plant systems.

Alternatively, these nucleic acids can be synthesized *in vitro* by well-known chemical synthesis techniques, as described in, *e.g.*, Carruthers, *Cold Spring Harbor Symp. Quant. Biol.* 47:411-418 (1982); Adams, *Am. Chem. Soc.* 105:661 (1983); Belousov, *Nucleic Acids Res.* 25:3440-3444 (1997); Frenkel, *Free Radic. Biol. Med.* 19:373-380 (1995); Blommers, *Biochemistry* 33:7886-7896 (1994); Narang, *Meth. Enzymol.* 68:90 (1979); Brown, *Meth. Enzymol.* 68:109 (1979); Beaucage, *Tetra. Lett.* 22:1859 (1981); U.S. Patent No. 4,458,066. Double-stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

Techniques for the manipulation of nucleic acids, such as, for example, for generating mutations in sequences, subcloning, labeling probes, sequencing, hybridization and the like are well described in the scientific and patent literature.

See, e.g., Sambrook, ed., *Molecular Cloning: a Laboratory manual* (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory (1989); *Current Protocols in Molecular Biology*, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); *Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I*,
5 Theory and Nucleic Acid Preparation, Tijssen, ed. Elsevier, N.Y. (1993).

Nucleic acids, vectors, capsids, polypeptides, and the like can be analyzed and quantified by any of a number of general means well known to those of skill in the art. These include, e.g., analytical biochemical methods such as NMR, spectrophotometry, radiography, electrophoresis, capillary electrophoresis, high performance liquid
10 chromatography (HPLC), thin layer chromatography (TLC), and hyperdiffusion chromatography, various immunological methods, e.g., fluid or gel precipitin reactions, immunodiffusion, immunoelectrophoresis, radioimmunoassays (RIAs), enzyme-linked immunosorbent assays (ELISAs), immuno-fluorescent assays, Southern analysis, Northern analysis, dot-blot analysis, gel electrophoresis (e.g., SDS-
15 PAGE), RT-PCR, quantitative PCR, other nucleic acid or target or signal amplification methods, radiolabeling, scintillation counting, and affinity chromatography.

Oligonucleotide primers are used to amplify nucleic acid encoding an olfactory receptor ligand-binding region. The nucleic acids described herein can also be cloned
20 or measured quantitatively using amplification techniques. Using exemplary degenerate primer pair sequences, (see below), the skilled artisan can select and design suitable oligonucleotide amplification primers. Amplification methods are also well known in the art, and include, e.g., polymerase chain reaction, PCR (PCR Protocols, a Guide to Methods and Applications, ed. Innis. Academic Press, N.Y.
25 (1990) and PCR Strategies, ed. Innis, Academic Press, Inc., N.Y. (1995), ligase chain reaction (LCR) (see, e.g., Wu, *Genomics* 4:560 (1989); Landegren, *Science* 241:1077,(1988); Barringer, *Gene* 89:117 (1990)); transcription amplification (see, e.g., Kwoh, *PNAS*, 86:1173 (1989)); and, self-sustained sequence replication (see, e.g., Guatelli, *PNAS*, 87:1874 (1990)); Q Beta replicase amplification (see, e.g.,
30 Smith, *J. Clin. Microbiol.* 35:1477-1491 (1997)); automated Q-beta replicase amplification assay (see, e.g., Burg, *Mol. Cell. Probes* 10:257-271 (1996)) and other RNA polymerase mediated techniques (e.g., NASBA, Cangene, Mississauga, Ontario); see also Berger, *Methods Enzymol.* 152:307-316 (1987); Sambrook;

Ausubel; U.S. Patent Nos. 4,683,195 and 4,683,202; Sooknanan, *Biotechnology* 13:563-564 (1995).

Once amplified, the nucleic acids, either individually or as libraries, may be cloned according to methods known in the art, if desired, into any of a variety of
5 vectors using routine molecular biological methods; methods for cloning *in vitro* amplified nucleic acids are described, *e.g.*, U.S. Pat. No. 5,426,039. To facilitate cloning of amplified sequences, restriction enzyme sites can be "built into" the PCR primer pair. For example, Pst I and Bsp E1 sites were designed into the exemplary primer pairs of the invention. These particular restriction sites have a sequence that,
10 when ligated, are "in-frame" with respect to the 7-membrane receptor "donor" coding sequence into which they are spliced (the ligand-binding region coding sequence is internal to the 7-membrane polypeptide, thus, if it is desired that the construct be translated downstream of a restriction enzyme splice site, out of frame results should be avoided; this may not be necessary if the inserted ligand-binding domain comprises
15 substantially most of the transmembrane VII region). The primers can be designed to retain the original sequence of the "donor" 7-membrane receptor (the Pst I and Bsp E1 sequence in the primers of the invention generate an insert that, when ligated into the Pst I/Bsp E1 cut vector, encode residues found in the "donor" mouse olfactory receptor M4 sequence). Alternatively, the primers can encode amino acid residues
20 that are conservative substitutions (*e.g.*, hydrophobic for hydrophobic residue, see above discussion) or functionally benign substitutions (*e.g.*, do not prevent plasma membrane insertion, cause cleavage by peptidase, cause abnormal folding of receptor, and the like).

The primer pairs are designed to selectively amplify ligand-binding regions of
25 olfactory receptor proteins. These domain regions may vary for different ligands, and more particularly odorants; thus, what may be a minimal binding region for one ligand, and more particularly odorants, may be too limiting for a second potential ligand. Thus, domain regions of different sizes comprising different domain structures may be amplified; for example, transmembrane (TM) domains II through
30 VII, III through VII, III through VI or II through VI, or variations thereof (*e.g.*, only a subsequence of a particular domain, mixing the order of the domains, and the like), of a 7-transmembrane OR.

As domain structures and sequence of many 7-membrane proteins, particularly olfactory receptors, are known, the skilled artisan can readily select domain-flanking and internal domain sequences as model sequences to design degenerate amplification primer pairs. For example, a nucleic acid sequence encoding domain regions II through VII can be generated by PCR amplification using a primer pair. To amplify a nucleic acid comprising transmembrane domain I (TM I) sequence, a degenerate primer can be designed from a nucleic acid that encodes the amino acid sequence LFLLYL3' (SEQ ID NO: 519). Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM III, TM I through TM IV, TM I through TM V, TM I through TM VI or TM I through TM VII).

To amplify a nucleic acid comprising a transmembrane domain III (TM III) sequence, a degenerate primer (of at least about 17 residues) can be designed from a nucleic acid that encodes the amino acid sequence M(A/G)(Y/F)DRYVAI 3' (SEQ ID NO: 520) (encoded by a nucleic acid sequence such as 5'-ATGG(G/C)CT(A/T)TGACCG(C/A/T)T(AT)(C/T)GT-3' (SEQ ID NO: 521)). Such a degenerate primer can be used to generate a binding domain incorporating TM III through TM IV, TM III through TM V, TM III through TM VI or TM III through TM VII.

To amplify transmembrane domain VI (TM VI) sequence, a degenerate primer (of at least about 17 residues) can be designed from nucleic acid encoding an amino acid sequence TC(G/A)SHL (SEQ ID NO: 522), encoded by a sequence such as 5'-AG(G/A)TGN(G/C)(T/A)N(G/C)C(G/A)CANGT-3' (SEQ ID NO: 522). Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM VI, TM II through TM VI, TM III through TM VI or TM IV through TM VI).

Paradigms to design degenerate primer pairs are well known in the art. For example, a CONsensus-DEgenerate Hybrid Oligonucleotide Primer (CODEHOP) (SEQ ID NO: 523) strategy computer program is accessible as <http://blocks.fhcrc.org/codehop.html>, and is directly linked from the BlockMaker multiple sequence alignment site for hybrid primer prediction beginning with a set of related protein sequences, as known olfactory receptor ligand-binding regions (*see, e.g., Rose, Nucleic Acids Res.* 26:1628-1635 (1998); *Singh, Biotechniques*, 24:318-19 (1998)).

Means to synthesize oligonucleotide primer pairs are well known in the art. "Natural" base pairs or synthetic base pairs can be used. For example, use of artificial nucleobases offers a versatile approach to manipulate primer sequence and generate a more complex mixture of amplification products. Various families of artificial nucleobases are capable of assuming multiple hydrogen bonding orientations through internal bond rotations to provide a means for degenerate molecular recognition. Incorporation of these analogs into a single position of a PCR primer allows for generation of a complex library of amplification products. *See, e.g., Hoops, Nucleic Acids Res.* 25:4866-4871 (1997). Nonpolar molecules can also be used to mimic the shape of natural DNA bases. A non-hydrogen-bonding shape mimic for adenine can replicate efficiently and selectively against a nonpolar shape mimic for thymine (*see, e.g., Morales, Nat. Struct. Biol.* 5:950-954 (1998)). For example, two degenerate bases can be the pyrimidine base 6H, 8H-3,4-dihydropyrimido[4,5-c][1,2]oxazin-7-one or the purine base N6-methoxy-2,6-diaminopurine (*see, e.g., Hill, PNAS*, 95:4258-63 (1998)). Exemplary degenerate primers of the invention incorporate the nucleobase analog 5'-Dimethoxytrityl-N-benzoyl-2'-deoxy-Cytidine, 3'-[(2-cyanoethyl)-(N,N-diisopropyl)]-phosphoramidite (the term "P" in the sequences, *see above*). This pyrimidine analog hydrogen bonds with purines, including A and G residues.

Exemplary primer pairs for amplification of olfactory receptor transmembrane domains II through VII include:

- (a) 5'-GGGGTCCGGAG(A/G)(C/G)(A/G)TA(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' (SEQ ID NO: 524) and
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 525).
- (b) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' (SEQ ID NO: 526); and
5'-GGGGCTGCAGACACC(AC/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 527)
- (c) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/C/T)A(A/G/C/T)(A/G/C/T)GG-3' (SEQ ID NO: 528) and
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 558)

Nucleic acids that encode ligand-binding regions of olfactory receptors may be generated by amplification (*e.g., PCR*) of appropriate nucleic acid sequences using

degenerate primer pairs. The amplified nucleic acid can be genomic DNA from any cell or tissue or mRNA or cDNA derived from olfactory receptor-expressing cells, *e.g.*, olfactory neurons or olfactory epithelium.

Isolation from olfactory receptor-expressing cells is well known in the art
5 (cells expressing naturally or inducibly expressing olfactory receptors can be used to express the hybrid olfactory receptors of the invention to screen for potential odorants and odorant effect on cell physiology, as described below). For example, cells can be identified by olfactory marker protein (OMP), an abundant cytoplasmic protein expressed almost exclusively in mature olfactory sensory neurons (*see, e.g.*, Buiakova,
10 *PNAS*, 93:9858-63 (1996)). Shirley, *Eur. J. Biochem.* 32:485-494 (1983), describes a rat olfactory preparation suitable for biochemical studies *in vitro* on olfactory mechanisms. Cultures of adult rat olfactory receptor neurons are described by Vargas, *Chem. Senses* 24:211-216 (1999). Because these cultured neurons exhibit typical voltage-gated currents and are responsive to application of odorants, they can also be
15 used to express the hybrid olfactory receptors of the invention for odorant screening (endogenous olfactory receptor can be initially blocked, if desired, by, *e.g.*, antisense, knockout, and the like). U.S. Patent No. 5,869,266 describes culturing human olfactory neurons for neurotoxicity tests and screening. Murrell, *J. Neurosci.* 19:8260-8270 (1999), describes differentiated olfactory receptor-expressing cells in
20 culture that respond to odorants, as measured by an influx of calcium.

In one embodiment, hybrid protein-coding sequences comprising nucleic acids ORs fused to the translocation sequences described herein may be constructed. Also provided are hybrid ORs comprising the translocation motifs and ligand-binding domains of olfactory receptors. These nucleic acid sequences can be operably linked
25 to transcriptional or translational control elements, *e.g.*, transcription and translation initiation sequences, promoters and enhancers, transcription and translation terminators, polyadenylation sequences, and other sequences useful for transcribing DNA into RNA. In construction of recombinant expression cassettes, vectors, transgenics, and a promoter fragment can be employed to direct expression of the
30 desired nucleic acid in all tissues. Olfactory cell-specific transcriptional elements can also be used to express the fusion polypeptide receptor, including, *e.g.*, a 6.7 kb region upstream of the M4 olfactory receptor coding region. This region was sufficient to direct expression in olfactory epithelium with wild type zonal restriction and

distributed neuronal expression for endogenous olfactory receptors (Qasba, *J. Neurosci.* 18:227-236 (1998)). Receptor genes are normally expressed in a small subset of neurons throughout a zonally restricted region of the sensory epithelium. The transcriptional or translational control elements can be isolated from natural
5 sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

In another embodiment, fusion proteins, either having C-terminal or, more preferably, N-terminal translocation sequences, may also comprise the translocation motif described herein. However, these fusion proteins can also comprise additional
10 elements for, *e.g.*, protein detection, purification, or other applications. Detection and purification facilitating domains include, *e.g.*, metal chelating peptides such as polyhistidine tracts or histidine-tryptophan modules or other domains that allow purification on immobilized metals; maltose binding protein; protein A domains that allow purification on immobilized immunoglobulin; or the domain utilized in the
15 FLAGS extension/affinity purification system (Immunex Corp, Seattle WA).

The inclusion of a cleavable linker sequences such as Factor Xa (*see, e.g.*, Ottavi, *Biochimie* 80:289-293 (1998)), subtilisin protease recognition motif (*see, e.g.*, Polyak, *Protein Eng.* 10:615-619 (1997)); enterokinase (Invitrogen, San Diego, CA), and the like, between the translocation domain (for efficient plasma membrane
20 expression) and the rest of the newly translated polypeptide may be useful to facilitate purification. For example, one construct can include a polypeptide-encoding nucleic acid sequence linked to six histidine residues followed by a thioredoxin, an enterokinase cleavage site (*see, e.g.*, Williams, *Biochemistry* 34:1787-1797 (1995)), and an amino terminal translocation domain. The histidine residues facilitate
25 detection and purification while the enterokinase cleavage site provides a means for purifying the desired protein(s) from the remainder of the fusion protein. Technology pertaining to vectors encoding fusion proteins and application of fusion proteins are well described in the scientific and patent literature (*see, e.g.*, Kroll, *DNA Cell. Biol.* 12:441-53 (1993)).

30 Expression vectors, either as individual expression vectors or as libraries of expression vectors, comprising the olfactory binding domain-encoding sequences may be introduced into a genome or into the cytoplasm or a nucleus of a cell and expressed by a variety of conventional techniques, well described in the scientific and patent

literature (see, e.g., Roberts, *Nature* 328:731 (1987); Berger *supra*; Schneider, *Protein Expr. Purif.* 6435:10 (1995); Sambrook; Tijssen; Ausubel). Product information from manufacturers of biological reagents and experimental equipment also provide information regarding known biological methods. The vectors can be isolated from
5 natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

The nucleic acids can be expressed in expression cassettes, vectors or viruses which are stably or transiently expressed in cells (e.g., episomal expression systems). Selection markers can be incorporated into expression cassettes and vectors to confer
10 a selectable phenotype on transformed cells and sequences. For example, selection markers can code for episomal maintenance and replication such that integration into the host genome is not required. For example, the marker may encode antibiotic resistance (e.g., chloramphenicol, kanamycin, G418, bleomycin, hygromycin) or herbicide resistance (e.g., chlorosulfuron or Basta) to permit selection of those cells
15 transformed with the desired DNA sequences (see, e.g., Blondelet-Rouault, *Gene* 190:315-17 (1997); Aubrecht, *J. Pharmacol. Exp. Ther.*, 281:992-97 (1997)). Because selectable marker genes conferring resistance to substrates like neomycin or hygromycin can only be utilized in tissue culture, chemoresistance genes are also used as selectable markers *in vitro* and *in vivo*.

20 A chimeric nucleic acid sequence may encode a ligand-binding domain within any 7-transmembrane polypeptide. 7-transmembrane receptors belong to a superfamily of transmembrane (TM) proteins having seven domains that traverse a plasma membrane seven times. Each of the seven domains spans the plasma membrane (TM I to TM VII). Because 7-transmembrane receptor polypeptides have
25 similar primary sequences and secondary and tertiary structures, structural domains (e.g., TM domains) can be readily identified by sequence analysis. For example, homology modeling, Fourier analysis and helical periodicity detection can identify and characterize the seven domains with a 7-transmembrane receptor sequence. Fast Fourier Transform (FFT) algorithms can be used to assess the dominant periods that
30 characterize profiles of the hydrophobicity and variability of analyzed sequences. To predict TM domains and their boundaries and topology, a "neural network algorithm" by "PHD server" can be used, as done by Pilpel, *Protein Science* 8:969-977 (1999); Rost, *Protein Sci.* 4:521-533 (1995). Periodicity detection enhancement and alpha

helical periodicity index can be done as by, *e.g.*, Donnelly, *Protein Sci.* 2:55-70 (1993). Other alignment and modeling algorithms are well known in the art, *see, e.g.*, Peitsch, *Receptors Channels* 4:161-164 (1996); Cronet, *Protein Eng.* 6:59-64 (1993) (homology and "discover modeling"); <http://bioinfo.weizmann.ac.il/>.

5 The library sequences include receptor sequences that correspond to TM ligand-binding domains, including, *e.g.*, TM II to VII, TM II to VI, TM III to VII, and TM III to VII, that have been amplified (*e.g.*, PCR) from mRNA of or cDNA derived from, *e.g.*, olfactory receptor-expressing neurons or genomic DNA.

Libraries of olfactory receptor ligand-binding TM domain sequences can
10 include a various TM domains or variations thereof, as described above. These sequences can be derived from any 7-transmembrane receptor. Because these polypeptides have similar primary sequences and secondary and tertiary structures, the seven domains can be identified by various analyses well known in the art, including, *e.g.*, homology modeling, Fourier analysis and helical periodicity (*see, e.g.*, Pilpel
15 *supra*), as described above. Using this information sequences flanking the seven domains can be identified and used to design degenerate primers for amplification of various combinations of TM regions and subsequences.

The present invention also includes not only the DNA and proteins having the specified amino acid sequences, but also DNA fragments, particularly fragments of,
20 for example, 40, 60, 80, 100, 150, 200, or 250 nucleotides, or more, as well as protein fragments of, for example, 10, 20, 30, 50, 70, 100, or 150 amino acids, or more.

Also contemplated are chimeric proteins, comprising at least 10, 20, 30, 50, 70, 100, or 150 amino acids, or more, of one of at least one of the olfactory receptors described herein, coupled to additional amino acids representing all or part of another
25 G protein receptor, preferably a member of the 7TM superfamily. These chimeras can be made from the instant receptors and a G protein receptor described herein, or they can be made by combining two or more of the present proteins. In one preferred embodiment, one portion of the chimera corresponds to and is derived from one or more of the domains of the seven transmembrane protein described herein, and the
30 remaining portion or portions come from another G protein-coupled receptor. Chimeric receptors are well known in the art, and the techniques for creating them and the selection and boundaries of domains or fragments of G protein-coupled receptors for incorporation therein are also well known. Thus, this knowledge of those skilled

in the art can readily be used to create such chimeric receptors. The use of such chimeric receptors can provide, for example, an olfactory selectivity characteristic of one of the receptors specifically disclosed herein, coupled with the signal transduction characteristics of another receptor, such as a well known receptor used in prior art assay systems.

For example, a domain such as a ligand-binding domain, an extracellular domain, a transmembrane domain (*e.g.*, one comprising seven transmembrane regions and corresponding extracellular and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc., can be covalently linked to a heterologous protein. For instance, an extracellular domain can be linked to a heterologous GPCR transmembrane domain, or a heterologous GPCR extracellular domain can be linked to a transmembrane domain. Other heterologous proteins of choice can include, *e.g.*, green fluorescent protein, β -gal, glutamate receptor, and the rhodopsin presequence.

Polymorphic variants, alleles, and interspecies homologs that are substantially identical to an olfactory receptor disclosed herein can be isolated using the nucleic acid probes described above. It is hypothesized that allelic differences in receptors may explain why there is a difference in olfactory sensation in different human subjects. Accordingly, the identification of such alleles may be significant, especially with respect to producing receptor libraries that adequately represent the olfactory capability of the human population, *i.e.*, which take into account allelic differences in different individuals. Alternatively, expression libraries can be used to clone olfactory receptors and polymorphic variants, alleles, and interspecies homologs thereof, by detecting expressed homologs immunologically with antisera or purified antibodies made against an olfactory polypeptide, which also recognize and selectively bind to the olfactory receptor homolog.

Also within the scope of the invention are host cells for expressing the ORs, fragments, or variants of the invention. To obtain high levels of expression of a cloned gene or nucleic acid, such as cDNAs encoding the olfactory receptors, fragments, or variants of the invention, one of skill typically subclones the nucleic acid sequence of interest into an expression vector that contains a strong promoter to direct transcription, a transcription/translation terminator, and if for a nucleic acid encoding a protein, a ribosome binding site for translational initiation. Suitable

bacterial promoters are well known in the art and described, *e.g.*, in Sambrook *et al.* However, bacterial or eukaryotic expression systems can be used.

Any of the well-known procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, polybrene, protoplast fusion, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g.*, Sambrook *et al.*) It is only necessary that the particular genetic engineering procedure used be capable of successfully introducing at least one gene into the host cell capable of expressing the olfactory receptor, fragment, or variant of interest.

After the expression vector is introduced into the cells, the transfected cells are cultured under conditions favoring expression of the receptor, fragment, or variant of interest, which is then recovered from the culture using standard techniques. Examples of such techniques are well known in the art. *See, e.g.*, WO 00/06593, which is incorporated by reference in a manner consistent with this disclosure.

D. Immunological Detection of OR Polypeptides

In addition to the detection of OR genes and gene expression using nucleic acid hybridization technology, one can also use immunoassays to detect ORs, *e.g.*, to identify olfactory receptor cells, and variants of OR family members. Immunoassays can be used to qualitatively or quantitatively analyze the ORs. A general overview of the applicable technology can be found in Harlow & Lane, *Antibodies: A Laboratory Manual* (1988).

1. Antibodies to OR family members

Methods of producing polyclonal and monoclonal antibodies that react specifically with a OR family member are known to those of skill in the art (*see, e.g.*, Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *supra*; Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986); and Kohler & Milstein, *Nature*, 256:495-97 (1975)). Such techniques include antibody preparation by selection of antibodies from libraries of recombinant antibodies in phage or similar vectors, as well as preparation of polyclonal and monoclonal antibodies by

immunizing rabbits or mice (*see, e.g., Huse et al., Science, 246:1275-81 (1989); Ward et al., Nature, 341:544-46 (1989)*).

A number of OR-comprising immunogens may be used to produce antibodies specifically reactive with a OR family member. For example, a recombinant OR protein, or an antigenic fragment thereof, can be isolated as described herein. Suitable antigenic regions include, *e.g.*, the conserved motifs that are used to identify members of the OR family. Recombinant proteins can be expressed in eukaryotic or prokaryotic cells as described above, and purified as generally described above. Recombinant protein is the preferred immunogen for the production of monoclonal or polyclonal antibodies. Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used as an immunogen. Naturally occurring protein may also be used either in pure or impure form. The product is then injected into an animal capable of producing antibodies. Either monoclonal or polyclonal antibodies may be generated, for subsequent use in immunoassays to measure the protein.

Methods of production of polyclonal antibodies are known to those of skill in the art. For example, an inbred strain of mice (*e.g.*, BALB/C mice) or rabbits may be immunized with the protein using a standard adjuvant, such as Freund's adjuvant, and a standard immunization protocol. The animal's immune response to the immunogen preparation is monitored by taking test bleeds and determining the titer of reactivity to the OR. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the antisera to enrich for antibodies reactive to the protein can be done if desired (*see Harlow & Lane, supra*).

Monoclonal antibodies may be obtained by various techniques familiar to those skilled in the art. Briefly, spleen cells from an animal immunized with a desired antigen may be immortalized, commonly by fusion with a myeloma cell (*see Kohler & Milstein, Eur. J. Immunol., 6:511-19 (1976)*). Alternative methods of immortalization include transformation with Epstein Barr Virus, oncogenes, or retroviruses, or other methods well known in the art. Colonies arising from single immortalized cells are screened for production of antibodies of the desired specificity and affinity for the antigen, and yield of the monoclonal antibodies produced by such cells may be enhanced by various techniques, including injection into the peritoneal cavity of a

vertebrate host. Alternatively, one may isolate DNA sequences which encode a monoclonal antibody or a binding fragment thereof by screening a DNA library from human B cells according to the general protocol outlined by Huse *et al.*, *Science*, 246:1275-1281 (1989).

5 Monoclonal antibodies and polyclonal sera are collected and titrated against the immunogen protein in an immunoassay, for example, a solid phase immunoassay with the immunogen immobilized on a solid support. Typically, polyclonal antisera with a titer of 10⁹ or greater are selected and tested for their cross reactivity against non-OR proteins, or even other OR family members or other related proteins from other
10 organisms, using a competitive binding immunoassay. Specific polyclonal antisera and monoclonal antibodies will usually bind with a K_d of at least about 0.1 mM, more usually at least about 1 pM, optionally at least about 0.1 pM or better, and optionally 0.01 pM or better.

Once OR family member specific antibodies are available, individual OR
15 proteins can be detected by a variety of immunoassay methods. For a review of immunological and immunoassay procedures, see *Basic and Clinical Immunology* (Stites & Terr eds., 7th ed. 1991). Moreover, the immunoassays of the present invention can be performed in any of several configurations, which are reviewed extensively in *Enzyme Immunoassay* (Maggio, ed., 1980); and Harlow & Lane, *supra*.

20 2. Immunological binding assays

OR proteins can be detected and/or quantified using any of a number of well recognized immunological binding assays (see, e.g., U.S. Patents 4,366,241; 4,376,110; 4,517,288; and 4,837,168). For a review of the general immunoassays, see also *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993);
25 *Basic and Clinical Immunology* (Stites & Terr, eds., 7th ed. 1991). Immunological binding assays (or immunoassays) typically use an antibody that specifically binds to a protein or antigen of choice (in this case an OR family member or an antigenic subsequence thereof). The antibody (e.g., anti-OR) may be produced by any of a number of means well known to those of skill in the art and as described above.

30 Immunoassays also often use a labeling agent to specifically bind to and label the complex formed by the antibody and antigen. The labeling agent may itself be one of the moieties comprising the antibody/antigen complex. Thus, the labeling agent may be a labeled OR polypeptide or a labeled anti-OR antibody. Alternatively, the

labeling agent may be a third moiety, such a secondary antibody that specifically binds to the antibody/OR complex (a secondary antibody is typically specific to antibodies of the species from which the first antibody is derived). Other proteins capable of specifically binding immunoglobulin constant regions, such as protein A or protein G may also be used as the label agent. These proteins exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species (*see, e.g., Kronval et al., J. Immunol., 111:1401-1406 (1973); Akerstrom et al., J. Immunol., 135:2589-2542 (1985)*). The labeling agent can be modified with a detectable moiety, such as biotin, to which another molecule can specifically bind, such as streptavidin.

10 A variety of detectable moieties are well known to those skilled in the art.

Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, optionally from about 5 minutes to about 24 hours. However, the incubation time will depend upon the assay format, antigen, volume of solution, concentrations, and the like. Usually, the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10°C to 40°C.

15

a. Non-competitive assay formats

Immunoassays for detecting an OR protein in a sample may be either competitive or noncompetitive. Noncompetitive immunoassays are assays in which the amount of antigen is directly measured. In one preferred "sandwich" assay, for example, the anti-OR antibodies can be bound directly to a solid substrate on which they are immobilized. These immobilized antibodies then capture the OR protein present in the test sample. The OR protein is thus immobilized is then bound by a labeling agent, such as a second OR antibody bearing a label. Alternatively, the second antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second or third antibody is typically modified with a detectable moiety, such as biotin, to which another molecule specifically binds, *e.g., streptavidin*, to provide a detectable moiety.

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b. Competitive assay formats

In competitive assays, the amount of OR protein present in the sample is measured indirectly by measuring the amount of a known, added (exogenous) OR

protein displaced (competed away) from an anti-OR antibody by the unknown OR protein present in a sample. In one competitive assay, a known amount of OR protein is added to a sample and the sample is then contacted with an antibody that specifically binds to the OR. The amount of exogenous OR protein bound to the antibody is inversely proportional to the concentration of OR protein present in the sample. In a particularly preferred embodiment, the antibody is immobilized on a solid substrate. The amount of OR protein bound to the antibody may be determined either by measuring the amount of OR protein present in a OR/antibody complex, or alternatively by measuring the amount of remaining uncomplexed protein. The amount of OR protein may be detected by providing a labeled OR molecule.

A hapten inhibition assay is another preferred competitive assay. In this assay the known OR protein is immobilized on a solid substrate. A known amount of anti-OR antibody is added to the sample, and the sample is then contacted with the immobilized OR. The amount of anti-OR antibody bound to the known immobilized OR protein is inversely proportional to the amount of OR protein present in the sample. Again, the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

c. Cross-reactivity determinations

Immunoassays in the competitive binding format can also be used for cross-reactivity determinations. For example, a protein at least partially encoded by the nucleic acid sequences disclosed herein can be immobilized to a solid support. Proteins (*e.g.*, OR proteins and homologs) are added to the assay that compete for binding of the antisera to the immobilized antigen. The ability of the added proteins to compete for binding of the antisera to the immobilized protein is compared to the ability of the OR polypeptide encoded by the nucleic acid sequences disclosed herein to compete with itself. The percent cross-reactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% cross-reactivity with each of the added proteins listed above are selected and pooled. The cross-reacting antibodies are optionally removed from the pooled antisera by immunoabsorption with the added considered proteins, *e.g.*, distantly related

homologs. In addition, peptides comprising amino acid sequences representing conserved motifs that are used to identify members of the OR family can be used in cross-reactivity determinations.

The immunoabsorbed and pooled antisera are then used in a competitive
5 binding immunoassay as described above to compare a second protein, thought to be perhaps an allele or polymorphic variant of a OR family member, to the immunogen protein (*i.e.*, OR protein encoded by the nucleic acid sequences disclosed herein). In order to make this comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding
10 of the antisera to the immobilized protein is determined. If the amount of the second protein required to inhibit 50% of binding is less than 10 times the amount of the protein encoded by nucleic acid sequences disclosed herein required to inhibit 50% of binding, then the second protein is said to specifically bind to the polyclonal antibodies generated to a OR immunogen.

15 Antibodies raised against OR conserved motifs can also be used to prepare antibodies that specifically bind only to GPCRs of the OR family, but not to GPCRs from other families.

Polyclonal antibodies that specifically bind to a particular member of the OR family, *e.g.*, AOLFR1, can be make by subtracting out cross-reactive antibodies using
20 other OR family members. Species-specific polyclonal antibodies can be made in a similar way. For example, antibodies specific to human AOLFR1 can be made by, subtracting out antibodies that are cross-reactive with orthologous sequences, *e.g.*, rat OR1 or mouse OR1.

d. Other assay formats

25 Western blot (immunoblot) analysis is used to detect and quantify the presence of OR protein in the sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that
30 specifically bind the OR protein. The anti-OR polypeptide antibodies specifically bind to the OR polypeptide on the solid support. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (*e.g.*, labeled sheep anti-mouse antibodies) that specifically bind to the anti-OR antibodies.

Other, assay formats include liposome immunoassays (LIA), which use liposomes designed to bind specific molecules (*e.g.*, antibodies) and release encapsulated reagents or markers. The released chemicals are then detected according to standard techniques (*see Monroe et al., Amer. Clin. Prod. Rev.*, 5:34-41 (1986)).

5 e. **Reduction of non-specific binding**

One of skill in the art will appreciate that it is often desirable to minimize non-specific binding in immunoassays. Particularly, where the assay involves an antigen or antibody immobilized on a solid substrate it is desirable to minimize the amount of non-specific binding to the substrate. Means of reducing such non-specific
10 binding are well known to those of skill in the art. Typically, this technique involves coating the substrate with a proteinaceous composition. In particular, protein compositions such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used with powdered milk being most preferred.

 f. **Labels**

15 The particular label or detectable group used in the assay is not a critical aspect of the invention, as long as it does not significantly interfere with the specific binding of the antibody used in the assay. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immunoassays and, in general, most any label useful in such
20 methods can be applied to the present invention. Thus, a label is any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include magnetic beads (*e.g.*, DYNABEADS™) (SEQ ID NO: 529), fluorescent dyes (*e.g.*, fluorescein isothiocyanate, Texas red, rhodamine, and the like), radiolabels (*e.g.*, ³H, ¹²⁵I, ³⁵S, ¹⁴C,
25 or ³²P), enzymes (*e.g.*, horseradish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic beads (*e.g.*, polystyrene, polypropylene, latex, *etc.*).

The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety
30 of labels may be used, with the choice of label depending on sensitivity required, ease of conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (*e.g.*, biotin) is covalently bound to the molecule. The ligand then binds to another molecules (*e.g.*, streptavidin) molecule, which is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. The ligands and their targets can be used in any suitable combination with antibodies that recognize a OR protein, or secondary antibodies that recognize anti-OR.

The molecules can also be conjugated directly to signal generating compounds, *e.g.*, by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidotases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, *etc.* Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, *e.g.*, luminol. For a review of various labeling or signal producing systems that may be used, *see* U.S. Patent No. 4,391,904.

Means of detecting labels are well known to those of skill in the art. Thus, for example, where the label is a radioactive label, means for detection include a scintillation counter or photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluorochrome with the appropriate wavelength of light and detecting the resulting fluorescence. The fluorescence may be detected visually, by means of photographic film, by the use of electronic detectors such as charge coupled devices (CCDs) or photomultipliers and the like. Similarly, enzymatic labels may be detected by providing the appropriate substrates for the enzyme and detecting the resulting reaction product. Finally simple colorimetric labels may be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of the target antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

E. Detection of Olfactory Modulators

Methods and compositions for determining whether a test compound specifically binds to a mammalian chemosensory, and more particularly, an olfactory receptor of the invention, both *in vitro* and *in vivo* are described below. Many aspects of cell physiology can be monitored to assess the effect of ligand-binding to a naturally-occurring or chimeric olfactory receptor. These assays may be performed on intact cells expressing an olfactory receptor, on permeabilized cells or on membrane fractions produced by standard methods.

Olfactory receptors are normally located on the specialized cilia of olfactory neurons. These receptors bind odorants and initiate the transduction of chemical stimuli into electrical signals. An activated or inhibited G protein will in turn alter the properties of target enzymes, channels, and other effector proteins. Some examples include the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G protein, phospholipase C by Gq and other cognate G proteins, and modulation of diverse channels by Gi and other G proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

The OR protein of the assay will typically be selected from a polypeptide having a sequence selected from SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID.

NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID.
NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID.
NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID.
NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID.
5 NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID.
NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID.
NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID.
NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID.
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Alternatively, the OR protein of the assay can be derived from a eukaryote host cell and can include an amino acid subsequence having at least about 30-40% amino acid sequence identity to SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID.

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Preferably, the amino acid sequence identity will be at least 50-75% preferably 85%, 90%, 95%, 96%, 97%, 98%, or 99%. Optionally, the polypeptide of the assays can comprise a domain of an OR protein, such as an extracellular domain, transmembrane region, transmembrane domain, cytoplasmic domain, ligand-binding domain, subunit association domain, active site, and the like. Either the OR protein or a domain thereof can be covalently linked to a heterologous protein to create a chimeric protein used in the assays described herein. As discussed *infra*, the family of ORs provided herein exhibits substantial sequence similarity at both the DNA and protein level, but also significant dissimilarity. In particular, the members possess an average percentage sequence identity to other members of the family when determined over the full length of the gene by about 30%. Moreover, different members of the genes at the protein level exhibit an average on the order of about 40% sequence identity to other members of the family when the full length protein sequences are compared. However, while there exist differences, there are characteristic similarities, *e.g.* the consensus sequence already mentioned, which further define members of this novel genus of receptors.

Modulators of OR activity can be tested using OR polypeptides as described above, either recombinant or naturally occurring. The protein can be isolated, expressed in a cell, expressed in a membrane derived from a cell, expressed in tissue or in an animal, either recombinant or naturally occurring. Modulation can be tested using one of the *in vitro* or *in vivo* assays described herein.

1. In vitro binding assays

Olfactory transduction can also be examined *in vitro* with soluble or solid state reactions, using a full-length OR or a chimeric molecule such as an extracellular domain or transmembrane region, or combination thereof, of a OR covalently linked
5 to a heterologous signal transduction domain, or a heterologous extracellular domain and/or transmembrane region covalently linked to the transmembrane and/or cytoplasmic domain of an OR. Furthermore, ligand-binding domains of the protein of interest can be used *in vitro* in soluble or solid state reactions to assay for ligand binding. In numerous embodiments, a chimeric receptor will be made that comprises
10 all or part of a OR polypeptide, as well an additional sequence that facilitates the localization of the OR to the membrane, such as a rhodopsin, *e.g.*, an N-terminal fragment of a rhodopsin protein, *e.g.* bovine or another mammalian rhodopsin.

Ligand binding to a OR protein, a domain, or chimeric protein can be tested in solution, in a bilayer membrane, attached to a solid phase, in a lipid monolayer, or in
15 vesicles. Binding of a modulator can be tested using, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index) hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties.

Receptor-G protein interactions can also be examined. For example, binding of the G protein to the receptor or its release from the receptor can be examined. For
20 example, in the absence of GTP, an activator will lead to the formation of a tight complex of a G protein (all three subunits) with the receptor. This complex can be detected in a variety of ways, as noted above. Such an assay can be modified to search for inhibitors, *e.g.*, by adding an activator to the receptor and G protein in the absence of GTP, which form a tight complex, and then screen for inhibitors by
25 looking at dissociation of the receptor-G protein complex. In the presence of GTP, release of the alpha subunit of the G protein from the other two G protein subunits serves as a criterion of activation.

An activated or inhibited G protein will in turn alter the properties of target enzymes, channels, and other effector proteins. The classic examples are the
30 activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G protein, phospholipase C by Gq and other cognate G proteins, and modulation of diverse channels by Gi and other G proteins.

Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

In another embodiment of the invention, a GTP γ S assay may be used. As described above, upon activation of a GPCR, the G α subunit of the G protein complex is stimulated to exchange bound GDP for GTP. Ligand-mediated stimulation of G protein exchange activity can be measured in a biochemical assay measuring the binding of added radioactively-labeled GTP γ ³⁵S to the G protein in the presence of a putative ligand. Typically, membranes containing the chemosensory receptor of interest are mixed with a complex of G proteins. Potential inhibitors and/or activators and GTP γ S are added to the assay, and binding of GTP γ S to the G protein is measured. Binding can be measured by liquid scintillation counting or by any other means known in the art, including scintillation proximity assays (SPA). In other assays formats, fluorescently-labeled GTP γ S can be utilized.

2. Fluorescence Polarization Assays

In another embodiment, Fluorescence Polarization ("FP") based assays may be used to detect and monitor odorant binding. Fluorescence polarization is a versatile laboratory technique for measuring equilibrium binding, nucleic acid hybridization, and enzymatic activity. Fluorescence polarization assays are homogeneous in that they do not require a separation step such as centrifugation, filtration, chromatography, precipitation or electrophoresis. These assays are done in real time, directly in solution and do not require an immobilized phase. Polarization values can be measured repeatedly and after the addition of reagents since measuring the polarization is rapid and does not destroy the sample. Generally, this technique can be used to measure polarization values of fluorophores from low picomolar to micromolar levels. This section describes how fluorescence polarization can be used in a simple and quantitative way to measure the binding of odorants to the olfactory receptors of the invention.

When a fluorescently labeled molecule is excited with plane polarized light, it emits light that has a degree of polarization that is inversely proportional to its molecular rotation. Large fluorescently labeled molecules remain relatively stationary during the excited state (4 nanoseconds in the case of fluorescein) and the polarization of the light remains relatively constant between excitation and emission. Small fluorescently labeled molecules rotate rapidly during the excited state and the

polarization changes significantly between excitation and emission. Therefore, small molecules have low polarization values and large molecules have high polarization values. For example, a single-stranded fluorescein-labeled oligonucleotide has a relatively low polarization value but when it is hybridized to a complementary strand, it has a higher polarization value. When using FP to detect and monitor odorant-binding which may activate or inhibit the olfactory receptors of the invention, fluorescence-labeled odorants or auto-fluorescent odorants may be used.

Fluorescence polarization (P) is defined as:

$$P = \frac{Int_{\parallel} - Int_{\perp}}{Int_{\parallel} + Int_{\perp}}$$

Where \parallel is the intensity of the emission light parallel to the excitation light plane and \perp is the intensity of the emission light perpendicular to the excitation light plane. P, being a ratio of light intensities, is a dimensionless number. For example, the Beacon ® and Beacon 2000™ System may be used in connection with these assays. Such systems typically express polarization in millipolarization units (1 Polarization Unit = 1000 mP Units).

The relationship between molecular rotation and size is described by the Perrin equation and the reader is referred to Jolley, M. E. (1991) in Journal of Analytical Toxicology, pp. 236-240, which gives a thorough explanation of this equation. Summarily, the Perrin equation states that polarization is directly proportional to the rotational relaxation time, the time that it takes a molecule to rotate through an angle of approximately 68.5°. Rotational relaxation time is related to viscosity (η), absolute temperature (T), molecular volume (V), and the gas constant (R) by the following equation:

$$Rotational\ Relaxation\ Time = \frac{3\eta V}{RT}$$

The rotational relaxation time is small (\approx 1 nanosecond) for small molecules (e.g. fluorescein) and large (\approx 100 nanoseconds) for large molecules (e.g. immunoglobulins). If viscosity and temperature are held constant, rotational relaxation time, and therefore polarization, is directly related to the molecular volume. Changes in molecular volume may be due to interactions with other molecules, dissociation, polymerization, degradation, hybridization, or conformational changes of the fluorescently labeled molecule. For example, fluorescence polarization has been

used to measure enzymatic cleavage of large fluorescein labeled polymers by proteases, DNases, and RNases. It also has been used to measure equilibrium binding for protein/protein interactions, antibody/antigen binding, and protein/DNA binding.

3. Solid state and soluble high throughput assays

5 In yet another embodiment, the invention provides soluble assays using molecules such as a domain such as ligand-binding domain, an extracellular domain, a transmembrane domain (*e.g.*, one comprising seven transmembrane regions and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc.; a domain that is covalently linked to a heterologous
10 protein to create a chimeric molecule; an OR protein; or a cell or tissue expressing an OR protein, either naturally occurring or recombinant. In another embodiment, the invention provides solid phase based in vitro assays in a high throughput format, where the domain, chimeric molecule, OR protein, or cell or tissue expressing the OR is attached to a solid phase substrate.

15 In the high throughput assays of the invention, it is possible to screen up to several thousand different modulators or ligands in a single day. In particular, each well of a microtiter plate can be used to run a separate assay against a selected potential modulator, or, if concentration or incubation time effects are to be observed, every 5-10 wells can test a single modulator. Thus, a single standard microtiter plate
20 can assay about 100 (*e.g.*, 96) modulators. If 1536 well plates are used, then a single plate can easily assay from about 1000 to about 1500 different compounds. It is also possible to assay multiple compounds in each plate well. Further, it is possible to assay several different plates per day; assay screens for up to about 6,000-20,000 different compounds is possible using the integrated systems of the invention. More
25 recently, microfluidic approaches to reagent manipulation have been developed.

The molecule of interest can be bound to the solid state component, directly or indirectly, via covalent or non covalent linkage, *e.g.*, via a tag. The tag can be any of a variety of components. In general, a molecule which binds the tag (a tag binder) is fixed to a solid support, and the tagged molecule of interest (*e.g.*, the olfactory
30 transduction molecule of interest) is attached to the solid support by interaction of the tag and the tag binder.

A number of tags and tag binders can be used, based upon known molecular interactions well described in the literature. For example, where a tag has a natural

binder, for example, biotin, protein A, or protein G, it can be used in conjunction with appropriate tag binders (avidin, streptavidin, neutravidin, the Fc region of an immunoglobulin, *etc.*). Antibodies to molecules with natural binders such as biotin are also widely available and appropriate tag binders (*see*, SIGMA Immunochemicals 5 1998 catalogue SIGMA, St. Louis MO).

Similarly, any haptenic or antigenic compound can be used in combination with an appropriate antibody to form a tag/tag binder pair. Thousands of specific antibodies are commercially available and many additional antibodies are described in the literature. For example, in one common configuration, the tag is a first antibody 10 and the tag binder is a second antibody which recognizes the first antibody. In addition to antibody-antigen interactions, receptor-ligand interactions are also appropriate as tag and tag-binder pairs. For example, agonists and antagonists of cell membrane receptors (*e.g.*, cell receptor-ligand interactions such as transferrin, c-kit, viral receptor ligands, cytokine receptors, chemokine receptors, interleukin receptors, 15 immunoglobulin receptors and antibodies, the cadherein family, the integrin family, the selectin family, and the like; *see, e.g.*, Pigott & Power, The Adhesion Molecule Facts Book I (1993)). Similarly, toxins and venoms, viral epitopes, hormones (*e.g.*, opiates, steroids, *etc.*), intracellular receptors (*e.g.*, which mediate the effects of various small ligands, including steroids, thyroid hormone, retinoids and vitamin D; 20 peptides), drugs, lectins, sugars, nucleic acids (both linear and cyclic polymer configurations), oligosaccharides, proteins, phospholipids and antibodies can all interact with various cell receptors.

Synthetic polymers, such as polyurethanes, polyesters, polycarbonates, polyureas, polyamides, polyethyleneimines, polyarylene sulfides, polysiloxanes, 25 polyimides, and polyacetates can also form an appropriate tag or tag binder. Many other tag/tag binder pairs are also useful in assay systems described herein, as would be apparent to one of skill upon review of this disclosure.

Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly gly sequences of between about 30 5 and 200 amino acids. Such flexible linkers are known to persons of skill in the art. For example, poly(ethelyne glycol) linkers are available from Shearwater Polymers, Inc. Huntsville, Alabama. These linkers optionally have amide linkages, sulfhydryl linkages, or heterofunctional linkages.

Tag binders are fixed to solid substrates using any of a variety of methods currently available. Solid substrates are commonly derivatized or functionalized by exposing all or a portion of the substrate to a chemical reagent that fixes a chemical group to the surface which is reactive with a portion of the tag binder. For example, groups that are suitable for attachment to a longer chain portion would include amines, hydroxyl, thiol, and carboxyl groups. Aminoalkylsilanes and hydroxyalkylsilanes can be used to functionalize a variety of surfaces, such as glass surfaces. The construction of such solid phase biopolymer arrays is well described in the literature. *See, e.g., Merrifield, J. Am. Chem. Soc.*, 85:2149-54 (1963) (describing solid phase synthesis of, *e.g., peptides*); Geysen *et al.*, *J. Immun. Meth.*, 102:259-74 (1987) (describing synthesis of solid phase components on pins); Frank & Doring, *Tetrahedron*, 44:60316040 (1988) (describing synthesis of various peptide sequences on cellulose disks); Fodor *et al.*, *Science*, 251:767-77 (1991); Sheldon *et al.*, *Clinical Chemistry*, 39(4):718-19 (1993); and Kozal *et al.*, *Nature Medicine*, 2(7):753759 (1996) (all describing arrays of biopolymers fixed to solid substrates). Non-chemical approaches for fixing tag binders to substrates include other common methods, such as heat, cross-linking by UV radiation, and the like.

4. Computer-based assays

Yet another assay for compounds that modulate OR protein activity involves computer assisted compound design, in which a computer system is used to generate a three-dimensional structure of an OR protein based on the structural information encoded by its amino acid sequence. The input amino acid sequence interacts directly and actively with a preestablished algorithm in a computer program to yield secondary, tertiary, and quaternary structural models of the protein. The models of the protein structure are then examined to identify regions of the structure that have the ability to bind, *e.g., ligands*. These regions are then used to identify ligands that bind to the protein.

The three-dimensional structural model of the protein is generated by entering protein amino acid sequences of at least 10 amino acid residues or corresponding nucleic acid sequences encoding a OR polypeptide into the computer system. The nucleotide sequence encoding the polypeptide, or the amino acid sequence thereof, can be any of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID

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NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,
20 SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID
NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,
SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID
NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,
SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID
25 NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,
SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID
NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269,
SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID
NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,
30 SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID
NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,
SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID
NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,

SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, 5 SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, 10 SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, 15 SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, 20 SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511, and conservatively modified versions thereof.

The amino acid sequence represents the primary sequence or subsequence of the protein, which encodes the structural information of the protein. At least 10 25 residues of the amino acid sequence (or a nucleotide sequence encoding 10 amino acids) are entered into the computer system from computer keyboards, computer readable substrates that include, but are not limited to, electronic storage media (*e.g.*, magnetic diskettes, tapes, cartridges, and chips), optical media (*e.g.*, CD ROM), information distributed by internet sites, and by RAM. The three-dimensional 30 structural model of the protein is then generated by the interaction of the amino acid sequence and the computer system, using software known to those of skill in the art. .

The amino acid sequence represents a primary structure that encodes the information necessary to form the secondary, tertiary and quaternary structure of the

protein of interest. The software looks at certain parameters encoded by the primary sequence to generate the structural model. These parameters are referred to as "energy terms," and primarily include electrostatic potentials, hydrophobic potentials, solvent accessible surfaces, and hydrogen bonding. Secondary energy terms include van der
5 Waals potentials. Biological molecules form the structures that minimize the energy terms in a cumulative fashion. The computer program is therefore using these terms encoded by the primary structure or amino acid sequence to create the secondary structural model.

The tertiary structure of the protein encoded by the secondary structure is then
10 formed on the basis of the energy terms of the secondary structure. The user at this point can enter additional variables such as whether the protein is membrane bound or soluble, its location in the body, and its cellular location, *e.g.*, cytoplasmic, surface, or nuclear. These variables along with the energy terms of the secondary structure are used to form the model of the tertiary structure. In modeling the tertiary structure, the
15 computer program matches hydrophobic faces of secondary structure with like, and hydrophilic faces of secondary structure with like.

Once the structure has been generated, potential ligand-binding regions are identified by the computer system. Three-dimensional structures for potential ligands are generated by entering amino acid or nucleotide sequences or chemical formulas of
20 compounds, as described above. The three-dimensional structure of the potential ligand is then compared to that of the OR protein to identify ligands that bind to the protein. Binding affinity between the protein and ligands is determined using energy terms to determine which ligands have an enhanced probability of binding to the protein.

25 Computer systems are also used to screen for mutations, polymorphic variants, alleles and interspecies homologs of OR genes. Such mutations can be associated with disease states or genetic traits. As described above, GeneChip™ and related technology can also be used to screen for mutations, polymorphic variants, alleles and interspecies homologs. Once the variants are identified, diagnostic assays can be used
30 to identify patients having such mutated genes. Identification of the mutated OR genes involves receiving input of a first nucleic acid or amino acid sequence of a OR gene, or conservatively modified versions thereof. The sequence is entered into the computer system as described above. The first nucleic acid or amino acid sequence is

then compared to a second nucleic acid or amino acid sequence that has substantial identity to the first sequence. The second sequence is entered into the computer system in the manner described above. Once the first and second sequences are compared, nucleotide or amino acid differences between the sequences are identified.

- 5 Such sequences can represent allelic differences in various OR genes, and mutations associated with disease states and genetic traits.

5. Cell-based binding assays

In a preferred embodiment, an OR polypeptide is expressed in a eukaryotic cell as a chimeric receptor with a heterologous, chaperone sequence that facilitates its maturation and targeting through the secretory pathway. In a preferred embodiment, 10 the heterologous sequence is a rhodopsin sequence, such as an N-terminal fragment of a rhodopsin. Such chimeric OR receptors can be expressed in any eukaryotic cell, such as HEK-293 cells. Preferably, the cells comprise a functional G protein, *e.g.*, G α 15, that is capable of coupling the chimeric receptor to an intracellular signaling pathway or to a signaling protein such as phospholipase C. Activation of such 15 chimeric receptors in such cells can be detected using any standard method, such as by detecting changes in intracellular calcium by detecting FURA-2 dependent fluorescence in the cell.

Activated GPCR receptors become substrates for kinases that phosphorylate 20 the C-terminal tail of the receptor (and possibly other sites as well). Thus, activators will promote the transfer of ^{32}P from gamma-labeled GTP to the receptor, which can be assayed with a scintillation counter. The phosphorylation of the C-terminal tail will promote the binding of arrestin-like proteins and will interfere with the binding of G proteins. The kinase/arrestin pathway plays a key role in the desensitization of 25 many GPCR receptors. For example, compounds that modulate the duration an olfactory receptor stays active would be useful as a means of prolonging a desired odor or cutting off an unpleasant one. For a general review of GPCR signal transduction and methods of assaying signal transduction, *see, e.g., Methods in Enzymology*, vols. 237 and 238 (1994) and volume 96 (1983); Bourne *et al.*, *Nature*, 30 10:349:117-27 (1991); Bourne *et al.*, *Nature*, 348:125-32 (1990); Pitcher *et al.*, *Annu. Rev. Biochem.*, 67:653-92 (1998).

OR modulation may be assayed by comparing the response of an OR polypeptide treated with a putative OR modulator to the response of an untreated

control sample. Such putative OR modulators can include odorants that either inhibit or activate OR polypeptide activity. In one embodiment, control samples (untreated with activators or inhibitors) are assigned a relative OR activity value of 100. Inhibition of an OR polypeptide is achieved when the OR activity value relative to the control is about 90%, optionally 50%, optionally 25-0%. Activation of an OR polypeptide is achieved when the OR activity value relative to the control is 110%, optionally 150%, 200-500%, or 1000-2000%.

Changes in ion flux may be assessed by determining changes in polarization (*i.e.*, electrical potential) of the cell or membrane expressing a OR protein. One means to determine changes in cellular polarization is by measuring changes in current (thereby measuring changes in polarization) with voltage-clamp and patch-clamp techniques, *e.g.*, the "cell-attached" mode, the "inside-out" mode, and the "whole cell" mode (*see, e.g.*, Ackerman *et al.*, *New Engl. J Med.*, 336:1575-1595 (1997)). Whole cell currents are conveniently determined using the standard. Other known assays include: radiolabeled ion flux assays and fluorescence assays using voltage-sensitive dyes (*see, e.g.*, Vestergaard-Bogind *et al.*, *J. Membrane Biol.*, 88:67-75 (1988); Gonzales & Tsien, *Chem. Biol.*, 4:269277 (1997); Daniel *et al.*, *J. Pharmacol. Meth.*, 25:185-193 (1991); Holevinsky *et al.*, *J. Membrane Biology*, 137:59-70 (1994)). Generally, the compounds to be tested are present in the range from 1 pM to 100 mM.

The effects of the test compounds upon the function of the polypeptides can be measured by examining any of the parameters described above. Any suitable physiological change that affects GPCR activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as transmitter release, hormone release, transcriptional changes to both known and uncharacterized genetic markers (*e.g.*, northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as Ca^{2+} , IP3, cGMP, or cAMP.

Preferred assays for GPCRs include cells that are loaded with ion or voltage sensitive dyes to report receptor activity. Assays for determining activity of such receptors can also use known agonists and antagonists for other G protein coupled receptors as negative or positive controls to assess activity of tested compounds. In

assays for identifying modulatory compounds (*e.g.*, agonists, antagonists), changes in the level of ions in the cytoplasm or membrane voltage will be monitored using an ion sensitive or membrane voltage fluorescent indicator, respectively. Among the ion-sensitive indicators and voltage probes that may be employed are those disclosed
5 in the Molecular Probes 1997 Catalog. For G protein coupled receptors, promiscuous G proteins such as G α 15 and G α 16 can be used in the assay of choice (Wilkie *et al.*, *PNAS*, 88:10049-53 (1991)). Such promiscuous G proteins allow coupling of a wide range of receptors.

Receptor activation typically initiates subsequent intracellular events, *e.g.*,
10 increases in second messengers such as IP₃, which releases intracellular stores of calcium ions. Activation of some G protein coupled receptors stimulates the formation of inositol triphosphate (IP₃) through phospholipase C-mediated hydrolysis of phosphatidylinositol (Berridge & Irvine, *Nature*, 312:315-21 (1984)). IP₃ in turn stimulates the release of intracellular calcium ion stores. Thus, a change in
15 cytoplasmic calcium ion levels, or a change in second messenger levels such as IP₃ can be used to assess G protein coupled receptor function. Cells expressing such G protein coupled receptors may exhibit increased cytoplasmic calcium levels as a result of contribution from both intracellular stores and via activation of ion channels, in which case it may be desirable although not necessary to conduct such assays in
20 calcium-free buffer, optionally supplemented with a chelating agent such as EGTA, to distinguish fluorescence response resulting from calcium release from internal stores.

Other assays can involve determining the activity of receptors which, when activated, result in a change in the level of intracellular cyclic nucleotides, *e.g.*, cAMP or cGMP, by activating or inhibiting enzymes such as adenylate cyclase. There are
25 cyclic nucleotide-gated ion channels, *e.g.*, rod photoreceptor cell channels and olfactory neuron channels that are permeable to cations upon activation by binding of cAMP or cGMP (*see, e.g.*, Altenhofen *et al.*, *PNAS*, 88:9868-72 (1991) and Dhallan *et al.*, *Nature*, 347:184-187 (1990)). In cases where activation of the receptor results in a decrease in cyclic nucleotide levels, it may be preferable to expose the cells to agents
30 that increase intracellular cyclic nucleotide levels, *e.g.*, forskolin, prior to adding a receptor-activating compound to the cells in the assay. Cells for this type of assay can be made by co-transfection of a host cell with DNA encoding a cyclic nucleotide-gated ion channel, GPCR phosphatase and DNA encoding a receptor (*e.g.*,

certain glutamate receptors, muscarinic acetylcholine receptors, dopamine receptors, serotonin receptors, and the like), which, when activated, causes a change in cyclic nucleotide levels in the cytoplasm.

In a preferred embodiment, OR protein activity is measured by expressing a
5 OR gene in a heterologous cell with a promiscuous G protein that links the receptor to a phospholipase C signal transduction pathway (*see* Offermanns & Simon, *J. Biol. Chem.*, 270:15175-15180 (1995)). Optionally the cell line is HEK-293 (which does not naturally express OR genes) and the promiscuous G protein is G α 15/G α 16 (Offermanns & Simon, *supra*). Modulation of olfactory transduction is assayed by
10 measuring changes in intracellular Ca²⁺ levels, which change in response to modulation of the OR signal transduction pathway via administration of a molecule that associates with a OR protein. Changes in Ca²⁺ levels are optionally measured using fluorescent Ca²⁺ indicator dyes and fluorometric imaging.

In one embodiment, the changes in intracellular cAMP or cGMP can be
15 measured using immunoassays. The method described in Offermanns & Simon, *J. Bio. Chem.*, 270:15175-15180 (1995), may be used to determine the level of cAMP. Also, the method described in Felley-Bosco *et al.*, *Am. J. Resp. Cell and Mol. Biol.*, 11:159-164 (1994), may be used to determine the level of cGMP. Further, an assay kit for measuring cAMP and/or cGMP is described in U.S. Patent 4,115,538, herein
20 incorporated by reference.

In another embodiment, phosphatidyl inositol (PI) hydrolysis can be analyzed according to U.S. Patent 5,436,128, herein incorporated by reference. Briefly, the assay involves labeling of cells with 3H-myoinositol for 48 or more hrs. The labeled cells are treated with a test compound for one hour. The treated cells are lysed and
25 extracted in chloroform-methanol-water after which the inositol phosphates were separated by ion exchange chromatography and quantified by scintillation counting. Fold stimulation is determined by calculating the ratio of cpm in the presence of agonist, to cpm in the presence of buffer control. Likewise, fold inhibition is determined by calculating the ratio of cpm in the presence of antagonist, to cpm in the
30 presence of buffer control (which may or may not contain an agonist).

In another embodiment, transcription levels can be measured to assess the effects of a test compound on signal transduction. A host cell containing an OR protein of interest is contacted with a test compound for a sufficient time to effect any

interactions, and then the level of gene expression is measured. The amount of time to effect such interactions may be empirically determined, such as by running a time course and measuring the level of transcription as a function of time. The amount of transcription may be measured by using any method known to those of skill in the art to be suitable. For example, mRNA expression of the protein of interest may be detected using northern blots or their polypeptide products may be identified using immunoassays. Alternatively, transcription based assays using reporter gene may be used as described in U.S. Patent 5,436,128, herein incorporated by reference. The reporter genes can be, e.g., chloramphenicol acetyltransferase, luciferase, '3-galactosidase and alkaline phosphatase. Furthermore, the protein of interest can be used as an indirect reporter via attachment to a second reporter such as green fluorescent protein (see, e.g., Mistili & Spector, *Nature Biotechnology*, 15:961-64 (1997)).

The amount of transcription is then compared to the amount of transcription in either the same cell in the absence of the test compound, or it may be compared with the amount of transcription in a substantially identical cell that lacks the OR protein of interest. A substantially identical cell may be derived from the same cells from which the recombinant cell was prepared but which had not been modified by introduction of heterologous DNA. Any difference in the amount of transcription indicates that the test compound has in some manner altered the activity of the OR protein of interest.

6. Transgenic non-human animals expressing olfactory receptors

Non-human animals expressing one or more olfactory receptor sequences of the invention, particularly human olfactory receptor sequences, can also be used for receptor assays. Such expression can be used to determine whether a test compound specifically binds to a mammalian olfactory transmembrane receptor polypeptide *in vivo* by contacting a non-human animal stably or transiently transfected with a nucleic acid encoding an olfactory receptor or ligand-binding region thereof with a test compound and determining whether the animal reacts to the test compound by specifically binding to the receptor polypeptide.

Use of the translocation domains of the invention in the fusion polypeptides generates a cell expressing high levels of olfactory receptor. Animals transfected or infected with the vectors of the invention are particularly useful for assays to identify and characterize odorants/ligands that can bind to a specific or sets of receptors. Such

vector-infected animals expressing libraries of human olfactory sequences can be used for *in vivo* screening of odorants and their effect on, *e.g.*, cell physiology (*e.g.*, on olfactory neurons), on the CNS (*e.g.*, olfactory bulb activity), or behavior.

Means to infect/express the nucleic acids and vectors, either individually or as
5 libraries, are well known in the art. A variety of individual cell, organ or whole animal parameters can be measured by a variety of means. For example, recording of stimulant-induced waves (bulbar responses) from the main olfactory bulb or accessory olfactory bulb is a useful tool for measuring quantitative stable olfactory responses. When electrodes are located on the olfactory bulb surface it is possible to record stable
10 responses over a period of several days (*see, e.g.*, Kashiwayanagi, *Brain Res. Protoc.* 1:287-291 (1997)). In this study, electroolfactogram recordings were made with a four-electrode assembly from the olfactory epithelium overlying the endoturbinates facing the nasal septum. Four electrodes were fixed along the dorsal-to-ventral axis of one turbinate bone or were placed in corresponding positions on four turbinate
15 bones and moved together up toward the top of the bone. *See also*, Scott, *J. Neurophysiol.* 77:1950-1962 (1997); Scott, *J. Neurophysiol.* 75:2036-2049 (1996); Ezech, *J. Neurophysiol.* 73:2207-2220 (1995). In other systems, fluorescence changes in nasal epithelium can be measured using the dye di-4-ANEPPS, which is applied on the rat's nasal septum and medial surface of the turbinates (*see, e.g.*, Youngentob, *J.*
20 *Neurophysiol.* 73:387-398 (1995)). Extracellular potassium activity (aK) measurements can also be carried out in *in vivo*. An increase in aK can be measured in the mucus and the proximal part of the nasal epithelium (*see, e.g.*, Khayari, *Brain Res.* 539:1-5 (1991)).

The OR sequences of the invention can be for example expressed in animal
25 nasal epithelium by delivery with an infecting agent, *e.g.*, adenovirus expression vector. Recombinant adenovirus-mediated expression of a recombinant gene in olfactory epithelium using green fluorescent protein as a marker is described by, *e.g.*, Touhara, *PNAS*, 96:4040-45 (1999).

The endogenous olfactory receptor genes can remain functional and wild-type
30 (native) activity can still be present. In other situations, where it is desirable that all olfactory receptor activity is by the introduced exogenous hybrid receptor, use of a knockout line is preferred. Methods for the construction of non-human transgenic

animals, particularly transgenic mice, and the selection and preparation of recombinant constructs for generating transformed cells are well known in the art.

Construction of a "knockout" cell and animal is based on the premise that the level of expression of a particular gene in a mammalian cell can be decreased or completely abrogated by introducing into the genome a new DNA sequence that serves to interrupt some portion of the DNA sequence of the gene to be suppressed. Also, "gene trap insertion" can be used to disrupt a host gene, and mouse embryonic stem (ES) cells can be used to produce knockout transgenic animals (*see, e.g.,* Holzschu, *Transgenic Res* 6:97-106 (1997)). The insertion of the exogenous is typically by homologous recombination between complementary nucleic acid sequences. The exogenous sequence is some portion of the target gene to be modified, such as exonic, intronic or transcriptional regulatory sequences, or any genomic sequence which is able to affect the level of the target gene's expression; or a combination thereof. Gene targeting via homologous recombination in pluripotent embryonic stem cells allows one to modify precisely the genomic sequence of interest. Any technique can be used to create, screen for, propagate, a knockout animal, *e.g., see* Bijvoet, *Hum. Mol. Genet.* 7:53-62 (1998); Moreadith, *J. Mol. Med.* 75:208-216 (1997); Tojo, *Cytotechnology* 19:161-165 (1995); Mudgett, *Methods Mol. Biol.* 48:167-184 (1995); Longo, *Transgenic Res.* 6:321-328 (1997); U.S. Patents Nos. 5,616,491; 5,464,764; 5,631,153; 5,487,992; 5,627,059; 5,272,071; WO 91/09955; WO 93/09222; WO 96/29411; WO 95/31560; WO 91/12650.

The nucleic acid libraries of the invention can also be used as reagents to produce "knockout" human cells and their progeny. Likewise, the nucleic acids of the invention can also be used as reagents to produce "knock-ins" in mice. The human or rat OR gene sequences can replace the orthologous ORs in the mouse genome. In this way, a mouse expressing a human or rat OR can be produced. This mouse can then be used to analyze the function of human or rat ORs, and to identify ligands for such ORs.

F. Modulators

The compounds tested as modulators of an OR family member can be any small chemical compound, or a biological entity, such as a protein, sugar, nucleic acid or lipid. Alternatively, modulators can be genetically altered versions of an OR gene.

Typically, test compounds will be small chemical molecules and peptides. Essentially any chemical compound can be used as a potential modulator or ligand in the assays of the invention, although most often compounds can be dissolved in aqueous or organic (especially DMSO-based) solutions are used. The assays are designed to
5 screen large chemical libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays). It will be appreciated that there are many suppliers of chemical compounds, including Sigma (St. Louis, MO), Aldrich (St. Louis, MO), Sigma-Aldrich (St. Louis, MO), Fluka
10 Chemika-Biochemica Analytika (Buchs, Switzerland) and the like.

The OR modulating compounds can be used in any number of consumer products, including, but not limited to, perfumes, fragrance compositions, deodorants, air fresheners, foods, drugs, *etc.*, or ingredients thereof, to thereby modulate the odor of the product, composition, or ingredient in a desired manner. As
15 one of skill in the art will recognize, OR modulating compounds can be used to enhance desirable odors, to block malodors, or a combination thereof.

In one preferred embodiment, high throughput screening methods involve providing a combinatorial chemical or peptide library containing a large number of potential therapeutic compounds (potential modulator or ligand compounds). Such
20 "combinatorial chemical libraries" or "ligand libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual odorant compositions.

25 A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis, by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (amino acids) in every possible way for a
30 given compound length (*i.e.*, the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (*see, e.g.*, U.S. Patent 5,010,175, Furka, *Int. J. Pept. Prot. Res.*, 37:487-93 (1991) and Houghton *et al.*, *Nature*, 354:84-88 (1991)). Other chemistries for generating chemical diversity libraries can also be used. Such chemistries include, but are not limited to: peptoids (*e.g.*, PCT Publication No. WO 91/19735), encoded peptides (*e.g.*, PCT Publication WO 93/20242), random bio-oligomers (*e.g.*, PCT Publication No. WO 92/00091), benzodiazepines (*e.g.*, U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *PNAS*, 90:6909-13 (1993)), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.*, 114:6568 (1992)), nonpeptidal peptidomimetics with glucose scaffolding (Hirschmann *et al.*, *J. Amer. Chem. Soc.*, 114:9217-18 (1992)), analogous organic syntheses of small compound libraries (Chen *et al.*, *J. Amer. Chem. Soc.*, 116:2661 (1994)), oligocarbamates (Cho *et al.*, *Science*, 261:1303 (1993)), peptidyl phosphonates (Campbell *et al.*, *J. Org. Chem.*, 59:658 (1994)), nucleic acid libraries (Ausubel, Berger and Sambrook, all *supra*), peptide nucleic acid libraries (U.S. Patent 5,539,083), antibody libraries (Vaughn *et al.*, *Nature Biotechnology*, 14(3):309-14 (1996) and PCT/US96/10287), carbohydrate libraries (Liang *et al.*, *Science*, 274:1520-22 (1996) and U.S. Patent 5,593,853), small organic molecule libraries (benzodiazepines, Baum, *C&EN*, Jan 18, page 33 (1993); thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pynrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337; benzodiazepines, 5,288,514, and the like).

Devices for the preparation of combinatorial libraries are commercially available (*see, e.g.*, 357 MPS, 390 MPS (Advanced Chem Tech, Louisville KY), Symphony (Rainin, Woburn, MA), 433A (Applied Biosystems, Foster City, CA), 9050 Plus (Millipore, Bedford, MA)). In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.*, ComGenex, Princeton, NJ; Tripos, Inc., St. Louis, MO; 3D Pharmaceuticals, Exton, PA; Martek Biosciences; Columbia, MD; *etc.*).

G. Methods for Representing and Predicting the Perception of Odor

The invention also preferably provides methods for representing the perception of odor (or taste) and/or for predicting the perception of odor (or taste) in a mammal, including in a human. Preferably, such methods may be performed by using the
5 receptors and genes encoding said olfactory receptors disclosed herein.

Also contemplated as within the invention, is a method of screening one or more compounds for the presence of an odor detectable by a mammal, comprising: contacting said one or more compounds with the disclosed receptors, preferably wherein the mammal is a human. Also contemplated as within the invention is a
10 method for representing olfactory perception of a particular smell in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n olfactory receptors of said vertebrate, where n is greater than or equal to 4; and generating from said values a quantitative representation of olfactory perception. The olfactory receptors may be an olfactory receptor disclosed herein, the
15 representation may constitute a point or a volume in n -dimensional space, may constitute a graph or a spectrum, and may constitute a matrix of quantitative representations. Also, the providing step may comprise contacting a plurality of recombinantly-produced olfactory receptors with a test composition and quantitatively measuring the interaction of said composition with said receptors.

Also contemplated as within the invention, is a method for predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n olfactory receptors of said vertebrate, where n is greater than or equal to 4,
25 for one or more molecules or combinations of molecules yielding known olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal, providing values X_1 to X_n representative of the quantitative stimulation of each of n olfactory receptors of
30 said vertebrate, where n is greater than or equal to 4, for one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding

unknown olfactory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal by comparing the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal to the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal. The olfactory receptors used in this method may include an olfactory receptor disclosed herein.

10 In another embodiment, novel molecules or combinations of molecules are generated which elicit a predetermined olfactory perception in a mammal by determining a value of olfactory perception in a mammal for a known molecule or combinations of molecules as described above; determining a value of olfactory perception in a mammal for one or more unknown molecules or combinations of molecules as described above; comparing the value of olfactory perception in a mammal for one or more unknown compositions to the value of olfactory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal; and combining two or more unknown molecules or combinations of molecules to form a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal. The combining step yields a single molecule or a combination of molecules that elicits a predetermined olfactory perception in a mammal.

25 In another embodiment of the invention, there is provided a method for simulating a fragrance, comprising: for each of a plurality of cloned olfactory receptors, preferably human receptors, ascertaining the extent to which the receptor interacts with the fragrance; and combining a plurality of compounds, each having a previously-ascertained interaction with one or more of the receptors, in amounts that together provide a receptor-stimulation profile that mimics the profile for the fragrance. Interaction of a fragrance with an olfactory receptor can be determined using any of the binding or reporter assays described herein. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds

substantially stimulate at least 75%, 80% or 90% of the receptors that are substantially stimulated by the fragrance.

In another preferred embodiment of the invention, a plurality of standard compounds are tested against a plurality of olfactory receptors to ascertain the extent to which the receptors each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on a data storage medium. The method may further comprise providing a desired receptor-stimulation profile for a scent; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the scent.

H. Kits

OR genes and their homologs are useful tools for identifying olfactory receptor cells, for forensics and paternity determinations, and for examining olfactory transduction. OR family member-specific reagents that specifically hybridize to OR nucleic acids, such as AOLFR1 probes and primers, and OR family member-specific reagents that specifically bind to an OR protein, *e.g.*, OR antibodies are used to examine olfactory cell expression and olfactory transduction regulation.

Nucleic acid assays for the presence of DNA and RNA for an OR family member in a sample include numerous techniques are known to those skilled in the art, such as southern analysis, northern analysis, dot blots, RNase protection, S1 analysis, amplification techniques such as PCR, and *in situ* hybridization. In *in situ* hybridization, for example, the target nucleic acid is liberated from its cellular surroundings in such a form so as to be available for hybridization within the cell, while preserving the cellular morphology for subsequent interpretation and analysis. The following articles provide an overview of the art of *in situ* hybridization: Singer *et al.*, *Biotechniques*, 4:230-50 (1986); Haase *et al.*, *Methods in Virology*, vol. VII, pp. 189-226 (1984); and *Nucleic Acid Hybridization: A Practical Approach* (Names *et al.*, eds. 1987). In addition, an OR protein can be detected with the various immunoassay

techniques described above. The test sample is typically compared to both a positive control (e.g., a sample expressing a recombinant OR protein) and a negative control.

The present invention also provides for kits for screening for modulators of OR family members. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise any one or more of the following materials: OR nucleic acids or proteins, reaction tubes, and instructions for testing OR activity. Optionally, the kit contains a biologically active OR receptor. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user.

EXAMPLES

Genomic, predicted amino acid sequence, and predicted coding sequences (cds), of novel G protein-coupled human odorant receptors, and classes of such receptors, are described. Each example describes a discrete protein and nucleic acid pair. Accordingly, Example 1 describes SEQ. ID. NOS. 1 and 2, for the human olfactory receptor protein designated AOLFR1, and the human DNA encoding AOLFR1, respectively; Example 2 describes SEQ. ID. NOS. 3 and 4, for the human olfactory receptor protein designated AOLFR2, and the human DNA encoding AOLFR2, respectively; and so on in the manner described, through the final Example sequence.

In the protein sequences presented herein, the one-letter code X or Xaa refers to any of the twenty common amino acid residues. In the DNA sequences presented herein, the one letter codes N or n refers to any of the of the four common nucleotide bases, A, T, C, or G.

EXAMPLES

AOLFR1 sequences:

MKTFSSFLQIGRNMHQGNQTTTTEFILLGFFKQDEHQNLLFVLFLGMYLVTVIGNGLIIVAISLD
TYLHTPMYFLANLSFADISSISNSVPKMLVNIQTKSQSISYESCITQMYFSIVFVIDNLLLGTM
AYDHFVAICHPLNYTILMRPRFGILLTVISWFLSNIIALHTLLLIQLLFCNHNTPHFFCDLAPLL
KLSCSDTLINELVLFIVGLSVIIFPFTLSFFSYVCIIRAVLRVSSTQGWKAFSTCGSHLTVVLLFY
GTTVGVYFFPSSTHPEDTDKIGAVLFTVVTMPINPFYISLRNKDMKGALRKLINRKISSL (SEQ ID
NO: 1)

ATGAAGACTTTTAGTTCCTTTCTTCAGATCGGCAGAAATATGCATCAAGGAAACCAAACCA
CCATCACTGAATTCATTCTCCTGGGATTTTCAAGCAGGATGAGCATCAAAACCTCCTCTTT
GTGCTTTTCTTGGGTATGTACCTGGTCACTGTGATTGGGAACGGGCTCATCATTGTGGCTA
TCAGCTTGGATACGTACCTTCATACCCCATGTATCTCTTCCTTGCCAATCTATCCTTTGCT
GATATTTCTCCTCCATTTCCAACCTCAGTCCCCAAATGCTGGTGAATATTCAAACCAAGAGTC

AATCCATCTCTTATGAGAGCTGCATCACACAGATGTACTTTTCTATTGTGTTTGTGCGTCATT
 GACAATTTGCTCTTGGGGACCATGGCCTATGACCACTTTGTGGCGATCTGCCACCCTCTGA
 ATTATACAATTTCTCATGCGGCCAGGTTCCGGCATTITGCTCACAGTCATCTCATGGTTCCTC
 AGTAATATTATTGCTCTGACACACACCCCTTCTGCTCATTCAATTGCTCTTCTGTAAACCACAA
 5 CACTCTCCACACTTCTTCTGTGACTTGGCCCCTCTGCTCAAACTGTCCTGTTTCAGATACAT
 TGATCAATGAGCTTGTGTTGTTTATTGTGGGTTTATCAGTTATCATCTTCCCTTTTACACTC
 AGCTTCTTTTCTATGTCTGCATCATCAGAGCTGTCCTGAGAGTATCTTCCACACAGGGAA
 AGTGGAAAGCCTTCTCCACTTGTGGCTCTCACCTGACAGTTGTATTACTGTTCTACGGAAC
 CATTGTAGGCGTGTACTTTTTCCCTCCTCCACTCACCTGAGGACACTGATAAGATTGGT
 10 GCTGTCCTATTCACTGTGGTGACACCCATGATAAAACCCCTTCATCTACAGCTTGAGGAATA
 AGGATATGAAAGGTGCCCTGAGAAAGCTCATCAATAGAAAAATTTCTTCCCTTTGA (SEQ
 ID NO: 2)

AOLFR2 sequences:

15 MMMVLRNLSMEPTFALLGFTDYPKLQIPLFLVFLLMYVITVVGNLGMIHINPKFHTPMYFFL
 SHLSFVDFCYSSIVTPKLEENLVMADKSIFYFSCMMQYFLSCTAVVTESFLLAVMAYDRFVAIC
 NPLLYTVAMSQRLCALLVAGSYLWGMFGPLVLLCYALRLNFGPNVINHFFCEY TALISVSGS
 DILPHLLLSFATFNEMCTLLILTSYVFIVTVLKIRSVSGRHKAFSTWASHLTAITIFHGTLFL
 YCVPSNKNRQTVKVASVFYTVVNPMLNPPYSLRNKDVKDADFVKLIHTQVPFH (SEQ ID NO:
 20 3)

ATGATGATGGTTTTAAGGAATCTGAGCATGGAGCCCACCTTTGCCCTTTTAGGTTTCACAG
 ATTACCCAAAGCTTCAGATTCTCTCTTCTTGTGTTTCTGCTCATGTATGTTATCACAGTG
 GTAGGAAACCTTGGGATGATCATAATAATCAAGATTAACCCCAAATTCACACTCCTATGT
 25 ACTTTTTCTTAGTCACCTCTCTTTTGTGATTTTTGTTACTCTTCCATTGTCACCTCCCAAGC
 TGCTTGAGAACTTGGTAATGGCAGATAAAAGCATCTTCTACTTTAGCTGCATGATGCAGTA
 CTTCTGCTGCACTGCTGTGGTGACAGAGTCTTCTTGCTGGCAGTGATGGCCTATGAC
 CGCTTTGTGGCCATCTGCAATCCTCTGCTTATACAGTGGCCATGTCACAGAGGCTCTGTG
 CCCTGCTGGTGGCTGGGTCATATCTCTGGGCGATGTTTGGCCCCTTGGTACTCCTTTGTTAT
 30 GCTCTCCGGTTAAACTTCTCTGGACCTAATGTAATCAACCACTTCTTTTGTGAGTATACTGC
 TCTCATCTCTGTGTCTGGCTCTGATATACTCATCCCCACCTGCTGCTTTTACGCTTCGCCA
 CCTTCAATGAGATGTGTACACTACTGATCATCCTCACTTCTTATGTTTTCATTTTTGTGACT
 GTACTAAAAATCCGTCTCTGTTAGTGGGCGCCACAAAGCCTTCTCCACCTGGGCCTCCCACC
 TGACTGCTATCACCATCTTCCATGGGACCATCCTTTTCTTTACTGTGTACCCAACTCCAAA
 35 AACTCTCGGCAAAACAGTCAAAGTGGCCTCTGTATTTTACACAGTTGTCAACCCCATGCTGA
 ACCCTCCGATCTACAGCCTAAGGAATAAAGACGTGAAGGATGCTTTCTGGAAGTTAATACA
 TACACAAGTTCATTTCCTGA (SEQ ID NO: 4)

AOLFR3 sequences:

40 MLLTDRNTSGTTFLLGFSDYPELQVPLFLVFLAIYNVTVLGNIGLIVIKINPKLHTPMYFFLSQ
 LSFVDFCYSSIIAPKMLVNLVVKDRITISFLGCVVQFFFCTFVVTESFLLAVMAYDRFVAICNPL
 LYTVDMQSQKLCVLLVVGSYAWGVSCSLELTCSALKLCFHGFNTINHFFCEFSLLSLSCSDTYI
 NQWLLFFLATFNEISTLLIVLTSYAFIVVTILKMRSVSGRRKAFSTCASHLTAITIFHGTLFLYCV
 PNSKNRHTVKVASVFYTVVIPMLNPLIYSLRNKDVKDTVTEILDTKVFSY (SEQ ID NO: 5)

45 ATGCTGCTGACAGATAGAAATACAAGTGGGACCACGTTACCCCTCTTGGGCTTCTCAGATT
 ACCCAGAACTGCAAGTCCCCTCTTCTGGTTTTTCTGGCCATCTACAATGTCACTGTGCTA
 GGGAAATATTGGGTTGATTGTGATCATCAAAATCAACCCCAAATGCATACCCCATGTACT
 TTTTCTCAGCCAACTCTCCTTTGTGGATTTCTGCTATTCTCCATCATTGCTCCCAAGATG
 50 TTGGTGAACCTTGTGTCAAAGACAGAACCATTTCATTTTTAGGATGCGTAGTACAATTCT
 TTTTCTTCTGTACCTTTGTGGTCACTGAATCCTTTTTATTAGCTGTGATGGCCTATGACCGC
 TTCGTGGCCATTTGCAACCTCTGCTCTACACAGTTGACATGTCCAGAAACTCTGCGTGC
 TGCTGGTTGTGGGATCCTATGCCTGGGGAGTCTCATGTTCTTGGAACTGACGTGCTCTGC
 TTTAAAGTTATGTTTTCATGGTTTCAACACAATCAATCACTTCTTCTGTGAGTTCTCCTCAC
 55 TACTCTCCCTTTCTGCTCTGATACTTACATCAACCAAGTGGCTGCTATTCTTCTTGGCCACC
 TTTAATGAAATCAGCACACTACTCATCGTTCTCACATCTTATGCGTTCATTGTTGTAACCAT

CCTCAAGATGCGTTCAAGTCAGTGGGCGCCGCAAAGCCTTCTCCACCTGTGCCTCCACCTG
 ACTGCCATCACCATCTTCCATGGCACCATCCTCTTCTTTACTGTGTGCCAACTCCAAAAA
 CTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGATCCCATGTTGAAT
 CCCCTGATCTACAGTCTGAGAAATAAAGATGTCAAGGATACAGTCACCGAGATACTGGAC
 5 ACCAAAGTCTTCTCTTACTGA (SEQ ID NO: 6)

AOLFR4 sequences:

MENQNNVTEFILLGLTENLELWKIFSAVFLVMYVATVLENLLIVVTITTSQSLRSPMYFFLTFLS
 LLDVMFSSVVPKVIIVDTLSKSTTISLKGCLTQLFVEHFFGGVGILLTVMAYDRYVAICKPLHY
 10 TIIMSPRVCCMLMVGGAWVGGFMHAMIQLLFMYQIPFCGPNIDHFIQDLFQLLTLACTDTHILGL
 LVTNLNGMMCVAFILILIASYTVILCSLSYSSKGRHKALSTCSSHLTVVVLFFVPCIFLYMRPV
 VTHPIDKAMAVSDSIITPMLNPLIYTLRNAEVKSAMKKLWMKWEALAGK (SEQ ID NO: 7)

ATGGAAAATCAAAAACATGTGACTGAATTCATTCTTCTGGGTCTCACAGAGAACCTGGAGC
 15 TGTGGAAAATATTTTCTGCTGTGTTTCTTGTTCATGTATGTAGCCACAGTGCTGGAAAATCT
 ACTTATTGTGGTAACTATTATCACAAGTCAGAGTCTGAGGTCACCTATGTATTTTTTCTTA
 CCTTCTTGTCCCTTTTGGATGTCATGTTCTCATCTGTCGTTGCCCAAGGTGATTGTAGAC
 ACCCTCTCCAAGAGCACTACCATCTCTCTCAAAGGCTGCCTCACCCAGCTGTTTGTGGAGC
 ATTTCTTTGGTGGTGTGGGGATCATCCTCCTCACTGTGATGGCCTATGACCGCTACGTGGC
 20 CATCTGTAAGCCCCTGCACTACACGATCATCATGAGTCCACGGGTGTGCTGCCTAATGGTA
 GGAGGGGCTTGGGTGGGGGGATTATGCACGCAATGATACAACTTCTCTTCATGTATCAAA
 TACCCTTCTGTGGTCTAATATCATAGATCACTTTATATGTGATTGTGTTTCAAGTTGTTGACA
 CTTGCCTGCACGGACACCCACATCCTGGGCCTCTTAGTTACCCTCAACAGTGGGATGATGT
 GTGTGGCCATCTTTCTTATCTTAATTGCGTCTACACGGTCATCCTATGCTCCCTGAAGTCT
 25 TACAGCTCTAAAGGGCGGCACAAAGCCCTCTCTACCTGCAGCTCCACCTCACGGTGGTTG
 TATTGTTCTTTGTCCCCTGTATTTTCTTGTACATGAGGCCTGTGGTCACTACCCCATAGAC
 AAGGCAATGGCTGTGTGCACTCAATCATCACCCCATGTAAATCCCTTGATCTATACAC
 TGAGGAATGCAGAGGTGAAAAGTGCCATGAAGAACTCTGGATGAAATGGGAGGCTTTGG
 CTGGGAAATAA (SEQ ID NO: 8)

30

AOLFR5 sequences:

MGKENCTTVAEFILLGLSDVPELRVCLFLLFLLIYGVTLNLANLGMIALIQVSSRLHTPMYFFLSH
 LSSVDFCYSSIIIVPKMLANIFNKDKAISFLGCMVQFYLFCTCVVTEVFLLAVMAYDRFVAICNPL
 35 LYTVTMSWKVRVELASCCYFCGTVCSLIHLCLALRIPFYRSNVINHHFCDLPPVLSLACSDITVN
 ETLFLVATL NESVTIMILTSYLLILTILKMGSABGRHKAFSTCASHLTAITVFHGTVLSIYCRP
 SSGNSGDADKVATVFYTVVIPMLNSVTYSLRNKDVKEALRKVMGSKIHS (SEQ ID NO: 9)

ATGGGCAAGGAAAACCTGCACCACTGTGGCTGAGTTCATTCTCCTTGGACTATCAGATGTCC
 CTGAGTTGAGAGTCTGCCTCTTCTGCTGTTCTTCTCATCTATGGAGTCACGTTGTTAGCC
 40 AACCTGGGCATGATTGCACTGATTCAAGTCAGCTCTCGGCTCCACACCCCATGTACTTTT
 TCCTCAGCCACTTGTCTCTGTAGATTCTGCTACTCTCAATAATTGTGCCAAAATGTTG
 GCTAATATCTTTAACAAGGACAAAGCCATCTCCTTCTAGGGTGCATGGTGCAATTCTACT
 TGTTTTGCACCTTGTGTGGTCACTGAGGTCTTCTGCTGGCCGTGATGGCCTATGACCGCTT
 GTGGCCATCTGTAACCTTTGCTATACACAGTCACCATGTCTTGGAAGGTGCGTGTGGAGC
 45 TGGCTTCTTGTGCTACTTCTGTGGGACGGTGTGTTCTCTGATTCAATTTGTGCTTAGCTCTT
 AGGATCCCCTTCTATAGATCTAATGTGATTAACCACTTTTCTGTGATCTACCTCCTGTCTT
 AAGTCTTGCTTGTCTGATATCACTGTGAATGAGACACTGCTGTTCTGGTGGCCACTTTG
 AATGAGAGTGTTACCATCATGATCATCCTCACCTCCTACCTGCTAATTCTCACCACCATCCT
 GAAGATGGGCTCTGCAGAGGGCAGGCACAAAGCCTTCTCCACCTGTGCTTCCACCTCACA
 50 GCTATCACTGTCTTCCATGGAACAGTCTTTCCATTTATTGCAGGCCCAGTTCAAGCAATA
 GTGGAGATGCTGACAAAGTGGCCACCGTGTCTACACAGTCGTGATTCTATGCTGAATC
 TGTGATCTACAGCCTGAGAAATAAAGATGTGAAAGAAGCTCTCAGAAAAGTGATGGGCTC
 CAAAATTCACCTCCTAG (SEQ ID NO: 10)

AOLFR6 sequences:

MMASERNQSSSTPTFILLGFSEYPEIQVPLFLVFLFVYTVTVVGNLGMIIIRLNSKLHTIMYFFLS
 HLSLTDFCFSTVVPKLEENLVVEYRTISFSGCIMQFCFACIFGVTETFMLAAMAYDRFVAVCK
 PLLYTTIMSQKLCALLVAGSYTWGIVCSLLTYFLLDLSESTFINNFICDHSVIVSASYSDPYIS
 5 QRLCFIIAFNEVSSLIILTSYMLIFTTIMKMRSASGRQKTFSTCASHLTAITFHGTILFLYCVPNP
 KTSSLIVTVASVFYTVAIPLNPLIYSLRNKDINNMFELVVTCLIYH (SEQ ID NO: 11)

ATGATGGCATCTGAAAGAAATCAAAGCAGCACACCCACTTTTATTCTCTTGGGTTTTTCAG
 AATACCCAGAAATCCAGGTTCCACTCTTTCTGGTTTTCTTGTTCTGCTACACAGTCACTGTA
 10 GTGGGGAACCTGGGCATGATAATAATCATCAGACTCAATTCAAAACCTCCATACAATCATGT
 ACTTTTTCCCTTAGTCACTTGTCTTGACAGACTTCTGTTTTTCCACTGTAGTTACACCTAAA
 CTGTTGGAGAACTTGGTTGTGGAATACAGAACCATCTCTTCTCTGGTTGCATCATGCAAT
 TTTGTTTTGCTTGCATTTTTGGAGTGACAGAACTTTCATGTTAGCAGCGATGGCTTATGAC
 CGTTTTGTGGCAGTTTGTAAACCCCTTGCTGTATACCACTATTATGTCTCAGAAGCTCTGTGC
 15 TCTTCTGGTGGCTGGGTCCTATACATGGGGGATAGTGTGCTCCCTGATACTCACATATTTT
 CTTCTTGACTTATCGTTTTGTGAATCTACCTTCATAAATAATTTTATCTGTGACCACTCTGT
 AATTGTTTTCTGCCTCCTACTCAGACCCCTATATCAGCCAGAGGCTATGCTTTATTATTGCCA
 TATTCAATGAGGTGAGCAGCCTAATTATCATTCTGACATCATATATGCTTATTTCACTACC
 ATTATGAAGATGCGATCTGCAAGTGGGCGCCAGAAAACCTTCTCCACCTGTGCCTCCCACC
 20 TGACAGCCATCACTATCTTCCATGGAATATCCTTTTCTTTACTGTGTTCTTAATCCTAAA
 ACTTCTAGCCTCATAGTTACAGTGGCTTCTGTGTTTTACACAGTGGCGATTCCAATGCTGA
 ACCCATTGATCTACAGCCTTAGGAACAAAGATATCAATAACATGTTTGAAAAATTAGTGT
 CACCAAATTGATTTACCACTGA (SEQ ID NO: 12)

AOLFR7 sequences:

MSYFYRLKLMKEAVLVKLPFTSLPLLQTLRSKSRDMEIKNYSSSTSGFILLGLSSNPQLQKPLF
 AIFLIMYLLAAVGNVLIIPAIYSDPRLHTPMYFFLSNLSFMDICFTTVIVPKMLVNFSETKVISY
 VGCLAQMYFFMAFGNTDSYLLASMAIDRLVAICNPLHYDVVMKPRHCLLMLLGSCSISHLHSL
 FRVLLMSRSLFCASHIHKHFFCDTQPVKLSCSDTSSSQMVVMTETLAIVTPFLCIIFSILRIMV
 30 TVLRIPSAAGKWKAFSTCGSHLTAVALFYGSIYVYFRPLSMYSVVRDRVATVMYTVVTPMLN
 PFYISLRNKDMKRGLKKLQDRIYR (SEQ ID NO: 13)

ATGAGCTATTTTTACAGGCTTAAGCTTATGAAAGAAGCTGTCTTGGTCAAACCTGCCCTTTA
 CATCTCTCCCACTGCTTCTCCAAACCTATCCAGGAAGTCCAGAGACATGGAGATAAAGAA
 35 CTACAGCAGCAGCACCTCAGGCTTCATCTCTGGGCTCTCTTCCAACCTCAGCTGCAG
 AAACCTCTCTTTGCCATCTTCTCATCATGTACTGCTCGCTGCGGTGGGAATGTGTCAT
 CATCCCGGCCATCTACTCTGACCCCAAGGCTCCACACCCCTATGTACTTTTTTCTCAGCAACT
 TGTCTTTTATGGATATCTGCTTCACAACAGTCATAGTGCCTAAGATGCTGGTGAATTTTCTA
 TCAGAGACAAAGGTTATCTCCTATGTGGGCTGCCTGGCCAGATGTACTTCTTTATGGCAT
 40 TTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCGGCTGGTGGCCATCTG
 CAACCCCTTACACTATGATGTGGTTATGAAACCACGGCATTGCCTGCTCATGCTATTGGGT
 TCTTGACAGCATCTCCACCTACATTCCCTGTTCCGCGTGCTACTTATGTCTCGCTTGTCTTT
 CTGTGCCTCTCACATCATTAAGCACTTTTTCTGTGACACCCAGCCTGTGCTAAAGCTCTCCT
 GCTCTGACACATCCTCCAGCCAGATGGTGGTGATGACTGAGACCTTAGCTGTCTATTGTGAC
 45 CCCCTTCTGTGTATCATCTTCTCCTACCTGCGAATCATGGTCACTGTGCTCAGAATCCCT
 CTGCAGCCGGGAAGTGGAAGGCCTTCTCTACCTGTGGCTCCACCTCACTGCAGTAGCCCT
 TTTCTATGGGAGTATTATTTATGTCTATTTTAGGCCCTGTCCATGTACTCAGTGGTTAGGG
 ACCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGAACCCCTTCTATCTACAG
 CCTGAGGAACAAAGATATGAAGAGGGGTTTGAAGAAATTACAGGACAGAATTTACCGGTA
 50 A (SEQ ID NO: 14)

AOLFR8 sequences:

MATSNHSSGAEFILAGLTQRPELQLPLFLFLGIYVTVVGNLGMIFLIALSSQLYPPVYYFLSH
 LSFIDLCSYSSVITPKMLVNFVPEENIISFLECITQLYFFLIFVIAEGYLLTAMEYDRYVAICRPLLY
 55 NIVMSHRVCSIMMAVVYSLGFLWATVHTTRMSVLSFCRSHTVSHYFCDILPLLTLSCSSTHINEI

LLFIIGGVNTLATTALVLISYAFIFSSILGIHSTEGQSKAFGTCSSHLLAVGIFFGSITFMFKPPSS
TTMEKEKVSSVFYITIIPMLNPLIYSLRNKDVKNALKKMTRGRQSS (SEQ ID NO: 15)

5 ATGGCTACTTCAAACCATTCCTTCAGGGGCTGAGTTTATCCTGGCAGGCTTGACACAACGCC
CAGAACTTCAACTGCCACTCTTCTCCTGTTCTTGGAAATATATGTGGTCACAGTGGTGGG
GAACCTGGGCATGATCTTCTTAATTGCTCTCAGTTCTCAACTTTACCCTCCAGTGTATTATT
TTCTCAGTCATTTGTCTTTTCAATTGATCTCTGCTACTCCTCTGTCAATTACCCCTAAGATGCTG
GTGAACCTTTGTTCCAGAGGAGAACATTATCTCCTTTCTGGAATGCATTACTCAACTTTATTT
CTTCTTATTTTTGTAATTGCAGAAGGCTACCTTCTGACAGCCATGGAATATGACCGTTAT
10 GTTGTCTATCTGTGCGCCACTGCTTTACAATATTGTCATGTCCACAGGGTCTGTTCCATAAT
GATGGCTGTGGTATACTCACTGGGTTTTCTGTGGGCCACAGTCCATACTACCCGCATGTCA
GTGTTGTCAATTCTGTAGGTCTCATACGGTCAGTCATTATTTTTGTGATATTCTCCCTTATT
GACTCTGTCTTGCTCCAGCACCCACATCAATGAGATTCTGCTGTTCAATTATTGGAGGAGTT
AATACCTTAGCAACTACACTGGCGGTCCTTATCTCTTATGCTTTTCATTTTCTCTAGTATCCT
15 TGGTATTCACTCCACTGAGGGGCAATCCAAAGCCTTTGGCACTGTAGCTCCCATCTCTTG
GCTGTGGGCATCTTTTTTGGGTCTATAACATTGATGTATTTCAGCCCCCTTCCAGCACTAC
TATGGAAAAAGAGAAGGTGTCTTCTGTGTTCTACATCACAATAATCCCCATGCTGAATCCT
CTAATCTATAGCCTGAGGAACAAGGATGTGAAAAATGCACTGAAGAAGATGACTAGGGGA
AGGCAGTCATCCTGA (SEQ ID NO: 16)

20

AOLFR9 sequences:

MLARNNSLVTEFILAGLTDRPEFWQPFLLFLVIYIVTMVGNLGLITLFLNSHLHTPMYYFLFN
LSFIDLCYSSVFTPKMLMNFVSKKNISNVGCMTRLFFFLFFVISECYMLTSMAYDRYVAICNPL
LYKVTMSHQVCSMLTFAAYIMGLAGATAHTGCMFRLTFCSANINHYLCDILPLLQLSCTSTYV
25 NEVVVLIVVGTNITVPSCITLISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMKY
SSGSMEQKGVFSVFYTNVVPMLNPLIYSLRNKDVKVALRKALIKIQRNIF (SEQ ID NO: 17)

ATGCTGGCTAGAAACAACCTCCTTAGTGACTGAATTTATTCTTGCTGGATTAACAGATCGTC
CAGAGTTCTGGCAACCCCTCTTTTTCTGTTCTTAGTGATCTACATTGTCACCATGGTAGGC
30 AACCTTGGCTTGATCACTCTTTTCGGTCTAAATTCTCACCTCCACACACCAATGTACTATTT
CCTCTTCAATCTCTCCTTCATTGATCTCTGTTACTCCTCTGTTTTCACTCCCCAAATGCTAAT
GAACTTTGTGTCAAAAAAGAATATTATCTCCAATGTTGGGTGCATGACTCGGCTGTTTTTC
TTTCTCTTTTTCGTCATCTCTGAATGTTACATGTTGACCTCAATGGCATATGATCGCTATGT
GGCCATCTGTAATCCATTGCTGTATAAGGTACCATGTCCCATCAGGTCTGTTCTATGCTCA
35 CTTTGTGCTTACATAATGGGATTGGCTGGAGCCACGGCCACACCGGGTGCATGTTTAG
ACTCACCTTCTGCAGTGCTAATATCATTAAACCATTACTTGTGTGACATACTCCCCCTCCTCC
AGCTTTCCTGCACCAGCACCTATGTCAACGAGGTGGTTGTTCTCATTGTTGTGGGTACTAA
TATCACGGTACCCAGTTGTACCATCCTCATTTCTTATGTTTTTATTGTCATGACTAGCATTCTTC
ATATCAAATCCACTCAAGGAAGATCAAAAGCCTTCAGTACTTGTAGCTCTCATGTCAATTGC
40 TCTGTCTCTGTTTTTGGGTGAGCGGCATTCTATGTATATTAAATATTCTTCTGGATCTATGG
AGCAGGGAAAAGTTTTTCTGTTTTCTACACTAATGTGGTGCCCATGCTCAATCCCCCTCATC
TACAGTTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAAAATTGAG
AGGAGAAATATATTCTAA (SEQ ID NO: 18)

45 **AOLFR10 sequences:**

MLARNNSLVTEFILAGLTDRPEFRQPLFFFLFLVIYIVTMVGNLGLIILFGLNSHLHTPMYYFLFN
SFIDLCYSSVFTPKMLMNFVSKKNISYVGCMTQLFFFLFFVISECYILTSMAYDRYVAICNPLLY
KVTMSHQVCSMLTFAAYIMGLAGATAHTGCMRLTFCSANINHYLCDILPLLQLSCTSTYVN
EVVVVLIVVGINIMVPSCITLISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMKY
50 SGSMEQKGVSSVFYTNVVPMLNPLIYSLRNKDVKVALRKALIKIQRNIF (SEQ ID NO: 19)

ATGCTGGCTAGAAACAACCTCCTTAGTGACTGAATTTATTCTTGCTGGATTAACAGATCGTC
CAGAGTTCCGGCAACCCCTCTTTTTCTGTTTCTAGTGATCTACATTGTCACCATGGTAGGC
AACCTTGGCTTGATCACTCTTTTCGGTCTAAATTCTCACCTCCACACACCAATGTACTATTT
55 CCTCTTCAATCTCTCCTTCATTGATCTCTGTTACTCCTCTGTTTTCACTCCCCAAATGCTAAT
GAACTTTGTATCAAAAAAGAATATTATCTCCTATGTTGGGTGCATGACTCAGCTGTTTTTCT

TTCTCTTTTTTGTGCTCTCTGAATGCTACATATTGACCTCAATGGCATATGATCGCTATGTG
 GCCATCTGTAATCCATTGCTGTATAAGGTCACCATGTCCCATCAGGTCTGTTCTATGCTCAC
 TTTTGCTGCTTACATAATGGGATTGGCTGGAGCCACGGCCACACCGGGTGCATGCTTAGA
 CTCACCTTCTGCAGTGCTAATATCATCAACCATTACTTGTGTGACATACTCCCCCTCCTCCA
 5 GCTTTCCTGCACCAGCACCTATGTCAACGAGGTGGTTGTTCTCATTGTTGTGGGTATTAAT
 ATCATGGTACCCAGTTGTACCATCCTCATTTCTTATGTTTTTCATTGTCACTAGCATTCTTCA
 TATCAAATCCACTCAAGGAAGATCAAAAGCCTTCAGTACTTGTAGCTCTCATGTCAATTGCT
 CTGTCTCTGTTTTTTGGGTGAGCGGCATTCATGTATATTAAATATTCTTCTGGATCTATGGA
 GCAGGGAAAAGTTTCTTCTGTTTTCTACACTAATGTGGTGCCCATGCTCAATCCTCTCATCT
 10 ACAGTTTGAGGAACAAGGATGTCAAAGTTCAGTCTGAGGAAAGCTCTGATTAAAATTGAGA
 GAAGAAATATATTCTAA (SEQ ID NO: 20)

AOLFR11 sequences:

MTLRNSSSVTEFILVGLSEQPELQLPLFLLFLGIYVFTVVGNLGLITLIGINPSLHTPMYFFLENLS
 15 FIDLCYSCVFTP KMLNDFVSESIISYVGCMTQLFFFCFFVNSECYVLVSMA YDRYVAICNP LLY
 MVTMSPRVCFLLMFGSYVVG FAGAMAHTGSM LRLTFCD SNVIDHYLCDVLP LLQLSCTSTHV
 SELVFFIVGVITMLSSISIVISYALILSNILCIPSAEGRSKAFSTWGS HIAVALFFGSGTFTYLTTS
 FPGSMNHGRFASVFYTNVVPMLNPSIYSLRNKDDKLALGKTLKRVLF (SEQ ID NO: 21)

20 ATGACTCTGAGAAACAGCTCCTCAGTGACTGAGTTTATCCTTGTTGGGATTATCAGAACAGC
 CAGAGCTCCAGCTCCCTCTTTCTTCTATTCTTAGGGATCTATGTGTTCACTGTGGTGGGC
 AACTTGGGCTTGATCACCTTAATTGGGATAAATCCTAGCCTTCACACCCCCATGTACTTTTT
 CCTCTTCAACTTGTCTTTATAGATCTCTGTTATTCTGTGTGTTTACCCCCAAAATGCTGA
 ATGACTTTGTTTTAGAAAGTATCATCTCTTATGTGGGATGTATGACTCAGCTATTTTTCTTC
 25 TGTTTTCTTGTCAATTCTGAGTGCTATGTGTTGGTATCAATGGCCTATGATCGCTATGTGGC
 CATCTGCAACCCCTGCTCTACATGGTCACCATGTCCCCAAGGGTCTGCTTTCTGCTGATGT
 TTGGTTCCTATGTGGTAGGGTTTGCTGGGGCCATGGCCCACTGGAAGCATGCTGCGACT
 GACCTTCTGTGATTCCAACGTCATTGACCATTATCTGTGTGACGTTCTCCCCCTCTTGACAGC
 TCTCCTGCACCAGCACCCATGTCACTGAGTGGTATTTTTCTATTGTTGGAGTAATCACC
 30 ATGCTATCCAGCATAAGCATCGTCATCTCTTACGCTTTGATACTCTCCAACATCCTCTGTAT
 TCCTTCTGCAGAGGGCAGATCCAAAGCCTTTAGCACATGGGGCTCCACATAATTGCTGTT
 GCTCTGTTTTTTGGGTGAGGGACATTACCTACTTAACAACATCTTTTCTGGCTCTATGAA
 CCATGGCAGATTTGCCTCAGTCTTTTACACCAATGTGGTTCCCATGCTTAACCCCTTCGATCT
 ACAGTTTGAGGAATAAGGATGATAAACTTGCCCTGGGCAAAACCCTGAAGAGAGTGCTCT
 35 TCTAA (SEQ ID NO: 22)

AOLFR12 sequences:

MERNHNPDCNVLNFFFADKKNKRRNFGQIVSDVGRICYSVSLSLGEPTTMGRNNLTRPSEFIL
 LGLSSRPEDQKPLFAVFLPIYLITVIGNLLILAIRSDTRLQTPMYFFLSILSFVDICYVTVIIPKMLV
 40 NFLSETKTISYGECLTQMYFFLAFGNTDSYLLAAMADRYVAICNPFHYITIMSHRCCVLLLVL
 FCIPHFHSLHILLTNQLIFCASNVIHFFCDDQPV LKLS CSSHFVKEITVMTEGLAVIMTPFSCIII
 SYLRILITVLKIPSAAGKRKAFTSCGSHLTVVTLFYGSISYVYFQPLSNYTVKDQIATIIYTVLTP
 MLNPFYISLRNKDMKQGLAKLMHRMKCQ (SEQ ID NO: 23)

45 ATGGAAAGAAACCACAATCCAGATAATTGTAATGTTTTAAATTTTTCTTTGCTGATAAGA
 AGAATAAAAAGGAGAAATTTTGACAGATTGTATCAGATGTTGGAAGAATCTGTTACAGTG
 TAGTTTATCTTTAGGTGAACCCACAACCTATGGGAAGAAATAACCTAACAAGACCCTCTGA
 ATTCATCCTCCTTGACTCTCCTCTCGACCTGAGGATCAGAAGCCGCTCTTTGCTGTGTTCC
 TCCCCATCTACCTTATCAGATGATAGGAAACCTGCTTATCATCCTGGCCATCCGCTCAGA
 50 CACTCGTCTCCAGACGCCCATGTACTTCTTTCTAAGCATCCTGTCTTTTGTGACATTTGCT
 ATGTGACAGTCATTATCCCTAAGATGCTGGTGAACCTTCTTATCAGAGACAAAGACCATCTC
 TTACGGTGAGTGTCTGACCCAGATGTACTTTTCTTAGCCTTTGGAAACACAGACAGTTAC
 CTGCTAGCAGCCATGGCCATTGACCGCTATGTGGCCATATGTAATCCCTTCCACTACATCA
 CCATTATGAGTCACAGATGCTGTGCTCTGCTTCTGGTTCTCTCCTTCTGCATTCCACATTTT
 55 CACTCCCTCCTGCACATTCTTCTGACTAATCAGCTCATCTTCTGTGCCTCCAATGTCATCCA
 TCACTTTTTCTGCGATGATCAACCAGTGCTAAAATTGTCCTGTTCCCTCCCATTTTGTCAAAG

AAATCACAGTAATGACAGAAGGCTTGGCTGTCATAATGACCCCGTTTTTCATGCATCATCAT
 CTCTTATTTAAGAATCCTCATCACTGTTCTGAAGATTCTTCAGCTGCTGGAAAGCGTAAA
 GCATTTTCTACCTGTGGCTCTCATCTCACAGTGGTGACCCTGTTTTATGGAAGCATTAGCTA
 TGTCTATTTTTCAGCCCCCTGTCCAATACTGTCAAGGATCAAATAGCAACAATTATCTAC
 5 ACCGTA CTGACTCCTATGCTAAATCCATTTATCTATAGTCTGAGGAACAAAGACATGAAGC
 AGGGTTTGGCAAAGTTGATGCACAGGATGAAATGTCAGTAA (SEQ ID NO: 24)

AOLFR13 sequences:

MDQKNGSSFTGFILLGFSDRPQLELVLFVVLIFYIFTLLGNKTIIVLSHLDPHLHNP MYFFFSNL
 10 SFLDLCYTTGIVPQLLVNLRGADKSISYGGCVVQLYISLGLGSTECVLLGVMAFDRYAAVCRPL
 HYTVVMHPCLYVLMASWSWVIGFANSLQLTVLILLTL CGRNKLEHFLCEVPPLKLACVDTT
 MNESELFVSVIII LPVALIIFSYSQIVRAVVRKISATGQRKVFGTCGSHLTVVSLFYGTAIYAY
 LQPGNNYSQDQGXISLFYTIITPMINPLIYTLRNKDVKGALKKVLWKNYDSR (SEQ ID NO:
 25)

15 ATGGATCAGAAAAATGGAAGTTCTTTCACTGGATTTATCCTACTGGGTTTCTCTGACAGGC
 CTCAGCTGGAGCTAGTCCTCTTTGTGGTTCTTTTGATCTTCTATATCTTCACTTTGCTGGGG
 AACAAAACCATCATTTGATTATCTCACTGGACCACATCTTCACAATCCTATGTATTTT
 CTTCTCCAACCTAAGCTTTTTGGATCTGTGTTACACAACCGGCATTGTTCCACAGCTCCTGG
 20 TTAATCTCAGGGGAGCAGACAAATCAATCTCCTATGGTGGTTGTGTAGTTCAGCTGTACAT
 CTCTCTAGGCTTGGGATCTACAGAATGCGTTCTCTTAGGAGTGATGGCATTGACCGCTAT
 GCAGCTGTTTGCAGGCCCTCCACTACACAGTAGTCATGCACCCTGTCTGTATGTGCTGA
 TGGCTTCTACTTCATGGGTCA TTGGTTTTGCCAACTCCCTATTGCAGACGGTGCTCATCTTG
 CTTTAACTTTGTGGAAGAAATAAATTAGAACACTTTCTTTGTGAGGTTCCTCCATTGCT
 25 CAAGCTTGCTGTGTTGACACTACTATGAATGAATCTGAACCTTCTTTGTGAGTGTCATTA
 TTCTTCTGTACCTGTTGCATTAATCATATTCTCCTATAGTCAGATTGTCAGGGCAGTCGTG
 AGGATAAAGTCAGCAACAGGGCAGAGAAAAGTGTGTTGGGACATGTGGCTCCACCTCACA
 GTGGTTTCCCTGTTCTACGGCACAGCTATCTATGCTTACCTCCAGCCCGCAACAATACTC
 TCAGGATCAGGGCAAGKTCATCTCTCTCTTCTACACCATCATTACACCCATGATCAACCCC
 30 CTCATATATACTGAGGAACAAGGATGTGAAAGGAGCACTTAAGAAGGTGCTCTGGAAG
 AACTACGACTCCAGATGA (SEQ ID NO: 26)

AOLFR14 sequences:

MALPLLLSPSCFASSQSLSSRMNSENLTAAVAPAEFVLLGITNRWDLRVALFLTCLPVYLVSL
 35 LGNMGMALLIRMDARLHTPMYFFLANLSLLDACYS SAIGPKMLVDLLLPRATIPYTACALQMF
 VFLAGLADTECCLLAAMAYDRYVAIRNPLLYTTAMSQRCLALLGASGLGGAVSAFVHTTLTF
 RLSFCRSRKINSFFCDIPLLAISCDTSLNELLFAICGFIQTATVLAITVSYGFIAGAVIHMRSVE
 GSRRAASTGGSHLTAVAMMYGTLIFMYLRPSSSYALD TDKMASVFYTLVIPSLNPLIYSLRNKE
 VKEALRQTWSRFHCPGQGSQ (SEQ ID NO: 27)

40 ATGGCCTTGCCATTGCTCTTATCTCCCTCCTGCTTTGCCTCTTCTCAGTCTCTGTCCAGTAG
 GATGAACTCAGAGAACCTCACCCGGGCGCGGTTGCCCTGCTGAATTCGTCCTCCTGGGG
 ATCACAAATCGCTGGGACCTGCGTGTGGCCCTCTTCTGACCTGCCTGCCTGTCTACCTGG.
 TGAGCCTGCTGGGAAACATGGGCATGGCGCTGCTGATCCGCATGGATGCCCGGCTCCACA
 45 CACCTATGTACTTCTTCTGGCCAACCTCTCCCTGCTGGATGCCTGCTATTCTCCGCCATC
 GGCCCCAAGATGCTAGTGGACCTGCTGCTGCCCCGAGCCACCATCCCTTACACAGCCTGTG
 CCCTCCAGATGTTTGTCTTTGCAGGTCTGGCTGATACTGAGTGTTGCTTGTGTCAGCCAT
 GGCCCTATGACCGCTACGTGGCCATCAGAAACCCACTTCTCTATACAACAGCTATGTCGCAG
 CGTCTATGCCTGGCCTTGCTGGGAGCATCAGGCCTGGGTGGGGCAGTGAGTGCCTTTGTT
 50 ACACAACCTCACCTTCCGCCTGAGCTTCTGCCGCTCCCGGAAGATCAATAGCTTCTTCTG
 CGATATCCCTCCACTGCTGGCCATCTCGTGCACTGACACCACTCAATGAACTCCTTCTCT
 TCGCCATCTGTGGCTTCATCCAGACAGCCACGGTGTTAGCTATCACGGTGCTTATGGCTT
 CATCGCTGGGGCTGTGATCCACATGCGCTCGGTGCGAGGCAGTCGCGCAGCAGCCCTCCAC
 CGGTGGTTCCACCTCACAGCCGTGGCCATGATGTACGGGACACTCATTTTCATGTACCTG
 55 CGCCCCAGCTCCAGCTATGCCCTGGACACTGACAAGATGGCCTCTGTGTTCTATACCCTGG

TCATCCCGTCTCTCAACCCACTCATCTACAGCCTCCGCAATAAGGAGGTCAAGGAGGCCCT
CAGGCAGACCTGGAGCCGATTCCACTGTCCAGGGCAGGGGTCCCAGTGA (SEQ ID NO: 28)

AOLFR15 sequences:

5 MRENNQSSSTLEFILLGVTGQQEQEDFFYLFLFIYPITLIGNLLIVLAICSDVRLHNP MYFLLANLS
LVDIFFSSVTIPKMLANHLLGSKSISFGGCLTQMYFMIALGNTDSYLAAMAYDRAVAISHPLH
YTTIMSPRSCITWLIAGSWVIGNANALPHTLLTASLSFCGNQEVANFYCDITPLLKLSGSDIHFHV
KMMYLGVGIFSVPLLCIIVSYIRVFSTVFQVPSTKGVLKAFSTCGSHLTVVSLYYGTVMGTYFR
PLTNYSLKDAVITVMYTAVT PMLNPFYSLRNRDMKAALRKLFNKRIS (SEQ ID NO: 29)

10 ATGAGGGAAAATAACCAGTCCTCTACACTGGAATTCATCCTCCTGGGAGTTACTGGTCAGC
AGGAACAGGAAGATTTCTTCTACATCCTCTTCTGTTTCAATTAACCCATCACATTGATTGGA
AACCTGCTCATTGTCTAGCCATTTGCTCTGATGTTGCGCTTCAACAACCCCATGTATTTCT
CCTTGCCAACCTCTCCTTGGTTGACATCTTCTTCTCATCGGTAACCATCCCTAAGATGCTGG
15 CCAACCATCTCTTGGGCAGCAAATCCATCTCTTTTGGGGGATGCCTAACGCAGATGTATTT
CATGATAGCCTTGGGTAACACAGACAGCTATATTTGGCTGCAATGGCATATGATCGAGCT
GTGGCCATCAGCCACCCACTTCACTACACAACAATTATGAGTCCACGGTCTTGTATCTGGC
TTATTGCTGGGTCTTGGGTGATTGGAAATGCCAATGCCCTCCCCACACTCTGCTCACAGC
TAGTCTGTCTTCTGTGGCAACCAGGAAGTGGCCAACCTTCTACTGTGACATTACCCCTTG
20 CTGAAGTTATCCTGTTCTGACATCCACTTTCATGTGAAGATGATGTACCTAGGGGTTGGCA
TTTTCTCTGTGCCATTACTATGCATCATTGTCTCCTATATTCGAGTCTTCTCCACAGTCTTCC
AGGTTCTTCCACCAAGGGCGTGCTCAAGGCCTTCTCCACCTGTGGTTCACCTCACGGT
TGTCTCTTTGTATTATGGTACAGTCATGGGCACGTATTTCCGCCCTTTGACCAATTATAGCC
TAAAAGACGCAGTGATCACTGTAATGTACACGGCAGTGACCCCAATGTTAAATCCTTTCAT
25 CTACAGTCTGAGAAATCGGGACATGAAGGCTGCCCTGCGGAAACTCTTCAACAAGAGAAT
CTCCTCGTAA (SEQ ID NO: 30)

AOLFR16 sequences:

30 MRRNCTLVTEFILLGLTSRRELQILLFTFLAIYMTVAVGNLGMIVLIQANAWLHMP MYFFLSH
LSFVDLCFSSNVTPKMLEIFLSEKKSISYPACLVQCYLFIALVHVEIYILAVMAFDRYMAICNPLL
YGSRMKS SVCSFLITVPYVYGALTGLMETMWTYNLAFCGPNEINH FYCADPPLIKLACSDTYN
KELSMFIVAGWNLSFSLFIICISYLYIFPAILKIRSTEGROKAFSTCGSHLTA VTIFYATLFFMYLR
PPSKESVEQGMVA VFYTTVIPMLNLIYSLRNKNVKEALIKELSMKIYFS (SEQ ID NO: 31)

35 ATGAGAAGAACTGCACGTTGGTGACTGAGTTCATTCTCCTGGGACTGACCACTCGCCGG
GAATTACAAATTCCTCTTCAAGCTGTTTCTGGCCATTTACATGGTCACGGTGGCAGGGA
ACCTTGGCATGATTGTCTCATCCAGGCCAACGCCTGGCTCCACATGCCCATGTACTTTTTCT
CTGAGCCACTTATCCTTCGTGGATCTGTGCTTCTCTCCAATGTGACTCCAAAGATGCTGG
AGATTTTCTTTTTCAGAGAAGAAAAGCATTTCTATCCTGCCTGTCTTGTGCACTGTACCTT
40 TTTATCGCCTTGGTCCATGTTGAGATCTACATCCTGGCTGTGATGGCCTTTGACCGGTACAT
GGCCATCTGCAACCCTCTGCTTTATGGCAGCAGAATGTCCAAGAGTGTGTCTCCTTCTCTC
ATCACGGTGCTTATGTGTATGGAGCGCTCACTGGCCTGATGGAGACCATGTGGACCTACA
ACCTAGCCTTCTGTGGCCCCAATGAAATTAATCACTTCTACTGTGCGGACCCACCACTGAT
TAAGCTGGCTTGTCTGACACCTACAACAAGGAGTTGTCAATGTTTATTGTGGCTGGCTGG
45 AACCTTTCTTTTCTCTCTTTCATCATATGTATTTCTACCTTTACATTTTCCCTGCTATTTTA
AAGATTGCTCTACAGAGGGCAGGCAAAAAGCTTTTCTACCTGTGGCTCCCATCTGACAG
CTGTCACTATATTCTATGCAACCTTTTCTTTCATGTATCTCAGACCCCCCTCAAAGGAATCT
GTTGAACAGGGTAAAATGGTAGCTGTATTTTATACACAGTAATCCCTATGCTGAACCTTA
TAATTTATAGCCTTAGAAATAAAAATGTAAAAGAAGCATTAATCAAAGAGCTGTCAATGA
50 AGATATACTTTTCTTAA (SEQ ID NO: 32)

AOLFR17 sequences:

55 MLNFTDVTEFILLGLTSRREWQVLFFIIFLVVYITMVGNIGMMVLIKVSPQLNNP MYFFLSHLS
FVDVWFSSNVTPKMLENLFSDDKKTITYAGCLVQCFIFIALVHVEIFILAAMAFDRYMAIGNPLL
YGSKM SRVVCIRLITFPYTYGFLTSLAATLWTYGLYFCGKIEINH FYCADPPLIKMACAGTFVKE

YTMILAGINFTYSLTVIISYLFILAILRMRS AEGRQKAFSTCGSHLTAVIIFYGTLIFMYLRRPTE
ESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 33)

5 ATGCTCAATTTACCGATGTGACAGAGTTCATTCTTTTGGGGCTAACGAGCCGTCGAGAAT
GGCAAGTTCTCTTCTTCATCATCTTTCTTGTGGTCTACATCATCACCATGGTGGGCAATATC
GGCATGATGGTGTTAATCAAGGTCAGTCTCAGCTTAACAACCCCATGTACTTTTCTCTCA
GTCACITGTCAATTTGTTGATGTGTGGTCTTTCTTCCAATGTCACCCCTAAAATGTTGGAAAAAC
CTGTTTTAGATAAAAAACAATTACTTATGCTGGTGTGTTAGTACAGTGTCTTCTTCTCAT
10 TGCTCTTGTCCATGTGGAAATTTTATTCTTGTCTGCGATGGCCTTTGATAGATACATGGCAA
TTGGGAATCCTCTGCTTTATGGCAGTAAAATGTCAAGGGTGTCTGTATTTCGACTGATTAC
TTTCCCTTACATTTATGGTTTTCTGACGAGTCTGGCAGCAACATTATGGACTTACGGCTTGT
ACTTCTGTGGAAAAATTGAGATCAACCATTTCTACTGTGCAGATCCACCTCTCATCAAAAT
GGCCTGTGCCGGGACCTTTGTAAAAGAATATACAATGATCATACTTGCCGGCATTAACCTC
ACATATTCCTGACTGTAATTATCATCTCTTACTTATTCATCCTCATTGCCATTCTGCGAAT
15 GCGCTCAGCAGAAGGAAGGCAGAAGGCCTTTTCCACATGTGGGTCCCATCTGACAGCTGT
CATTATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCACAGAGGAGTCTGTG
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCCATGTTGAATCCCATGA
TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT
GTAA (SEQ ID NO: 34)

20

AOLFR18 sequences:

MSNTNGSAITEFILLGLTDCPELQSLFVFLVYLVTLGNLGMIMLMRLDSRLHTPMYFFLT
NLAFLVLCYTSNATPQMSTNIVSEKTISFAGCFTQCYFIALLLTFYMLAAMA YDRYVAIYDP
LRYSVKTSRRVCICLATFPYVYGFSDFLQAILTFRLTFCRSNVINHFYCADPPLIKLSCSDTYVK
25 EHAMFISAGFNLSSSLTIVLVSYAFILAILRIKSAEGRHKAFTSTCGSHMMAVTLFYGTLFCMYI
RPPTDKTVEESKIIAVFYTFVSPVLNPLIYSLRNKDVKQALKNVLR (SEQ ID NO: 35)

30 ATGTCCAACACAAATGGCAGTGCAATCACAGAATTCATTTTACTTGGGCTCACAGATTGCC
CGGAATCCAGTCTCTGCTTTTTGTGCTGTTTCTGGTGTGTTACCTCGTCACCCCTGCTAGGC
AACCTGGGCATGATAATGTTAATGAGACTGGACTCTCGCCTTCACACGCCCATGTACTTCT
TCCTCACTAACTTAGCCTTTGTGGATTTGTGCTATACATCAAATGCAACCCCGCAGATGTC
GACTAATATCGTATCTGAGAAGACCATTTCTTTGTGCTGGTGTGCTTTACACAGTGCTACATTT
TCATTGCCCTTCTACTCACTGAGTTTTACATGCTGGCAGCAATGGCCTATGACCGCTATGT
GGCCATATATGACCTCTGCGCTACAGTGTGAAAACGTCCAGGAGAGTGTGCTGCTTG
35 GCCACATTTCCCTATGTCTATGGCTTCTCAGATGGACTCTCCAGGCCATCCTGACCTCCG
CCTGACCTTCTGTAGATCCAATGTCATCAACCACCTTCTACTGTGCTGACCCGCCGCTCATT
AGCTTTCTTGTCTGATACTTATGTCAAAGAGCATGCCATGTTTATCTGCTGGCTTCAAC
CTCTCCAGCTCCCTCACCATCGTCTTGGTGTCTATGCCTTCATTCTTGTGCCATCCTCCG
GATCAAATCAGCAGAGGGAAGGCACAAGGCATTCTCCACCTGTGGTTCCCATATGATGGC
40 TGTCACCCTGTTTTATGGGACTCTTTTTGCATGTATATAAGACCACCAACAGATAAGACT
GTTGAGGAATCTAAAATAATAGCTGTCTTTTACACCTTTGTGAGTCCGGTACTTAATCCAT
TGATCTACAGTCTGAGGAATAAAGATGTGAAGCAGGCCTTGAAGAATGTCTGAGATGA
(SEQ ID NO: 36)

45 **AOLFR19 sequences:**

METKNYSSSTSGFILLGLSSNPQLQKPLFAIFLIMYLLTAVGNVLIIIAIYSDPRLHTPMYFFLSNL
SFMDICFTTVIVPKMLVNFLSETKIISYVGCLIQMYFFMAFGNTDSYLLASMAIDRLVAICNPLH
YDVVMKPWHCLLMMLGSCSISHLHSLFRVLLMSRLSFCASHIHKHFFCDTQPVKLKSCSDTSSSQ
MVVMTETLAVIVTPFLCTIFS YLQIIVTVLRIPSAAGKWKAFTSTCGSHLTVVVLFYGSVIVYFR
50 PLSMYSVMKGRVATVMYTVVTPMLNPFIIYSLRNKDMKRGLKLRHRIYS (SEQ ID NO: 37)

ATGGAGACAAAGAATTATAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCCTCTCTTCCA
ACCCTAAGCTGCAGAAACCTCTCTTTGCCATCTTCTCATCATGTACCTACTCACTGCGGTG
GGGAATGTGCTCATCATCCTGGCCATCTACTCTGACCCAGGCTCCACACCCCTATGTACT
55 TTTTCTCAGCAACTTGTCTTTTATGGATATCTGCTTCAACAGTCATAGTGCCTAAGATG
CTGGTGAATTTTCTATCAGAGACAAAGATTATCTCTTATGTGGGCTGCCTGATCCAGATGT

ACTTCTTCATGGCATTGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCG
 GCTGGTGGCCATCTGCAACCCCTTACACTATGATGTGGTTATGAAACCATGGCATTGCCTA
 CTCATGCTATTGGGTTCTTGCAGCATCTCCACCTACATTCCCTGTCCGCGTGCTACTTAT
 GTCTCGCTTGTCTTTCTGTGCCTCTCACATCATTAAAGCACTTTTTCTGTGACACCCAGCCTG
 5 TGCTAAAGCTCTCCTGCTCTGACACATCCTCCAGCCAGATGGTGGTGATGACTGAGACCTT
 AGCTGTCAATTGTGACCCCTTCTGTGTACCATCTTCTCTACCTGCAAATCATCGTCACTG
 TGCTCAGAATCCCTCTGACGCCGGGAAGTGAAGGCCTTCTCTACCTGTGGCTCCACCT
 CACTGTAGTGGTCTGTTCTATGGGAGTGTCTATGTCTATTTTAGGCCTCTGTCCATGT
 ACTCAGTGATGAAGGGCCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGA
 10 ACCCTTTCATCTACAGCCTGAGGAACAAAGATATGAAAAGGGGTTTGAAGAAATTAAGAC
 ACAGAATTTACTCATAG (SEQ ID NO: 38)

AOLFR20 sequences:

MVEENHTMKNEFILTGFTDHPCLKTLLFVFFAIYLITVVGNI SLVALIFTHCRLHTPMYIFLGN
 15 LALVDSCCACAITPKMLENFFSEGKRISLYECAVQFYFLCTVETADCFLLAAVAYDRYVAICNP
 LQYHIMMSKKLCIQMTTGAFIAGNLHSMIHVGLVFRLVFCGLNHINHFYCDTLPYRLSCVDPF
 INELVLFIFSGSVQVFTIGSVLISYLYILLTIFRMKSKEGRAKAFSTCASHFSSVSIFYSGIFFLYIRP
 NLLEEGNDIPAAILFTIVVPLNPFIFYSLRNKEVISVLRKILLKIKSQGSVNK (SEQ ID NO: 39)

20 ATGGTTGAAGAAAATCATACCATGAAAATGAGTTTATCCTCACAGGATTTACAGATCACC
 CTGAGCTGAAGACTCTGCTGTTTGTGGTGTCTTTGCCATCTATCTGATCACCGTGGTGGG
 GAATATTAGTTTGGTGGCACTGATATTTACACACTGTCGGCTTCACACACCAATGTACATC
 TTTCTGGGAAATCTGGCTCTTGTGGATTCTTGTCTGTGCCTGTGCTATTACCCCCAAAATGTT
 AGAGAACTTCTTTCTGAGGGCAAAGGATTTCCCTCTATGAATGTGCAGTACAGTTTTAT
 25 TTTCTTTCAGCTGTGGAACTGCAGACTGCTTTCTTCTGGCAGCAGTGGCCTATGACCGCT
 ATGTGGCCATCTGCAACCCACTGCAGTACCACATCATGATGTCCAAGAACTCTGCATTCA
 GATGACCACAGGCGCCTTCATAGCTGGAATCTGCATTCCATGATTTCATGTAGGGCTTGTA
 TTTAGGTTAGTTTTCTGTGGATTGAATCACATCAACCACTTTTACTGTGATACTCTTCCCTT
 GTATAGACTCTCCTGTGTTGACCCCTTTCATCAATGAAGTGGTCTATTCTCTCAGGTT
 30 CAGTTCAAGTCTTTACCATAGGTAGTGTCTTAATATCTTATCTCTATATTCTTCTACTATT
 TTCAGAATGAAATCCAAGGAGGGAAGGGCCAAAGCCTTTTCTACTTGTGCATCCCACTTTT
 CATCAGTTTCATTATTCTATGGATCTATTTTTTCTTATACATTAGACCAAATTTGCTTGAA
 GAAGGAGGTAATGATATACCAGCTGCTATTTTATTTACAATAGTAGTTCCTTACTAAATC
 CTTTCATTTATAGTCTGAGAAACAAGGAAGTAATAAGTGTCTTAAGAAAAATTCTGCTGAA
 35 AATAAAATCTCAAGGAAGTGTGAACAAATGA (SEQ ID NO: 40)

AOLFR21 sequences:

MEPRKNVTDVLLGFTQNPKEQKVLVFMFLFYILTMVGNLLIVVTVTVSETLGSPMSFFLAGL
 40 TFIDIIYSSSISPRLLISDLFFGNNSISFQSFMAQLFIEHLFGGSEVFLLLVMA YDRYVAICKPLHYLV
 IMRQWVCVLLLVVSWVGGFLQSVFQLSIYGLPFCGPNVIDHFFCDMYPLKLACTDTHVIGLL
 VVANGGLSCTIAFLLLISYGVILHSLKKLSQKGRQKAHSTCSSHITVVVFFVPCIFMCARPAR
 TFSIDKSVSVFYTVITPMLNPLIYTLRNSEMTSAMKKL (SEQ ID NO: 41)

45 ATGGAGCCAAGGAAAAATGTGACTGACTTTGTCTCTTGGGCTTCACACAGAATCCAAAG
 GAGCAGAAAGTACTTTTTGTTATGTTCTTGCTCTTCTACATTTTGACCATGGTGGGCAACCT
 GCTCATTGTAGTGACCGTAAGTGTGAGTGTGAGACCTGGGCTCACCAATGTCCTTCTTCTT
 GCTGGCTTAACATTTATAGATATCATTTATTCTTTCATCCATTTCCCCCAGATTGATTTTCA
 CTTGTTCTTTGGGAATAATTCCATATCCTTCCAATCTTTCATGGCCAGCTCTTTATCGAGC
 50 ACCTTTTTGGTGGGTGAGAGGTCTTCTCTGTTGGTGATGGCCTATGACCGCTATGTGGC
 CATCTGTAAGCCCTTGCATTATTTGGTTATCATGAGACAATGGGTGTGTGTTTTGCTGCTG
 GTAGTGTCTGGGTTGGAGGATTTCTGCAATCAGTATTTCAACTTAGCATTATTTATGGGC
 TCCCATTCTGTGGCCCAATGTCATTGATCATTTTTTCTGTGACATGTATCCCTTATTGAAA
 CTGGCCTGCACTGACACCCATGTTATTGGCCTCTTAGTGGTGGCCAATGGAGGACTGTCTT
 GCACTATTGCGTTTCTGCTCTTACTCATCTCTTATGGTGTCTATCCTGCACTCTCTAAAGAAA
 55 CTTAGTCAGAAAGGGAGGCAAAAAGCCCACTCAACCTGCAGTTCCCACATCACTGTGGTTG
 TCTTCTCTTTGTTCTTGTATTTTTATGTGTGCTAGACCTGCTAGGACCTTCTCCATTGAC

AAATCAGTGAGTGTGTTTTATACAGTCATAACCCCAATGCTGAACCCCTTAATCTACACTC
TGAGAAATTCTGAGATGACAAGTGCTATGAAGAAGCTTTAG (SEQ ID NO: 42)

AOLFR22 sequences:

5 MRXXNXXTEFVLLGFSQDPGVXKALFVMFLLTYXXTVVGNLLIVVDIIASPLGSPMYFFLAC
LSFIDAAYSTTISPKLIVGLFCDKKTISFQCGMGQLFIDHFFGGAEVFLVVMACDRYVAICKPL
HYLTIMNRQVCFLLLVXXMIGGFVHSAFQIVVYSLPFCGPXVIVHFSCDMHPLLELACTDTYFI
GLTVVVNSGAICMVIFNLLISYGVILSSLKTYSQEKRGKALSTCSSGSTVVVLFVPCIFYVRP
10 VSNFPIDKFMTVFYTIITHMLSPLIYTLRNSEMRNAIEKLLGKKLTIFIIGGVSVLM (SEQ ID NO:
43)

ATGAGACANNNNNAACAATATNACAGAATTTGTCCTCCTGGGCTTTTCTCAGGATCCTGGTG
TGNNNAAAGCATTATTTGTCATGTTTTACTCACATACNNNNNNACAGTGGTGGGGAACCT
GCTCATTGTNGTGGATATTATTGCCAGCCCTTNNTTGGGTTCCCAATGTATTTCTTCCTTG
15 CCTGCCTGTCATTTATAGATGCTGCATATTCCTACTACCATTTCTCCCAAGTTAATTGTAGGC
TTATTCTGTGATAAAAAGACTATTTCCCTCCAAGGTTGCATGGGCCAGCTATTTATAGACC
ATTTCTTTGGTGGGGCTGAGGTCTTCCTTCTGGTGGTGATGGCCTGTGATCGCTATGTGGC
CATCTGTAAGCCACTGCACTATTTGACCATCATGAATCGACAGGTTTGCTTCCTTCTGTTGG
TNNTNNCCATGATTGGAGGTTTTGTACATTCTGCGTTTCAAATTGTTGTGTACAGTCTCCCT
20 TTCTGTGGTCCCNATGTCATTGTTTCATTTTCAGTTGTGACATGCACCCATTACTGGAACCTGGC
ATGCACTGACACCTACTTTATAGGCCTCACTGTTGTTGTCAATAGTGGAGCAATCTGTATG
GTCATTTTCAACCTTCTGTAAATCTCCTATGGAGTCATCCTAAGCTCCCTTAAACTTACAG
TCAGGAAAAGAGGGGTAAAGCCTTGTCTACCTGCAGCTCCGGCAGTACCGTTGTGTCTC
TTTTTTGTACCCTGTATTTTCATATATGTTAGACCTGTTTCAAACCTTCTACTGATAAGTT
25 CATGACTGTGTTTTATACCATATCACACACATGCTGAGTCCTTTAATATATACGTTGAGA
AATTCAGAGATGAGAAATGCTATAGAAAACTCTTGGGTAAAAAGTTAACTATATTTATTA
TAGGAGGAGTGTCCGTCCTCATGTAG (SEQ ID NO: 44)

AOLFR23 sequences:

30 MAKNNLTRVTEFILMGFMDHPKLEIPLFLVFLSFYLVTLGNVGMIMLIQVDVKLYTPMYFFLS
HLSLLDACYTSVITPQILATLATGKTVISYGHCAAQFFLFTICAGTECFLLAVMAYDRYAAIRNP
LLYTVAMNPRLCWSLVVGAYVCGVSGAILRTTCTFLSFCKDNQINFFCCLPPLKLACSDTA
NIEIVIFFGNFVILANASVILISYLLIKTILKVKSSGGRAKTFSTCASHITAVAFFGALIFMYLQS
GSGKSLEEDKVVSVFYTVVIPMLNPLIYSLRNKDVKDAFRKVARRLQVSLSM (SEQ ID NO: 45)

35 ATGGCCAAGAATAATCTCACCAGAGTAACCGAATTCATTCTCATGGGCTTTATGGACCACC
CCAAATTGGAGATTCCCCTCTTCTGGTGTTCCTGAGTTTCTACCTAGTCACCCTTCTTGGG
AATGTGGGGATGATTATGTTAATCCAAGTAGATGTCAAACCTCTACACCCCAATGTACTTCT
TCCTGAGCCACCTCTCCCTGCTGGATGCCTGTTACACCTCAGTCATCACCCCTCAGATCCTA
40 GCCACATTGGCCACAGGCAAAACGGTCATCTCTACGGCCACTGTGCTGCCAGTTCCTTT
TATTCACCATCTGTGCAGGCACAGAGTGCTTTCTGCTGGCAGTGATGGCCTATGATCGCTA
TGCTGCCATTGCAACCCACTGCTCTATACCGTGGCCATGAATCCCAGGCTCTGCTGGAGC
CTGGTGGTAGGAGCCTATGTCTGTGGGGTGTGAGGAGCCATCCTGCGTACCCTTGCACCT
TCACCCTCTCCTTCTGTAAGGACAATCAAATAAACTTCTTCTTCTGTGACCTCCCACCCCTG
45 CTGAAGCTTGCCTGCAGTGACACAGCAAACATCGAGATTGTCATCATCTTCTTTGGCAATT
TTGTGATTTTGGCCAATGCCTCCGTCATCCTGATTTCTATCTGCTCATCATCAAGACCATT
TTGAAAGTGAAAGTCTTCAGGTGGCAGGGCCAAGACTTTCTCCACATGTGCCTCTCACATCA
CTGCTGTGGCCCTTTTCTTTGGAGCCCTTATCTTCATGTATCTGCAAAGTGGCTCAGGCAAA
TCTCTGGAGGAAGACAAAGTCGTGTCTGTCTTCTATACAGTGGTCATCCCCATGCTGAACC
50 CTCTGATCTACAGCTTAAGAAACAAAGATGTAAAGACGCCTTCAGAAAGGTCGCTAGGA
GACTCCAGGTGTCCCTGAGCATGTAG (SEQ ID NO: 46)

AOLFR25 sequences:

55 METGNLTWVSDFVFLGLSQTRELQRFLFVYITTVMGNILIITVTSDSLHTPMYFLLRN
LAVLDLCFSSVTAPKMLVDLLSEKKTISYQCGMGQIFFHFLGGAMVFFLSVMAFDRLLAISRP
RYVTVMNTQLWVGLVVATWVGGFVHSIVQLALMLPLPFCGPNILDNFYCDVPQVRLACTDT

SILLEFLKISNSGLLDVWVFFLLMSYLFILVMLRSHPGEARRKAASTCTTHIVVSMIFVPSIYLY
 ARPFTPFMDKLV SIGHTVMTPLNPMIYTLRNQDMQAAVRRLGRHLV (SEQ ID NO: 47)

5 ATGGAACAGGGAACCTCACGTGGGTATCAGACTTTGTCTTCCTGGGGCTCTCGCAGACTC
 GGGAGCTCCAGCGTTTCTGTCTAATGTTCCCTGTTTGTCTACATCACCAGTGTATGGGA
 AACATCCTTATCATCATCAGTGACCTCTGATTCCCAGCTCCACACACCCATGTACTTTCT
 GCTCCGAAACCTGGCTGTCTAGACCTCTGTTTCTCTTCAGTCACTGCTCCCAAATGCTAG
 TGGACCTCCTCTCTGAGAAGAAAACCATCTCTTACCAGGGCTGCATGGGTGAGATCTTCTT
 10 CTTCCACTTTTTGGGAGGTGCCATGGTCTTCTTCCTCTCAGTGATGGCCTTTGACCGCCTCA
 TTGCCATCTCCCGCCCCCTCCGCTATGTCACCGTCATGAACACTCAGCTCTGGGTGGGCT
 GGTGGTAGCCACCTGGGTGGGAGGCTTTGTCCACTCTATTGTCCAGCTGGCTCTGATGCTC
 CCACTGCCCTTCTGTGGCCCCAACATTTGGATAACTTCTACTGTGATGTTCCCCAAGTACT
 GAGACTTGCTGCACTGACACCTCACTGCTGGAGTTCTCAAGATCTCCAACAGTGGGCTG
 CTGGATGTCGTCTGTTCTTCTCCTCCTGATGTCCTACTTATTCATCCTGGTGTGCTGAG
 15 GTCACATCCAGGGGAGGCAAGAAGGAAGGCAGCTTCCACCTGCACACCCACATCATCGT
 GGTTCATGATCTTCGTTCCAAGCATTTACCTCTATGCCCGGCCCTTCACTCCATTCCCTA
 TGGACAAGCTTGTGTCCATCGGCCACACAGTCATGACCCCCATGCTCAACCCCATGATCTA
 TACCCTGAGGAACCAGGACATGCAGGCAGCAGTGAGAAGATTAGGGAGACACCGGCTGGT
 TTGA (SEQ ID NO: 48)

20

AOLFR26 sequences:

MAAKNSSVTEFILEGLTHQPLRPLFLFLGFYTVTVVGNLGLITLIGLNSHLHTPMYFFLFNLS
 LIDFCFSTTTTPKMLMSFVSRKNISFTGCMTQLFFCFFVVSSEFILLSAMAYDRYVAICNPPLYT
 25 VTMSQVCLLLLLGAYGMGFAGAMAHGTGIMNLTFCADNLVNHFMCDILPILLESCNSSSYM
 ELVVFVVAVDVGMPIVTVFISYALILLSLHNSSTEGRSKAFSTCSSHIVVSLFFGSGAFMYLKP
 LSILPLEQKGVSSLFYTHVPVLNPLIYSLRNKDKVALRRTLGRKIFS (SEQ ID NO: 49)

ATGGCAGCCAAAACTCTTCTGTGACAGAGTTTATCCTCGAAGGCTTAACCCACCAGCCGG
 GACTGCGGATCCCCCTCTTCTCCTGTTTCTGGGTTCCTACACGGTCACCGTGGTGGGGAA
 30 CCTGGGCTTGATAACCTGATTGGGCTGAACCTCTCACCTGCACACTCCCATGTACTTCTTCC
 TTTTAACTCTCTTTAATAGATTTCTGTTTCTCCACTACCATCACTCCCAAAATGCTGATG
 AGTTTTGTCTCAAGGAAGAACATCTTCTTCCAGGGTGTATGACTCAGCTCTTCTTCTT
 CTGCTTCTTTGTCGTCTCTGAGTCCTTCATCCTGTGCGATGGCGTATGACCGCTACGTGG
 CCATGTGTAACCCACTGTTGTACACAGTCACCATGTCTTGCCAGGTGTGTTTGTCTTTTG
 35 TTGGGTGCCTATGGGATGGGGTTTGCTGGGGCCATGGCCACACAGGAAGCATAATGAAC
 CTGACCTTCTGTGCTGACAACCTTGTCATTCATGTGTGACATCCTTCTCCTTGGA
 GCTCTCCTGCAACAGCTCTTACATGAATGAGCTGGTGGTCTTTATTGTGGTGGCTGTTGAC
 GTTGAATGCCCATTTGCACTGTCTTTATTCTTATGCCCTCATCCTCTCCAGCATTCTACA
 CAACAGTTCTACAGAAGGCAGGTCCAAAGCCTTATGACTTGCAGTTCCACATAATTGTA
 40 GTTCTCTTTTCTTTGGTTCTGGTGCTTTCATGTATCTCAAACCCCTTTCCATCCTGCCCTC
 GAGCAAGGGAAAGTGTCTCCTGTTCTATACCATAATAGTCCCCGTGTTAAACCCATTAA
 TCTATAGCTTGAGGAACAAGGATGTCAAAGTTGCCCTGAGGAGAACTTTGGGCAGAAAAA
 TCTTTTCTTAA (SEQ ID NO: 50)

AOLFR27 sequences:

MPSQNYSISEFNLFGFSAFPQHLLPILFLLYLLMFLFTLLGNLLIMATIWIEHRLHTPMYFLCTL
 SVSEILFTVAITPRMLADLLSTHHSITFVACANQMFFSFMFGFTHSFLLLVMGYDRYVAICHPLR
 YNVLMSPRDCAHLVACTWAGGSVMGMMVTTIVFHLTFGCSNVIHHFFCHVLSLLKLACENKT
 SSVIMGVMLVCVTALIGCLFLIILSYVFIVAAILRIPSAEGRHKTFSTCVSHLTVVVTHYSFASFIY
 50 LKPKGLHSMYSDALMATTYTVFTPLSPIIFSLRNKELKNAINKNFYRKFCPPSS (SEQ ID NO:
 51)

ATGCCTAGTCAGAACTATAGCATCATATCTGAATTTAACTCTTTGGCTTCTCAGCCTTCCC
 CCAGCACCTCCTGCCCATCTTGTTCCTGCTGTACCTCCTGATGTTCTGTTACATTGCTGG
 55 GCAACCTTCTCATCATGGCCACAATCTGGATTGAACACAGACTCCACACACCCATGTACCT
 CTTCTGTGCACCTCTCCGTCTCTGAGATTCTGTTCACTGTGCCATCACCCCTCGCATGC

TGGCTGATCTGCTTTCCACCCATCATTCCATCACCTTTGTGGCTTGTGCCAACCAGATGTTC
 TTCTCCTTCATGTTTGGCTTCACTCACTCCTTCCTTCTCCTGGTCATGGGCTATGATCGCTA
 TGTGGCCATCTGCCACCCACTGCGTTACAATGTGCTCATGAGCCCCCGTGA CTGTGCCCAT
 CTTGTGGCCTGTACCTGGGCTGGTGGCTCAGTCATGGGGATGATGGTGACAACGATAGTTT
 5 TCCACCTCACTTTCTGTGGGTCTAATGTGATCCACCATTCTTCTGTGTCATGTGCTTTCCCTCT
 TGAAGTTGGCCTGTGAAAACAAGACATCATCTGTCATCATGGGTGTGATGCTGGTGTGTGT
 CACAGCCCTGATAGGCTGTTTATTCCTCATCATCCTCTCCTATGTCTTCATTGTGGCTGCCA
 TCTTGAGGATTCCCTCTGCCGAAGGCCGGCACAAGACATTTTCTACGTGTGTATCCACCT
 CACTGTGGTGGTCACGCACTATAGTTTTCCTCCTTTATCTACCTCAAGCCCAAGGGCTCC
 10 ATTCTATGTACAGTGACGCTTGATGGCCACCACCTATACTGTCTTCACCCCTTCCTTAGC
 CCAATCATTTTTCAGCCTAAGGAACAAGGAGCTGAAGAATGCCATAAATAAAAACTTTTACA
 GAAAATTCTGTCTCTCAAGTTCCTGA (SEQ ID NO: 52)

AOLFR28 sequences:

15 MPNFTDVTEFTLLGLTCRQELQVLFFVFLAVYMITLLGNIGMIILISISPQLQSPMYFFLSHLSF
 ADVCFSSNVTPKMLENLLSEKTI SYVGLVQCYFFIAVHVHVEVYLAVMAFD RYMAGCXPLL
 YGSKMSRTVCVRLISVXYXYGFSVSLICTLW TYGLYFCGNFEINH FYCADPPLIQIACGRVHIKE
 ITMIVIAGINF TYSLSVLISYTLIVVAVLRMR SADGRRKAFSTCGSHLTAVSMFYGTPIFMYLR
 RPTEESVEQGKMVA VFYTTVIPMLNPMIYSLRNKDVKEAVNKAITKTYVRQ (SEQ ID NO: 53)

20 ATGCCTAATTTACGGATGTGACAGAATTTACTCTCCTGGGGCTGACCTGTCTGTCAGGAGC
 TACAGGTTCTCTTTTTTGTGGTGTTCTAGCGGTTTACATGATCACTCTGTTGGGAAATATT
 GGTATGATCATTTTATTAGCATCAGTCCTCAGCTTCAGAGTCCCATGTACTTTTTCTGAG
 TCATCTGTCTTTTGC GGACGTGTGCTTCTCCTCCAACGTTACCCCCAAAATGCTGGAAAAC T
 25 TATTATCAGAGACAAAAACCATTTCTATGTGGGATGCTTGGTGCACTGCTACTTTTTCAT
 TGCCGTTGTCCACGTGGAGGTCTATATCCTGGCTGTGATGGCCTTTGACAGGTACATGGCC
 GGCTGCAANCCTCTGCTTTATGGCAGTAAAATGTCTAGGACTGTGTGTGTTCCGGCTCATCT
 CTGTGNNNTATGNNTATGGATTCTCTGTGACGCTAATATGCACACTATGGACTTATGGCTT
 ATACTTCTGTGGAACTTTGAAATCAATCACTTCTATTGTGCAGATCCCCCTCTCATCCAGA
 30 TGCCTGTGGGAGAGTGCACATCAAAGAAATCACAATGATTGTTATTGCTGGAATTAAC TT
 CACATATCCCTCTCGGTGGTCCTCATCTCCTACACTCTCATTGTAGTAGCTGTGCTACGCA
 TGGCTCTGCCGATGGCAGGAGGAAGGCGTTCTCCACCTGTGGGTCCC ACTTGACGGCTGT
 TTCTATGTTTTATGGGACCCCATCTTCATGTATCTCAGGAGACCCACTGAGGAATCCGTA
 GAGCAGGGCAAAATGGTGGCTGTGTTTTACACCACAGTAATTCCTATGTTGAATCCCATGA
 35 TCTACAGTCTGAGAAATAAGGATGTAAAAGAAGCAGTCAACAAAGCAATCACCAAGACAT
 ATGTGAGGCAGTAA (SEQ ID NO: 54)

AOLFR29 sequences:

40 MMSFAPNASHSPVFLLLGFSRANISYTLFFLFLAIYLTTLGNVTLVLLISWDSRLHSPMYYLLR
 GLSVIDMGLSTVTL PQLLAHLVSHYPTIPAARCLAQFFFFYAFGVTDTLVIAVMALDRYVAICD
 PLHYALVMNHQRCACLLALSWVVSILHTMLRVGLVPLCWTGDAGGNVNLPHFFCDHRPLLR
 ASCSDIHSNELAIFFE GGF LMLGPCALIVLSYVRIGAAILRLPSAAGRRAVSTCGSHLT MVGFL
 YGTIICVYFQPPFQNSQYQDMVASV MYTAITPLANPFVYSLHNKDVKGALCRLLEWVKVDP
 (SEQ ID NO: 55)

45 ATGATGAGCTTTGCCCCTAATGCTTCACACTCTCCGGTTTTTTTGTCTCCTGGGTTCTCGAG
 AGCTAACATCTCCTACACTCTCCTCTTCTTCTGTTCTGGCTATTTACCTGACCACCATAC
 TGGGGAATGTGACACTGGTGCTGCTCATCTCCTGGGACTCCAGACTGCACTCACCCATGTA
 TTATCTGCTTCGTGGCCTCTCTGTGATAGACATGGGGCTATCCACAGTTACACTGCCCCAG
 50 TTGCTGGCCCAATTTGGTCTCTCATTACCCAACCATTCCTGCTGCCCGCTGCTTGGCTCAGTT
 CTTTTCTTCTATGCATTTGGGGTTACAGATACACTTGTGCTTGTGCTGCTGCTGCTGATC
 GCTATGTGGCCATCTGTGACCCCTGCACTATGCTTTGGTAATGAATCACCAACGGTGTGCTG
 CTGCTTACTAGCCTTGAGCTGGGTGGTGTCCATACTGCACACCATGTTGCGTGTGGGACTC
 GTCCTGCCTCTTTGCTGGACTGGGGATGCTGGGGGCAACGTTAACCTTCCTCACTTCTTTTG
 55 TGACCACCGGCCACTTCTGCGAGCCTCTTGTCTGACATACATTCTAATGAGCTGGCCATA
 TTCTTTGAGGGTGGCTTCCTTATGCTGGGCCCTGTGCCCTCATTGTACTCTCTTATGTCCG

AATTGGGGCCGCTATTCTACGTTTGCCTTCAGCTGCTGGTCGCCGCCGAGCAGTCTCCACC
TGTGGATCCCACCTCACCATGGTTGGTTTCCTCTACGGCACCATCATTTGTGTCTACTTCCA
GCCTCCCTTCCAGAACTCTCAGTATCAGGACATGGTGGCTTCAGTAATGTATACTGCCATT
ACACCTTTGGCCAACCCATTTGTGTATAGCCTCCACAATAAGGATGTCAAGGGTGCACCTCT
5 GCAGGCTGCTTGAATGGGTGAAGGTAGACCCCTGA (SEQ ID NO: 56)

AOLFR30 sequences:

MGFLSPMHPCRPPTQRRMAAGNHSTVTEFLKGLTKRADLQLPLFLLFLGIYLVTTVGNLGMIT
LICLNSQLHTPMYYFLSNLSLMDLCYSSVITPKMLVNFVSEKNISYAGCMSQLYFFLVFVIAEC
10 YMLTVMAYDRYVXXCHPLLNYIIMSHHTCLLLVAVVYAIGLIGSTIETGLMLKLPYCEHLISHY
FCDILPLMKLSCSSTYDVEMTVFFSAGFNIVTSLTVLVSYTFILSSILGISTTEGRSKAFSTCSSHL
AAVGMFYGSTAFMYLKPSTISSLTQENVASVFYTTVPMLNPLIYSLRNKEVKAAVQKTLRGK
LF (SEQ ID NO: 57)

15 ATGGGGTTCTTGTCTCCCATGCATCCCTGCAGGCCTCCCACCCAGAGGAGAATGGCTGCAG
GAAATCACTCTACAGTGACAGAGTTCATTCTCAAGGGTTTAACGAAGAGAGCAGACCTCC
AGCTCCCCCTCTTTCTCCTCTTCCTCGGGATCTACTTGGTCACCATCGTGGGGAACTGGGC
ATGATCACTCTAATTTGTCTGAACCTCAGCTGCACACCCCATGTACTACTTTCTCAGCAA
TCTGTCACTCATGGATCTCTGCTACTCTCCGTCATTACCCCTAAGATGCTGGTGAACCTTTG
20 TGTGAGAGAAAAACATCATCTCCTACGCAGGGTGCATGTCACAGCTCTACTTCTTCCTTGT
TTTTGTCAATGCTGAGTGTTACATGCTGACAGTGATGGCCTACGACCGCTATGTTGNCNTC
TGCCACCTTTGCTTTACAACATCATTATGTCTCATCACACCTGCCTGCTGCTGGTGGCTGT
GGTCTACGCCATCGGACTCATTGGCTCCACAATAGAACTGGCCTCATGTTAAACTGCCCT
TATTGTGAGCACCTCATCAGTCACTACTTCTGTGACATCCTCCCTCTCATGAAGCTGTCTCTG
25 CTCTAGCACCTATGATGTTGAGATGACAGTCTTCTTTTCGGCTGGATTCAACATCATAGTC
ACGAGCTTAACAGTTCTTGTTCCTTACACCTTCATTCTCTCCAGCATCCTCGGCATCAGCAC
CACAGAGGGGAGATCCAAAGCCTTCAGCACCTGCAGCTCCCACCTTGCAGCCGTGGGAAT
GTTCTATGGATCAACTGCATTATGTACTTAAACCCTCCACAATCAGTTCCTTGACCCAG
GAGAATGTGGCCTCTGTGTTCTACACCACGGTAATCCCCATGTTGAATCCCCTAATCTACA
30 GCCTGAGGAACAAGGAAGTAAAGGCTGCCGTGCAGAAAACGCTGAGGGGTAAACTGTTTT
GA (SEQ ID NO: 58)

AOLFR31 sequences:

MGTGNDTTVVEFTLLGLSEDTTVCAILFLVFLGIYVVTLMGNISIVLIRRSHELLHTPMYIFLCHL
35 AFVDIGYSSSVTPVMLMSFLRKETSLPVAGCVAQLCSVVTFGTAECFLAAMAYDRYVAICSP
LLYSTCMSPGVCILVGMSYLGCVNAWTFIGCLRLSFCGPNKVNHHFCDYSPLLKACSHDF
TFEIIPISSGSIIVATVCVIAISYTYILITLKMHSYKGRHKAFTSTSHLTAVTLFYGTITFIYVMP
KSSYSTDQNKVVSVFYTVVIPMLNPLIYSLRNKEIKGALKRELRIKIFS (SEQ ID NO: 59)

40 ATGGGGACTGGAAATGACACCACTGTGGTAGAGTTTACTCTTTTGGGGTTATCTGAGGATA
CTACAGTTTGTGCTATTTTATTTCTTGTGTTTCTAGGAATTTATGTTGTCACCTTAATGGGT
AATATCAGCATAATTGTATTGATCAGAAGAAGTCATCATCTTCATACACCCATGTACATTT
TCCTCTGCCATTTGGCCTTTGTAGACATTGGGTACTCCTCATCAGTCACACCTGTCATGCTC
ATGAGCTTCCTAAGGAAAGAAACCTCTCTCCCTGTTGCTGGTTGTGTGGCCCAGCTCTGTT
45 CTGTAGTGACGTTTGGTACGGCCGAGTGCTTCTGCTGGCTGCCATGGCCTATGATCGCTA
TGTGGCCATCTGCTCACCCCTGCTCTACTCTACCTGCATGTCCCCTGGAGTCTGCATCATCT
TAGTGGGCATGTCTACCTGGGTGGATGTGTGAATGCTTGGACATTCAATTGGCTGCTTATT
AAGACTGTCCTTCTGTGGGCCAAATAAAGTCAATCACTTTTCTGTGACTATTACCACTTT
TGAAGCTTGCTTGTTCCCATGATTTTACTTTTGAAATAATTCCAGCTATCTCTTCTGGATCT
50 ATCATTGTGGCCACTGTGTGTGTCATAGCCATATCCTACATCTATATCCTCATCACCATCCT
GAAGATGCACTCCACCAAGGGCCGCCACAAGGCCTTCTCCACCTGCACCTCCCACCTCACT
GCAGTCACTCTGTTCTATGGGACCATTACCTTCATTTATGTGATGCCCAAGTCCAGTCACTC
AACTGACCAGAACAAAGGTGGTGTCTGTGTTCTACACCGTGGTGATTCCCATTGTAACCCC
CTGATCTACAGCCTCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTAGAATA
55 AAAATATTTTCTTGA (SEQ ID NO: 60)

AOLFR32 sequences:

MNSLKDGNHTALTGFILLGLTDDPILRVILFMILSGNLSIILIRISSQLHHPMYFFLSHLAFADM
 AYSSSVTPNMLVNFLVERNTVSYLGCAIQLGSAFFATVECVLLAAMAYDRFVAICSPLLYSTK
 MSTQVSVQLLLVVYIAGFLIAVSYTTSFYLLFCGPNQVNHFFCDFAPLLELSCSDISVSTVVLST
 5 SSGSIIVTVCVIAVCYIYLITLKMIRSTEGHHKAFSTCTSHLTVVTLFYGTITFIYVMPNFSYST
 DQNKVSVLYTVVIPMLNPLIYSLRNKEIKGALKRELVRKILSHDACYFSRTSNNIT (SEQ ID
 NO: 61)

10 ATGAATTCCTGAAGGACGGGAATCACACCGCTCTGACGGGGTTCATCCTATTGGGCTTAA
 CAGATGATCCAATCCTTCGAGTCATCCTCTTCATGATCATCCTATCTGGTAATCTCAGCATA
 ATTATCTTATCAGAATTTCTTCTCAGCTCCATCATCCTATGTATTTCTTTCTGAGCCACTT
 GGCTTTTGCTGACATGGCCTATTCATCTTCTGTACACCCCAACATGCTTGTAACATTCCTGG
 TGGAGAGAAAATACAGTCTCCTACCTTGGATGTGCCATCCAGCTTGGTTGACGGCTTTCTT
 TGCAACAGTCGAATGCGTCCTTCTGGCTGCCATGGCCTATGACCGCTTTGTGGCAATTTGC
 15 AGTCCACTGCTTTATTCAACCAAAATGTCCACACAAGTCAGTGTCCAGCTACTCTTAGTAG
 TTTACATAGCTGGTTTTCTCATTGCTGTCTCTATACTACTTCTTCTATTTTTTACTCTTCT
 GTGGACCAAAATCAAGTCAATCATTTTTTCTGTGATTTGCTCCCTTACTTGAACCTCTCTGT
 TCTGATATCAGTGTCTCCACAGTTGTTCTCTCATTTTCTTCTGGATCCATCATTGTGGTCAC
 TGTGTGTGTCATAGCCGTCTGCTACATCTATATCCTCATCACCATCCTGAAGATGCGCTCCA
 20 CTGAGGGGGCACCACAAGGCCTTCTCCACCTGCACTTCCACCTCACTGTGGTTACCCTGTT
 CTATGGGACCATTACCTTCATTTATGTGATGCCCAATTTTAGCTACTCAACTGACCAGAAC
 AAGGTGGTGTCTGTGTTGTACACAGTGGTGATTCCCATGTTGAACCCCTGATCTACAGCC
 TCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTGTTAGAAAAATACTTTCTC
 ATGATGCTTGTTATTTTAGTAGAACTCAAATAATGATATTACATAG (SEQ ID NO: 62)

25

AOLFR34 sequences:

MLEGVEHLLLLLLTDVNSKELQSGNQTSVSHFILVGLHHPQLGAPLFLAFLVITYLLTVSGNG
 LIILTVDIRLHRPMCLFLCHLSFLDMTISCAIVPKMLAGFLLGSRHSFGGCVIQLFSFHLGCT
 ECFLYTLMAFYDRFLAICKPLHYATIMTHRVCNLSALGTWLGGTIHSFQTSFVRLPFCGPNRV
 30 DYIFCDIPAMRLACADTAINELVTFADIGFLALTCFMLILTSYGYVAAILRIPSADGRRNAFST
 CAAHLTVVIVYYVPCTFIYLRPCSQEPLDGVVAVFYTVITPLNSIYTLCKEMKAALQRLGG
 HKEVQPH (SEQ ID NO: 63)

35 ATGTTAGAGGGTGTGAGCATCTCCTTCTGCTACTTCTTTTGACAGATGTGAACAGCAAGG
 AACTGCAAAGTGGAACAGACTTCTGTGTCTCACTTCATTTTGGTGGGCTGCACCAACC
 ACCACAGCTGGGAGCGCACTCTTCTTAGCTTCTTCTGTCATCTATCTCCTCACTGTTTCTG
 GAAATGGGCTCATCATCCTCACTGTCTTAGTGGACATECGGCTCCATCGTCCCATGTGCTT
 GTTCTGTGTCACTCTCCTTCTTGGACATGACCATTTCTTGTGCTATTGTCCCAAGATGC
 TGGCTGGCTTTCTTGGGTAGTAGGATTATCTCCTTGGGGGCTGTGTAATCCAACATTTT
 40 TCTTTCCATTTCTTGGGCTGTACTGAGTGCTTCTTTACACACTCATGGCTTATGACCGTTT
 CCTTGCCATTTGTAAGCCCTTACACTATGCTACCATCATGACCCACAGAGTCTGTAACCTCC
 TGGCTTTAGGCACCTGGCTGGGAGGGACTATCCATTCATTTTCCAAACAAGTTTGTATT
 CCGGCTGCCCTTCTGTGGCCCCAATCGGGTGCAGTACATCTTCTGTGACATTCTGCCATGC
 TGCCTTAGCCTGCGCCGATACGGCCATCAACGAGCTGGTCACCTTTCAGACATTGGCTT
 45 CCTGGCCCTCACCTGCTTCATGCTCATCCTCACTTCTATGGCTATAATTGTAGCTGCCATCC
 TGCGAATTCGGTCAGCAGATGGGCGCCGCAATGCCTTCTCCACTTGTGCTGCCACCTCAC
 TGTGTGCTATTGTTTACTATGTGCCCTGCACCTTCATTTACCTGCGGCCTTGTTCACAGGAGC
 CCCTGGATGGGGTGGTAGCTGTCTTTTACACTGTCACTACTCCCTTGCTTAACCTCCATCATC
 TACACACTGTGCAACAAAGAAATGAAGGCAGCATTACAGAGGCTAGGGGGCCACAAGGAA
 50 GTGCAGCCTCACTGA (SEQ ID NO: 64)

AOLFR35 sequences:

MEPLNRTEVSEFFLKGFSGYPALHLLFPLCSAMYLVTLLGNTAIMAVSVLDIHLHTPVYFFLG
 NLSTLDICYTPTFVPLMLVHLLSSRKTISFAVCAIQMCLSLSTGSTECLLAITAYDRYLAICQPL
 55 RYHVLMSHRLCVLLMGAAWVLCCLKSVTEMVISMRLPFCGHVVSHTCKILAVLKLACGNT
 SVSEDFLLAGSILLPVPLAFICLSYLLILATILRVPSAARCKAFSTCLAHLAVVLLFYGTIIFMY

LKPKSKEAHISDEVFTVLYAMVTTMLNPTTYSLRNKEVKEAARKVWGRSRASR (SEQ ID NO: 65)

5 ATGGAGCCGCTCAACAGAACAGAGGTGTCCGAGTTCTTTCTGAAAGGATTTTCTGGCTACC
CAGCCCTGGAGCATCTGCTCTTCCCTCTGTGCTCAGCCATGTACCTGGTGACCCCTCCTGGG
GAACACAGCCATCATGGCGGTGAGCGTGCTAGATATCCACCTGCACACGCCCCGTGTACTTC
TTCTGGGCAACCTCTCTACCTGGACATCTGCTACACGCCCCACCTTTGTGCTCTGATGCT
GGTCCACCTCCTGTCATCCCGGAAGACCATCTCCTTTGCTGTCTGTGCCATCCAGATGTGTC
TGAGCCTGTCCACGGGCTCCACGGAGTGCTGCTACTGGCCATCACGGCCTATGACCGCTA
10 CCTGGCCATCTGCCAGCCACTCAGGTACCAGTGCTCATGAGCCACGGCTCTGCGTGCTG
CTGATGGGAGCTGCCTGGGTCTCTGCCTCCTCAAGTCGGTGACTGAGATGGTCATCTCCA
TGAGGCTGCCCTTCTGTGGCCACCACGTGGTCAGTCACTTACCTGCAAGATCCTGGCAGT
GCTGAAGCTGGCATGCGGCAACACGTGCGTCAGCGAAGACTTCTGCTGGCGGGCTCCAT
CCTGCTGCTGCCTGTACCCCTGGCATTCTGCTGCTCCTACTTGCTCATCCTGGCCACCA
15 TCCTGAGGGTGCCCTCGGCCGCCAGGTGCTGCAAGCCTTCTCCACCTGCTTGGCACACCT
GGCTGTAGTGCTGCTTTTCTACGGCACCATCATCTTCATGTACTTGAAGCCCAAGAGTAAG
GAAGCCCATCTCTGATGAGGTCTTACAGTCCTCTATGCCATGGTCACGACCATGCTGA
ACCCACCATCTACAGCTGAGGAACAAGGAGGTGAAGGAGGCCGCCAGGAAGGTGTGGG
GCAGGAGTCGGGCCTCCAGGTGA (SEQ ID NO: 66)

20

AOLFR36 sequences:

MYLVTVLRNLLSILAVSSDSHPHTPMYFFLSNLCWADIGFTLATVPKMIVDMGSHSKVISYGG
CLTQMSFLVLFACIVDMFLTVMAYDCFVAICRPLHYPVIVNPHLCVFFVLVSFFLSLLDSQLHS
WIVLQFTFFKNVEISNFVCEPSQLKLASYDSVINSIFYDNTMFGFLPISGILLSYKIVPSILRIS
25 SSDGKYKAFSACGCHLAVVCLFYGTGIGVYLTSAVAPPLRNGMVASVMYAVVTPMLNPFYIS
LRNRDIQSALWRVCNKTVESHDLFHPFSCVVEKGPHSIPTSANPAP (SEQ ID NO: 67)

30 ATGTATCTGGTCACGGTGCTGAGGAACCTGCTCAGCATCCTGGCTGTCAGCTCTGACTCCC
ACCCCCACACACCCATGTACTTCTTCTTCCAACTGTGCTGGGCTGACATCGGTTTCACC
TTGGCCACGGTTCCTCAAAATGATTGTGGACATGGGGTCGCATAGCAAAGTCATCTCTTATG
GGGGCTGCCTGACACAGATGTCTTTCTTGGTACTTTTTGCATGTATAGTAGACATGTTCTT
GACTGTGATGGCTTATGACTGCTTTGTAGCCATCTGTCGCCCTCTGCACTACCCAGTCATC
GTGAATCCTCACCTCTGTGCTTCTTCTGTTTGGTGTCTTTTCTTACCTGTTGGATTCC
CAGCTGCACAGTTGGATTGTGTTACAATTCACTTCTTCAAGAATGTGGAATCTCTAATT
35 TTGTCTGTGAGCCATCTCAACTTCTCAAGCTTGCCTCTTATGACAGCGTCATCAATAGCATA
TTCATATATTTTGATAATACTATGTTTGGTTTTCTTCCCATTTTCAAGGATCCTTTTGTCTTAC
TATAAAATTGTCCCTCCATTCTAAGGATTTCATCATCAGATGGGAAGTACAAAGCCTTCT
CAGCCTGTGGCTGTCACCTGGCAGTTGTTTGCTTATTTTATGGAACAGGCATTGGCGTGTA
CCTGACTTCAGCTGTGGCACCACCCCTCAGGAATGGTATGGTGGCGTCAGTGATGTACGCT
40 GTGGTCACCCCATGCTGAACCCTTTCATCTACAGCCTGAGAAACAGGGACATTCAAAGTG
CCCTGTGGAGGGTGTGCAACAAAACAGTCGAATCTCATGATCTGTTCCATCCTTTTTCTTG
TGTGGTTGAGAAAGGGCAACCACATTCAATCCCTACATCTGCAAATCCTGCCCCCTTAG
(SEQ ID NO: 68)

AOLFR37 sequences:

45 MEKANETSPVMGFVLLRLSAHPELEKTFVLLILMYLVILLGNGVLILVTILDSRLHTPMYFFLG
NLSFLDICFTTSSVPLVLDSTLPQETISFSACAVQMALSFAMAGTECLLSMMAFDTRYVAICNP
LRYSVIMSKAAYMPMAASSWAIGGAASVVHTSLAIQLPFCGDNVINHFTCEILAVLKLACADIS
INVISMEVTNVIFLGVPVLFISFSYVFITILRIPSAEGRKKVFSTCSAHLTVVIVFYGTLLFFMYG
50 KPKSKDSMGADKEDLSKLIPLFYGVVTPMLNPIIYSLRNKDVKAAVRLLRPKGFTQ (SEQ ID
NO: 69)

55 ATGGAAAAAGCCAATGAGACCTCCCCTGTGATGGGGTTCGTTCTCCTGAGGCTCTCTGCCC
ACCCAGAGCTGGAAAAGACATTCTTCGTGCTCATCCTGCTGATGTACCTCGTGATCCTGCT
GGGCAATGGGGTCTCATCCTGGTGACCATCCTTGACTCCCGCCTGCACACGCCCCATGTAC
TTCTTCTAGGGAACCTCTCCTTCTGGACATCTGCTTCACTACCTCCTCAGTCCCACTGGT

CCTGGACAGCTTTTTGACTCCCCAGGAAACCATCTCCTTCTCAGCCTGTGCTGTGCAGATG
 GCACTCTCCTTTGCCATGGCAGGAACAGAGTGCTTGCTCCTGAGCATGATGGCATTGTATC
 GCTATGTGGCCATCTGCAACCCCTTAGGTACTCCGTGATCATGAGCAAGGCTGCCTACAT
 GCCCATGGCTGCCAGCTCCTGGGCTATTGGTGGTGCTGCTTCCGTGGTACACACATCCTTG
 5 GCAATTCAGCTGCCCTTCTGTGGAGACAATGTCATCAACCACTTACCTGTGAGATTCTGG
 CTGTTCTAAAGTTGGCCTGTGCTGACATTTCCATCAATGTGATCAGCATGGAGGTGACGAA
 TGTGATCTTCTAGGAGTCCCGTTCTGTTTCATCTTTCTCCTATGTCTTCATCATCACCA
 CCATCCTGAGGATCCCCTCAGCTGAGGGGAGGAAAAAGGTCTTCTCCACCTGCTCTGCCCA
 CCTCACCCTGGTGATCGTCTTCTACGGGACCTTATTCTTCATGTATGGGAAGCCTAAGTCT
 10 AAGGACTCCATGGGAGCAGACAAAGAGGATCTTTCAGACAAACTCATCCCCCTTTTCTATG
 GGGTGGTGACCCGATGCTCAACCCCATCATCTATAGCCTGAGGAACAAGGATGTGAAGG
 CTGCTGTGAGGAGACTGCTGAGACCAAAAGGCTTCACTCAGTGA (SEQ ID NO: 70)

AOLFR38 sequences:

15 MYLVTVLRNLLILAVSSDHLHTPMCFFLSNLCWADIGFTSAMVPMIVDMQSHSRVISYAGC
 LTQMSFFVLFIACIEDMLLTVMAYDRFVAICHPLHYPVIMNPHLGVFLVLSFFLSLLDSQLHSW
 IVLQFTFFKNVEISNFVCDPSQLNLACSDSVINSIFTYLD SIMFGFLPISGILLSYANNVPSILRISS
 SDRKSKAFSTCGSHLAVVCLFYGTGIGVYLTSAVSPPRNGVVASVMYAVVTPLMNPFTYSLR
 NRDIQSALWRLRSRTVESHDLLSQDLLHPFSCVGEKGQPH (SEQ ID NO: 71)
 20
 ATGTACCTGGTCACGGTGCTGAGGAACCTGCTCATCATCCTGGCTGTCAGCTCTGACTCCC
 ACCTCCACACCCCCATGTGCTTCTTCTCTCCAACCTGTGCTGGGCTGACATCGGTTTCACC
 TCGGCCATGGTTCCCAAGATGATTGTGGACATGCAGTCGCATAGCAGAGTCATCTTTATG
 CGGGCTGCCTGACACAGATGTCTTTCTTTGTCCTTTTGCATGTATAGAAGACATGCTCCTG
 25 ACAGTGATGGCCTATGACCGATTTGTGGCCATCTGTACCCCTGCACTACCCAGTCATCA
 TGAATCCTCACCTTGGTGTCTTCTTAGTTTTGGTGTCTTTTCTCAGCCTGTTGGATTCC
 CAGCTGCACAGTTGGATTGTGTTACAATTACCTTCTTCAAGAATGTGGAATCTCCAATT
 TTGCTGTGACCCATCTCAACTTCTCAACCTTGCTGTTCTGACAGTGTCTCATCAATAGCATA
 TTCATATATTTAGATAGTATTATGTTTGGTTTTCTTCCCATTTTCAGGGATCCTTTTGTCTTAC
 30 GCTAACAATGTCCCCTCCATTCTAAGAATTTTCATCATCAGATAGGAAGTCTAAAGCCTTCT
 CCACCTGTGGCTCTCACCTGGCAGTTGTTTGCTTATTTTATGGAACAGGCATTGGCGTGTA
 CCTGACTTCAGCTGTGTACCAACCCCCCAGGAATGGTGTGGTGGCATCAGTGATGTACGCT
 GTGGTCACCCCATGCTGAACCTTTTCATCTACAGCCTGAGAAATAGGGACATTCAAAGTG
 CCCTGTGGAGGCTGCGCAGCAGAACAGTCGAATCTCATGATCTGTTATCTCAAGATCTGCT
 35 CCATCCTTTTTCTTGTGTGGGTGAGAAAGGTCAACCACATTAA (SEQ ID NO: 72)

AOLFR39 sequences:

MGVKNHSTVTEFLLSGLTEQAEQLPLFCLFLGIYTVTVVGNLSMISIRLNRLHTPMYYFLSS
 LSFLDFCYSSVITPKMLSGFLCRDRSISYSGCMIQLFFFCVCVISECYMLAAMACDRYVAICSP
 40 LYRVIMSPRVCSLLVAAVFSVGFTDAVIHGGCILRLSFCGSNIKHIFCDIVPLIKLSCSSTYDEL
 LIFVIGGFNMVATSLTIIISYAFILTSILRIHKKGRCKAFSTCSSHLTAVLMFYGSLMSMYLKPAS
 SSSLTQEKVSSVFYTTVILMLNPLIYSLRNNEVRNALMKLLRRKISLSPG (SEQ ID NO: 73)
 ATGGGTGTAAAAAACCATTCCACAGTGACTGAGTTTCTTCTTTTCAGGATTAACCTGAACAAG
 45 CAGAGCTTCAGCTGCCCTCTTCTGCCTCTTCTTAGGAATTTACACAGTTACTGTGGTGGG
 AAACCTCAGCATGATCTCAATTATTAGGCTGAATCGTCAACTTCATACCCCATGTACTAT
 TTCCTGAGTAGTTTGTCTTTTTTAGATTTCTGCTATTCTTCTGTCTATTACCCCTAAAAATGCT
 ATCAGGGTTTTTATGCAGAGATAGATCCATCTCCTATTCTGGATGCATGATTACAGCTGTTTT
 TTTTCTGTGTTTGTGTTATTTCTGAATGCTACATGCTGGCAGCCATGGCCTGCGATCGCTAC
 50 GTGGCCATGTCAGCCCACTGCTCTACAGGTCATCATGTCCCCTAGGGTCTGTTCTCTGC
 TGGTGGCTGTGCTTCTCTCAGTAGGTTTCACTGATGCTGTGATCCATGGAGGTGTATACT
 CAGGTTGTCTTTCTGTGGATCAAACATCATTAACATTATTTCTGTGACATTGTCCCTCTTA
 TTAAACTCTCCTGCTCCAGCACTTATATTGATGAGCTTTTGATTTTTGTCTATTGGTGGATTT
 AACATGGTGGCCACAAGCCTAACAATCATTATTTTCATATGCTTTTATCCTCACCAGCATCCT
 55 GCGCATCCACTCTAAAAAGGGCAGGTGCAAAGCGTTTAGCACCTGTAGCTCCACCTGACA
 GCTGTTCTTATGTTTTATGGGTCTCTGATGTCCATGTATCTCAAACCTGCTTCTAGCAGTTC

ACTCACCCAGGAGAAAGTATCCTCAGTATTTTATACCACTGTGATTCTCATGTTGAATCCC
TTGATATATAGTCTGAGGAACAATGAAGTAAGAAATGCTCTGATGAAACTTTTAAGAAGA
AAAATATCTTTATCTCCAGGATAA (SEQ ID NO: 74)

5 **AOLFR40 sequences:**

MSNATLLTAFILTGPHAPGLDAPLFGIFLVVYVLTVLGNLLLLVIRVDSHLHTPMYYFLTNLS
FIDMWFTVTVPKMLMTLVSPSGRTISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAIISYPL
RYTNMMTGRSCALLATGTWLSGSLHSAVQTLTFHLPYCGPNQIQHYFCDAPPILKLACADTS
ANEMVIFVNIGLVASGCFVLIVLSYVSIVCSILRRTSEGRHRAFQTCASHCIVVLCFFGPGLFIYL
10 RPSGRDALHGVVAVFYTTLTPLFNPVVYTLRNKEVKKALLKLKNGSVFAQGE (SEQ ID NO:
75)

ATGTCCAACGCCACCTACTGACAGCGTTCATCCTCACGGGCCTTCCCCATGCCCCAGGGC
TGGACGCCCCCTCTTTGGAATCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
15 CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCTCA
CCAACCTGTCCTTCATTGACATGTGGTCTCCACTGTCACGGTGCCCCAAATGCTGATGAC
CTTGGTGTCCCCAAGCGGCAGGACTATCTCCTCCACAGCTGCGTGGCTCAGCTCTATTTTT
TCCACTTCTGGGGAGCACCGAGTGTTCCTCTACACAGTCATGTCCTATGATCGCTACCT
GGCCATCAGTTACCCGCTCAGGTACACCAACATGATGACTGGGCGCTCGTGTGCCCTCCTG
20 GCCACCGGCACCTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCC
ATTTGCCCTACTGTGGACCCAACCAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCT
GAAACTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTGAATATTGGGCTA
GTGGCCTCGGGCTGCTTTGTCTGATAGTGCTGTCTATGTGTCCATCGTCTGTTCCATCCT
GCGGATCCGCACCTCAGAGGGGAGGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGTATC
25 GTGGTCTTTGCTTCTTTGGCCCTGGTCTTTTCAATTTACCTGAGGCCAGGCTCCAGGGACGC
CTTGCATGGGGTTGTGGCCGTTTCTACACCACGCTGACTCCTCTTTTCAACCCTGTTGTGT
ACACCCTGAGAAACAAGGAGGTAAAGAAAGCTCTGTTGAAGCTGAAAAATGGGTCACTAT
TTGCTCAGGGTGAATAG (SEQ ID NO: 76)

30 **AOLFR41 sequences:**

MNPENWTQVTSFVLLGFPSHLLIQFLVFLGLMVTYIVTATGKLLIIVLSWIDQRLHIQMYFFLRN
FSFLELLLVTVVVPKMLVVILTDHTISFVSCIQSYLYFFLGTTDFLLAVMSLDRLYLAI CRPLR
YETLMNGHVCSQLVLASWLAGFLWVLCPTVLMASLPFCGPNIDHFFRDSWPLRLSCGDTH
LLKLVAFMLSTLVLLGSLALTSVSYACILATVLRAPTA AERRKAFSTCASHLTVVVIYGSSIFLY
35 IRMSEAQSKLLNK GASVLSCHITPLLPNFIFTLRNDKVQQALREALGWPRLTAVMKLRVTSQRK
(SEQ ID NO: 77)

ATGAACCCTGAAAACTGGACTCAGGTAACAAGCTTTGTCTTCTGGGTTTCCCCAGTAGCC
ACCTCATACAGTTCCTGGTGTTCCTGGGGTTAATGGTGACCTACATTGTAACAGCCACAGG
40 CAAGCTGCTAATTATTGTGCTCAGCTGGATAGACCAACGCCTGCACATACAGATGTACTTC
TTCCTGCGGAATTTCTCCTTCCTGGAGCTGTTGCTGGTAACTGTTGTGGTTCCCAAGATGCT
TGTCGTCATCCTCACGGGGGATCACACCATCTCATTGTGCTGCTGCTATCCAGTCCCTACC
TCTACTTCTTTCTAGGCACCACTGACTTCTTCTCTTGGCCGTCATGTCTCTGGATCGTTAC
CTGGCAATCTGCCGACCACTCCGCTATGAGACCCTGATGAATGGCCATGTCTGTTCCCAAC
45 TAGTGCTGGCCTCCTGGCTAGCTGGATTCTCTGGGTCCTTTGCCCCACTGTCCTCATGGCC
AGCCTGCCTTTCTGTGGCCCCAATGGTATTGACCACTTCTTTCGTGACAGTTGGCCCTTGCT
CAGGCTTTCTGTGGGGACACCCACCTGCTGAACTGGTGGCTTTTCATGCTCTCTACGTTG
GTGTTACTGGGCTCACTGGCTCTGACCTCAGTTTCCTATGCCTGCATTCTTGCCACTGTTCT
CAGGGCCCCCTACAGCTGCTGAGCGAAGGAAAGCGTTTCCACTTGCGCCTCGCATCTTACA
50 GTGGTGGTCATCATCTATGGCAGTTCCATCTTTCTCTACATTCGTATGTCAGAGGCTCAGTC
CAAACTGCTCAACAAAGGTGCCTCCGTCCTGAGCTGCATCATCACACCCCTCTTGAACCCA
TTCATCTTCACTCTCCGCAATGACAAGGTGCAGCAAGCACTGAGAGAAGCCTTGGGGTGGC
CCAGGCTCACTGCTGTGATGAACTGAGGGTCACAAGTCAAAGGAAATGA (SEQ ID NO:
78)

55

AOLFR42 sequences:

MNPANHSQVAGFVLLGLSQVWELRFVFFTVFSAVYFMTVVGNLLIVVIVTSDPHLHTTMYFLL
 GNLSFLDFCYSSITAPRMLVDLLSGNPTISFGGCLTQLFFHFHFIGGKIFLLTVMAYDRYIAISQPL
 HYTLIMNQTVCALLMAASWVGFIHSIVQIALTIQLPFCGPKLDNFYCDVPQLIKLACTDTFV
 5 LELLMVSNNGLVTLMLCFLVLLGSYALLVMLRSHSREGRSKALSTCASHIAVVTLIFVPCIYVY
 TRPFRTPMDKAVSVLYTIVTPMLNPAIYTLRNKEVIMAMKKLWRRKKDPIGPLEHRPLH
 (SEQ ID NO: 79)

ATGAATCCAGCAAATCATTCCCAGGTGGCAGGATTTGTTCTACTGGGGCTCTCTCAGGTTT
 10 GGGAGCTTCGGTTTGTCTTCTTCACTGTTTTCTCTGCTGTGTATTTTATGACTGTAGTGGGA
 AACCTTCTTATTGTGGTCATAGTGACCTCCGACCCACACCTGCACACAACCATGTATTTCT
 CTTGGGCAATCTTTCTTCTTCTGGACTTTTGTCTACTCTTCCATCACAGCACCTAGGATGCTGG
 TTGACTTGCTCTCAGGCAACCTACCATTTCTTTGGTGGATGCCTGACTCAACTCTTCTTC
 TTCCACTTCATTGGAGGCATCAAGATCTTCTGCTGACTGTCTATGGCGTATGACCGCTACA
 15 TTGCCATTTCCAGCCCCTGCACTACAGCTCATTATGAATCAGACTGTCTGTGCACTCCTT
 ATGGCAGCCTCCTGGGTGGGGGGCTTCATCCACTCCATAGTACAGATTGCATTGACTATCC
 AGCTGCCATTCTGTGGGCCTGACAAGCTGGACAACCTTTTATTGTGATGTGCCTCAGCTGAT
 CAAATTGGCCTGCACAGATACCTTTGTCTTAGAGCTTTAATGGTGTCTAACAATGGCCTG
 GTGACCCCTGATGTGTTTTCTGGTGCTTCTGGGATCGTACACAGCACTGCTAGTCATGCTCC
 20 GAAGCCACTCACGGGAGGGCCGAGCAAGGCCCTGTCTACCTGTGCCTCTCACATTGCTGT
 GGTGACCTTAATCTTTGTGCCTTGCTCTACGTCTATACAAGGCCCTTTTCGGACATTCCTCCA
 TGGACAAGGCCGTCTCTGTGCTATACAAATTGTCAACCCCATGCTGAATCCTGCCATCTA
 TACCCTGAGAAACAAGGAAGTGATCATGGCCATGAAGAAGCTGTGGAGGAGGAAAAAGG
 ACCCTATTGGTCCCCTGGAGCACAGACCCTTACATTAG (SEQ ID NO: 80)

25

AOLFR43 sequences:

MQKPQLLVPIATSNGLVHAAYFLLVGIPGLGPTIHFWLAFPLCFMYALATLGNLTIVLIIRVE
 RRLHEPMYLFLAMLSTIDLVLSSITMPKMASLFLMGIQEIEFNICLAQMFLIHALSAVESAVLLA
 MAFDRFVAICHPLRHASVLTGCTVAKIGLSALTRGFVFFFLPFLKWLSCYQHTVTHSFCLHQ
 30 DIMKLSCTDTRVNVVYGLFIILSVMGVDSLFIGFSYILILWAVLELSSRRRAALKAFNTCISHLCAV
 LVFYVPLIGLSVVHRLGGPTSLHVMANTYLLPPVNVNPLVYGAKTKEICSRVLCMFSGQGGK
 (SEQ ID NO: 81)

ATGCAGAAGCCCCAGCTCTTGGTCCCTATCATAGCCACTTCAAATGGAAATCTGGTCCACG
 35 CAGCATACTTCCTTTTGGTGGGTATCCCTGGCCTGGGGCCTACCATACACTTTTGGCTGGCT
 TTCCCACCTGTGTTTTATGTATGCCTTGGCCACCCTGGGTAACCTGACCATTGTCCTCATCAT
 TCGTGTGGAGAGGCGACTGCATGAGCCCATGTACCTCTTCTGGCCATGCTTTCCACTATT
 GACCTAGTCCCTCTCCTCTATCACCATGCCCAAGATGGCCAGTCTTTTCTGATGGGCATCCA
 GGAGATCGAGTTCAACATTTGCCTGGCCAGATGTTCTTATCCATGCTCTGTGAGCCGTG
 40 GAGTCAGCTGTCTGCTGGCCATGGCTTTTGACCGCTTTGTGGCCATTGGCCACCCATTGC
 GCCATGCTTCTGTGCTGACAGGGGTGACTGTGGCCAAGATTGGACTATCTGCCCTGACCAG
 GGGGTTTGTATTCTTCTTCCCACTGCCCTTCATCCTCAAGTGGTTGTCTACTGCCAAACAC
 ATACTGTACACACTCCTTCTGTCTGCACCAAGATATTATGAAGCTGTCTGTACTGACAC
 CAGGGTCAATGTGGTTTATGGACTCTTCATCATCCTCTCAGTCATGGGTGTGGACTCTCTCT
 45 TCATTGGCTTCTCATATATCCTCATCCTGTGGGCTGTTTTGGAGCTGTCTCTCGGAGGGCA
 GCACTCAAGGCTTTCAACACCTGCATCTCCACCTCTGTGCTGTTCTGGTCTTCTATGTACC
 CCTCATTGGGCTCTCGGTGGTGCATAGGCTGGGTGGTCCCACCTCCCTCCTCCATGTGGGT
 ATGGCTAATACTACTTGCTGCTACCACTGTAGTCAACCCCTTGTCTATGGAGCCAAGA
 CCAAAGAGATCTGTTCAAGGTCCTCTGTATGTTCTCACAAGGTGGCAAGTGA (SEQ ID
 50 NO: 82)

AOLFR44 sequences:

MSSCNFTHATFVLIGIPGLEKAHFWVGFPLLSMYVVMFNGNCIVVFIVRTERS LHAPMYLFLC
 MLAADLALSTSTMPKILALFWFDSREISFEACLTQMFFIHALSAIESTILLAMAFDRYVAICHPL
 55 RHA AVLNNVTVAQIGIVAVVRGSLFFFLPLLKRLAFCHSNVLSHSYCVHQDVMKLAYADTLP
 NVVYGLTAILVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLAIFYVPLIGLS

VVHRFGNSLHPVVRVVMGDIYLLLPVINPIHYGAKTKQIRTRVLAMFKISCDKDLQAVGGK
(SEQ ID NO: 83)

5 ATGAGTTCCTGCAACTTCACACATGCCACCTTTGTGCTTATTGGTATCCCAGGATTAGAGA
AAGCCCATTCTGGGTTGGCTTCCCCCTCCTTTCCATGTATGTAGTGGCAATGTTTGGAAAC
TGCATCGTGGTCTTCATCGTAAGGACGGAACGCAGCCTGCACGCTCCGATGTACCTCTTTC
TCTGCATGCTTGACGCCATTGACCTGGCCTTATCCACATCCACCATGCCTAAGATCCTTGCC
CTTTTCTGGTTTGATTCCCGAGAGATTAGCTTTGAGGCCTGTCTTACCCAGATGTTCTTTAT
10 TCATGCCCTCTCAGCCATTGAATCCACCATCCTGCTGGCCATGGCCTTTGACCGTTATGTGG
CCATCTGCCACCCACTGCGCCATGCTGCAGTGTCTCAACAATACAGTAACAGCCAGATTGG
CATCGTGGCTGTGGTCCGCGGATCCCTCTTTTTCCTTCCACTGCCTCTGCTGATCAAGCGGC
TGGCCTTCTGCCACTCCAATGTCTCTCGCACTCCTATTGTGTCCACCAGGATGTAATGAA
GTTGGCCTATGCAGACACTTTGCCCAATGTGGTATATGGTCTTACTGCCATTCTGCTGGTC
15 ATGGGCGTGGACGTAATGTTTCATCTCCTTGTCTATTTTCTGATAATACGAACGGTTCTGC
AACTGCCTTCCAAGTCAGAGCGGGCCAAGGCCTTTGGAACCTGTGTGTGCACACATTGGTGT
GGTACTCGCCTTCTATGTGCCACTTATTGGCCTCTCAGTGGTACACCGCTTTGGAAACAGC
CTTCATCCCATTTGTGCGTGTGTGTCATGGGTGACATCTACCTGCTGCTGCCTCCTGTCACTAA
TCCCATCATCTATGGTGCCAAAACCAAACAGATCAGAACACGGGTGCTGGCTATGTTCAAG
20 ATCAGCTGTGACAAGGACTTGCAGGCTGTGGGAGGCAAGTGA (SEQ ID NO: 84)

AOLFR45 sequences:

MLPSNTTSTHPAVFLLVGIPGLEHLHAWISIPFCFAYTLALLGNCTLLFIQADAALHEPMYLFLA
MLATIDLVLSTTLPKMLAIFWFRDQEIFFACLVMFFLHSFSIMESAULLAMAFDRYVAICKP
LHYTTVLTGSLITKIGMAAVARAVTLMTPFLRRFHYCRGPVIAHCYCEHMAVVRLACGDT
25 SFNNIYGIAVAMFSVVDLLFVILSYVFLQAVLQLASQEARYKAFGTCVSHIGAILSTYTPVVIS
SVMHRVARHAAPRVHILLAIFYLLFPPMVNPITYGVKTKQIREYVLSLFQRKNM (SEQ ID NO:
85)

30 TGGAAACAAGAGGTAATCTTTGCAGGTGGGATAGCACAGGTTGAACTCTAATCATATATA
CTGTAGAAGGTATATATAGAAGGTGAAGAAGCCCTGTAAAAATTGACAAGGAGATTTCCTCA
GGAGCCATGCTTCCCTCTAATATCACCTCAACACATCCAGCTGTCTTTTGTGGTAGGAAT
TCCTGGTTTGGAAACACCTGCATGCCTGGATCTCCATCCCCTTCTGCTTTGCTTATACTCTGG
CCCTGCTAGGCAACTGTACCCTTCTCTTATTATCCAGGCTGATGCAGCCCTCCATGAACCC
ATGTACCTCTTTCTGGCCATGTTGGCAACCATTGACTTGGTTCTTTCTTCTACAACGCTGCC
35 CAAAATGCTTGCCATATTCTGGTTTCAAGGATCAGGAGATCAACTTCTTTGCTGTCTGGTC
CAGATGTTCTTCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGCTGCTGGCCATGGCCTT
TGACCGCTATGTGGCCATCTGCAAGCCATTGCACTACACGACGGTCTGACTGGGTCCCTC
ATCACCAGATTGGCATGGCTGCTGTGGCCCGGGCTGTGACACTAATGACTCCACTCCCCT
TCCTGCTCAGACGCTTCCACTACTGCCGAGGCCAGTGATTGCCATTGCTACTGTGAACA
40 CATGGCTGTGGTAAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATTGCT
GTGGCCATGTTTAGTGTGGTGTGGACCTGCTCTTGTATCCTGTCTTATGTCTTCATCCT
TCAGGCAGTTCTCCAGCTTGCTCTCAGGAGGCCGCTACAAAGCATTGTTGGGACATGTGTG
TCTCACATAGGTGCCATCCTGTCCACCTACACTCCAGTAGTCATCTCTTCAGTCATGCACCG
TGTAGCCCGCCATGCTGCCCTCGTGTCCACATACTCCTTGCTATTTTCTATCTCCTTTTCC
45 CACCCATGGTCAATCCTATCATATATGGAGTCAAGACCAAGCAGATTCTGTAGTATGTGCT
CAGTCTATTCCAGAGAAAGAACATGTAGATGGATAGTTCTCTTTTATCCCACTTGCCA
AGTAATGAGAATGCTGGATTGGGGTTGAGGGGAAAAATCTAAATAGGAAAATTGCAGAGT
ATCTTTGACAATTCTTAGTATGATAAGGAAAATGAGGTTTCATTCTCACAGATCTACGA
GTCAGGTCAAACCAGGAGTGCACCTATAGTCTGGTCTGATAGTAGAGGTTTGACCTTCCCA
50 TTGTCATAGACTCATCATGGCTAAGGAAGACAAACCTCTCAAAGTGGTATTGTAATCTG
GGTGAAAGACAGTAGGACCTTTATTGGCTGAGATTGGCCCAAACAGCTGAGTC (SEQ ID
NO: 86)

AOLFR46 sequences:

55 MNIKHCGWHMIHTWLNIREDDSDFKNFIGQIQGLSGNPHSTTSRMYFLCFCTSLLGFKVHWV
SRLIXKLYMASPNNDSTAPVSEFLICFPNFQSWQHWLSLPLSLFLAMGANTLLITIQLAS

LHQPLYLLSLLSLLDIVLCLTVIPKVLAIWFVDFLRISFPACFLQMFIMNSFLTMESCTFMVMA
YDRYVAICHPLRYPSTTDQFVARAVVFIARNAFVSLPVPMLSARLRYCAGNIKNKICSNLSVS
KLSCDDITFNQLYQFVAGWTLLGSDLILIVISYFILKVVLRIKAEGAVAKALSTCGSHFILFFS
TVLLVLVITNLARKRIPDPVILLNLHHLIPPALNPVYGVRTKEIKQIQIQLLRL (SEQ ID NO:
5 87)

ATGAATATAAAACATTGTGGCTGGCATATGATACATACTTGGTTAAATATAAGGGAGGAT
GATGACAGTGATTTTAAAACTTTATTGGACAGATACAGGGCCTCAGTGGAACCCACACT
CTACTACGTCTAGAATGTACTTTTTATGTTTCTGTACTTCTCTACTAGGTTTTAAGGTACAC
10 TGGGTCTCCAGATTGATCANGAACTTTACATGGCATCTCCCAACAATGACTCCACTGCCC
CAGTCTCTGAATTCTCTCATCTGCTTCCCCAACTTCCAGAGCTGGCAGCACTGGTTGTCT
CTGCCCCCTCAGCCTTCTCTTCTCTGGCCATGGGAGCTAACACCACCCTCCTGATCACCAT
CCAGCTGGAGGCCTCTCTGCACCAGCCCCTGTACTACCTGCTCAGCCTCCTCTCCCTGCTGG
ACATCGTGCTCTGCCTCACCGTCATCCCCAAGGTCCTGGCCATCTTCTGGTTTGACCTCAGG
15 TCGATCAGCTTCCCAGCCTGCTTCTCCAGATGTTTCATCATGAACAGTTTTTTGACCATGGA
GTCCTGCACGTTTCATGGTCATGGCCTATGACCGTTATGTGGCCATCTGCCATCCATTGAGA
TACCCGTCTATCATCACTGACCAGTTTGTGGCTAGGGCCGTGGTCTTTGTTATAGCCCGGA
ATGCCTTTGTTTCTCTTCTGTTCCCATGCTTTCTGCCAGGCTCAGATACTGTGCAGGAAAC
ATAATCAAGAACTGCATCTGCAGTAACCTGTCTGTGTCCAACTCTCTTGTGATGACATCA
20 CTTTCAATCAGCTCTACCAGTTTGTGGCAGGCTGGACTCTGTTGGGCTCTGATCTTATCCTT
ATTGTTATCTCCTATTCTTTTATATTGAAAGTTGTGCTTAGGATCAAGGCCGAGGGTGCTGT
GGCCAAGGCCTTGAGCACGTGTGGTTCCCACTTCATCCTCATCCTCTTCTTTCAGCACAGTCC
TGCTGGTTCTGGTCATCACTAACCTGGCCAGGAAGAGAATTCTCCAGATGTCCCCATCCT
GCTCAACATCCTGCACCACCTCATTCCCCCAGCTCTGAACCCCATGTTTATGGTGTGAGA
25 ACCAAGGAGATCAAGCAGGGAATCCAAAACCTGCTGAAGAGGTTGTAA (SEQ ID NO: 88)

AOLFR47 sequences:

MSASNTLTHPTAFLLVGIPGLEHLHIWISIPFLAYTLALLGNCTLLLIHQADAALHEPMYLFLA
MLAAIDLVLSSALPKMLAIFWFRDREINFFACLAQMFFLHSFSIMESAVLLAMAFDRYVAICK
30 PLHYTKVLTGSLITKIGMAAVARAVTLMTPLPFLLRCFHYCRGPVIAHCYCEHMAVVRACGD
TSFNNTYGVAVAMFIVLDLLLVILSYFILQAVLLLASQEARYKAFGTCVSHIGAILAFYTTVVIS
SVMHRVARHAAPHVHILLANFYLLFPPMVNPVYGVKTKQIRESILGVFPRKDM (SEQ ID NO:
89)

ATGTCAGCCTCCAATATCACCTTAACACATCCAACCTGCCTTCTTGTGGTGGGGATTCCAG
GCCTGGAACACCTGCACATCTGGATCTCCATCCCTTTCTGCTTAGCATATACACTGGCCCTG
CTTGGAACCTGCACTCTCCTTCTCATCATCCAGGCTGATGCAGCCCTCCATGAACCCATGT
ACCTCTTTCTGGCCATGTTGGCAGCCATCGACCTGGTCCTTTCTCCTCAGCACTGCCCCAA
ATGCTTGCCATATTCTGGTTCAGGGATCGGGAGATAAACTTCTTGCCTGTCTGGCCCAGA
40 TGTCTCTCCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGCTGCTGGCCATGGCCTTTGAC
CGCTATGTGGCTATCTGCAAGCCACTGCACTACACCAAGGTCCTGACTGGGTCCCTCATCA
CCAAGATTGGCATGGCTGCTGTGGCCCGGGCTGTGACACTAATGACTCCACTCCCCTTCTCT
GCTGAGATGTTTCCACTACTGCCGAGGCCAGTGATCGCTCACTGCTACTGTGAACACATG
GCTGTGGTGAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATCGCTGTGG
45 CCATGTTTATTGTGGTGTGGACCTGCTCCTTGTATCCTGTCTTATATCTTTATCTTTCAG
GCAGTTCTACTGCTTGCTCTCAGGAGGCCCGCTACAAGGCATTTGGGACATGTGTCTCTC
ATATAGGTGCCATCTTAGCCTTCTACACAAGTGTGGTCATCTCTTCAGTCATGCACCGTGTA
GCCCCCATGCTGCCCCCTCATGTCCACATCCTCCTTGCCAATTTCTATCTGCTCTTCCCACC
CATGGTCAATCCATAATCTATGGTGTCAAGACCAAGCAAATCCGTGAGAGCATCTTGGGA
50 GTATTCCCAAGAAAGGATATGTAG (SEQ ID NO: 90)

AOLFR48 sequences:

MMVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFL
CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFIAHSLSGMESTVLLAMAFDRYVAICH
55 PLRHATVLTLPVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNLSHSYCLHQDVMKLACDDI
RVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGLTREAAKAFGTCVSHVCAVFIFYVPFGLSM

VHRFSKRSDSPLPVILANTYLLVPPVLNPVYGVKTKRILRLRFHVATHASEP (SEQ ID NO: 91)

5 ATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCATCCTAATAGGCCTCC
CTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTGTGCTCCCTCTACCTTATTGCT
GTGCTAGGTAACCTTGACAATCATCTACATTGTGCGGACTGAGCACAGCCTGCATGAGCCCA
TGTATATATTTCTTTGCATGCTTTAGGCATTGACATCCTCATCTCCACCTCATCCATGCCC
AAAATGCTGGCCATCTTCTGGTTCAATTCCACTACCATCCAGTTTGATGCTTGTCTGTCTACA
10 GATGTTTGGCATCCACTCCTTATCTGGCATGGAATCCACAGTGCTGCTGGCCATGGCTTTT
GACCGCTATGTGGCCATCTGTCACCCACTGCGCCATGCCACAGTACTTACGTTGCCCTCGTG
TCACCAAAATTGGTGTGGCTGCTGTGGTGGGGGGCTGCACTGATGGCACCCCTTCTGT
CTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATATCCTTTCCCATTCCTACTGCCTACACC
AAGATGTCATGAAGCTGGCCTGTGATGATATCCGGGTCAATGTCGTCTATGGCCTTATCGT
15 CATCATCTCCGCCATTGGCCTGGACTCACTTCTCATCTCCTTCTCATATCTGCTTATTCTTA
AGACTGTGTTGGGCTTGACACGTGAAGCCAGGCCAAGGCATTTGGCACTTGGCTCTCTCA
TGTGTGTGCTGTGTTTATATTCTATGTACCTTTTATTGGATTGTCCATGGTGCATCGCTTTA
GCAAGCGGCGTGACTCTCCGCTGCCCGTCATCTTGCCAATATCTATCTGCTGGTTCCTCCT
GTGCTCAACCCAATTGTCTATGGAGTGAAGACAAAGGAGATTCGACAGCGCATCCTTCGA
CTTTTCCATGTGGCCACACACGCTTCAGAGCCCTAG (SEQ ID NO: 92)

20

AOLFR49 sequences:

MLTFHNVCSPSSFWLTGIPGLES�HVWLSIPFGSMYLVAVVGNVTILAVVKIERSLHQPMYFF
LCMLAAILDLVLSSTIPKLLGIFWFGACDIGLDACLGQMFLIHCFAVESGIFLAMAFDRYVAIC
NPLRHSMLVLTYYTVVGRGLVSLRGVLYIGPLPLMRLRLPLYKTHVISHSYCEHMAVVALTC
25 GDSRVNNVYGLSIGFLVLILDSVAIAASYVMIFRAVMGLATPEARLKTGTCASHLCAILIFYVP
IAVSSLIHRFGQCVPPVHTLLANFYLLIPILNPVYAVRTKQIRESLLQIPRIEMKIR (SEQ ID
NO: 93)

30 ATGCTCACTTTTTCATAATGTCTGCTCAGTACCCAGCTCCTTCTGGCTCACTGGCATCCCAGG
GCTGGAGTCCCTACACGTCTGGCTCTCCATCCCCTTTGGCTCCATGTACCTGGTGGCTGTG
GTGGGGAATGTGACCATCCTGGCTGTGGTAAAGATAGAACGCAGCCTGCACCAGCCCATG
TACTTTTTCTTGTGCATGTTGGCTGCCATTGACCTGGTTCTGTCTACTTCCACTATACCCAA
ACTTCTGGGAATCTTCTGGTTCCGTGCTTGTGACATTGGCCTGGACGCCTGCTTGGGCCAA
ATGTTCCCTTATCCACTGCTTTGCCACTGTTGAGTCAGGCATCTTCCCTGCCATGGCTTTTGA
35 TCGCTACGTGGCCATCTGCAACCCACTACGTCATAGCATGGTGCTCACTTATACAGTGGTG
GGTCGTTTGGGGCTTGTCTCTCCTCCGGGTGTTCTCTACATTGGACCTCTGCCTCTGAT
GATCCGCCTGCGGCTGCCCTTTATAAAACCCATGTTATCTCCACTCCTACTGTGAGCAC
ATGGCTGTAGTTGCCTTGACATGTGGCGACAGCAGGGTCAATAATGTCTATGGGCTGAGC
ATCGGCTTTCTGGTGTGATCCTGGACTCAGTGGCTATTGCTGCATCCTATGTGATGATTTT
40 CAGGGCCGTGATGGGGTTAGCCACTCCTGAGGCTAGGCTTAAACCCCTGGGGACATGCGC
TTCTCACCTCTGTGCCATCCTGATCTTTTATGTTCCCATGCTGTTTCTTCCCTGATTCACCG
ATTTGGTCAGTGTGTGCTCCTCCAGTCCACACTCTGCTGGCCAACTTCTATCTCCTCATTC
CTCCAATCCTCAATCCCATTTGTCTATGCTGTTGCGACCAAGCAGATCCGAGAGAGCCTTCT
CCAAATACCAAGGATAGAAATGAAGATTAGATGA (SEQ ID NO: 94)

45

AOLFR50 sequences:

MNLSFFSFLKSLIMALSNSSWRLPQPSFFLVGIPGLEESQHWIALPLGILYLLALVGNVTILFII
WMDPSLHQSMYLFSLMLAAILDVASSTAPKALAVLLVRAQEIGYTVCLIQMFTHAFSSMES
GVLVAMALDRYVAICHPLHHSTILHPGVIGHIGMVVLVRGLLLLPFLILLRKLIFCQATIIGHAY
50 CEHMAVVKLACSETTVNRAYGLTVALLVGLDVLAIGVSYAHILQAVLKVPNEARLKAFST
CGSHVCVILVFYIPGMFSFLTHRFGHHVPHVHVLLAILYRLVPPALNPLVYRVKTQKIHQ
(SEQ ID NO: 95)

55 ATGAATTTGGATTCTTTTTCTCTTTCCTCCTCAAGTCATTGATAATGGCACTTAGCAATTC
CAGCTGGAGGCTACCCAGCCTTCTTTTTCTGGTAGGAATCCGGGTTTAGAGGAAAGC
CAGCACTGGATCGCACTGCCCTGGGCATCCTTTACCTCCTTGTCTAGTGGGCAATGTTA

CCATTCTCTTCATCATCTGGATGGACCCATCCTTGACCAATCTATGTACCTCTTCCTGTCC
 ATGCTAGCTGCCATCGACCTGGTGTGGCCTCCTCCACTGCACCCAAAGCCCTGCAGTGC
 TCCTGGTTCGTGCCAAGAGATTGGTTACACTGTCTGCCTGATCCAGATGTTCTTCACCCAT
 GCATTCTCCTCCATGGAGTCAAGGGTACTTGTGGCCATGGCTCTGGATCGCTATGTAGCCA
 5 TTTGTCACCCCTTGACCAATTCCACAATCCTGCATCCAGGGGTCATAGGGCACATCGGAAT
 GGTGGTGTGGTGCAGGGGATTACTACTCCTCATCCCTTCCTCATTCTGTTGCGAAAACCT
 ATCTTCTGCCAAGCCACCATCATAGGCCATGCCTATTGTGAACATATGGCTGTTGTGAAAC
 TTGCCTGCTCAGAAACCACAGTCAATCGAGCTTATGGGCTGACTGTGGCCTTGCTTGTGGT
 TGGGCTGGATGTCTGGCCATTGGTGTTCCTATGCCACATTCTCCAGGCAGTGTGTAAG
 10 GTACCAGGAAATGAGGCCCGACTTAAGGCCTTAGCACATGTGGCTCTCATGTTTGTGTCA
 TCCTGGTCTTCTATATCCCGGAATGTTCTCCTTCCTCACTCACCCTTTGGTCATCATGTA
 CCCCATCACGTCCATGTTCTTCTGGCCATACTGTATCGCCTTGTGCCACCTGCACTCAATCC
 TCTTGTCTATAGGGTGAAGACCCAGAAGATCCACCAGTGA (SEQ ID NO: 96)

15 **AOLFR51 sequences:**

MCQQILRDCILLIHLHCINRKKVSLVMLGPAYNHTMETPASFLLVGIPGLQSSHLWLAISLSAM
 YIALLGNTIIVTAIWMDSTRHEPMYCFLCVLAAVDIVMASSVVPKMVSIFCSGDSISFSACFTQ
 MFFVHLATAVETGLLLTMAFDRYVAICKPLHYKRILTPQVMLGMSMAITIRAIATPLSWMVS
 HLPFCGSNVVVHSYCEHIALARLACADVPVSSLYSLIGSSLMVGSDVAFIAASYILLKAVFGLSS
 20 KTAQLKALSTCGSHVGMALYYLPGMASIYAAWLGQDVVPLHTQVLLADLYVIIPATLNPITY
 GMRTKQLRERIWSYLMHVLFDHNSNLGS (SEQ ID NO: 97)

ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTTTGTGCATTAACAGGA
 AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC
 25 CTTCTCCTTGTGGGTATCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGA
 GTGCATGTACATCATAGCCCTGTTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA
 TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGGACATGTTA
 TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG
 CTTTAGTGCTTGTTCCTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG
 30 CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA
 GAATTCTCAGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT
 AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTCTGTGGCTCCAATGTGGTT
 GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA
 GCAGTCTCTACAGTCTGATTGGTTCCTCTCTATGGTGGGCTCTGATGTGGCCTTCATTGCT
 35 GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA
 AGCATTAAACACATGTGGCTCCCATGTGGGGGTTATGGCTTTGTAATCTACCTGGGATG
 GCATCCATCTATGCGGCCTGGTTGGGGCAGGATGTAGTGCCCTTGACACCCAAAGTCCTGC
 TAGCTGACCTGTACGTATCATCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC
 CAAACAAGTGGGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATTCCAAC
 40 CTGGGTTTCATGA (SEQ ID NO: 98)

AOLFR52 sequences:

MLGPAYNHTMETPASFLLVGIPGLQSSHLWLAISLSAMYTTALLGNTLIVTAIWMDSTRHEPMY
 CFLCVLAAVDIVMASSVVPKMVSIFCSGDSISFSACFTQMFFVHLATAVETGLLLTMAFDRYV
 45 AICKPLHYKRILTPQVMLGMSMAVTIRAVTFMTPLSWMMNHLPFCGSNVVVHSYCKHIALAR
 LACADVPVSSLYSLIGSSLMVGSDVAFIAASYILLRAVFDLSSKTAQLKALSTCGSHVGMALY
 YLPGMASIYAAWLGQDIVPLHTQVLLADLYVIIPATLNPITYGMRTKQLLEGIWSYLMHFLFDH
 SNLGS (SEQ ID NO: 99)

50 ATGCTGGGTCCAGCTTACAACCACACAATGGAAACCCCTGCCTCCTTCTCCTTGTGGGTA
 TCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGAGTGCCATGTACATCAC
 AGCCCTGTTAGGAAACACCCTCATCGTGACTGCAATCTGGATGGATTCCAATCGGCATGAG
 CCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTATGGCCTCCTCCGTGGT
 ACCCAAGATGGTGAGCATCTTCTGCTCGGGAGACAGCTCCATCAGCTTTAGTGCTTGTTC
 55 ACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGGCTGCTGCTGACCATGG
 CTTTGTACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGAGAATTCTCAGCCTCA

AGTGATGCTGGGAATGAGTATGGCCGTCACCATCAGAGCTGTCACATTCATGACTCCACTG
 AGTTGGATGATGAATCATCTACCTTTCTGTGGCTCCAATGTGGTTGTCCACTCCTACTGTAA
 GCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCAGCAGTCTCTACAGTCTG
 ATTGGTTCCCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCTGCCTCCTATATCTTAAT
 5 TCTCAGGGCAGTATTTGATCTCTCCTCAAAGACTGCTCAGTTGAAAGCATTAAAGCATGT
 GGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATGGCATCCATCTATGCGG
 CCTGGTTGGGGCAGGATATAGTGCCCTTGACACCCAAAGTGCTGCTAGCTGACCTGTACGT
 GATCATCCCAGCCACTTTAAATCCCATCATCTATGGCATGAGGACCAAACAATTGCTGGAG
 10 GGAATATGGAGTTATCTGATGCACTTCTCTTTGACCACTCCAACCTGGGTTCATGA (SEQ
 ID NO: 100)

AOLFR54 sequences:

MSDSNLSDNHLPDTFFLTGIPGLEAAHFWIAIPFCAMYLVALVGNAALILVIAMDNALHAPMY
 LFLCLSLTDLALSSTTVPKMLAILWLHAGEISFGGCLAQMFCVHSIYALESSILLAMAFDRYVA
 15 ICNPLRYTTILNHAVIGRIGFVGLFRSVAIVSPFILLRRLPYCGHRVMTHTYCEHMGIA RLACA
 NITVNIVYGLTVALLAMGLDSILIAISYGFIHAFVHLP SHDAQHKALSTCGSHIGIILVFYPAFF
 SFLTHRFHHEVPKHVHIFLANLYVLVPPVLNPILYGARTKEIRSRLKLLHLGKTSI (SEQ ID
 NO: 101)

ATGTCAGATTCCAACCTCAGTGATAACCATCTTCCAGACACCTTCTTCTTAACAGGGATCC
 CAGGGCTGGAGGCTGCCCATTCTGGATTGCCATCCCTTTCTGTGCCATGTATCTTGTAGC
 ACTGGTTGGAAATGCTGCCCTCATCCTGGTCATTGCCATGGACAATGCTCTTCATGCACCT
 ATGTACCTCTTCTCTGCCTTCTCTCACTCACAGACCTGGCTCTCAGTTCTACCACTGTGCC
 CAAGATGCTGGCCATTTTGTGGCTCCATGCTGGTGAGATTTCCTTTGGTGGATGCCTGGCC
 25 CAGATGTTTTGTGTCCATTCTATCTATGCTCTGGAGTCCTCGATTCTACTTGCCATGGCCTT
 TGATAGGTATGTGGCTATCTGTAACCCATTAAGGTATACAACCATTTCAACCATGCTGTC
 ATAGGCAGAAATTGGCTTTGTGGGCTATTCCGTAGTGTGGCTATTGTCTCCCCCTTCATCTT
 CTGTGCTGAGGCGACTCCCCTACTGTGGTCACCGTGTGATGACACACACATACTGTGAGCAT
 ATGGGCATCGCCCGACTGGCCTGTGCCAACATCACTGTCAATATTGTCTATGGGCTAACTG
 30 TGGCTCTGCTGGCCATGGGACTGGATTCCATTCTCATTGCCATTTCTATGGCTTTATCCTC
 CATGCAGTCTTTACCTTCCATCTCATGATGCCCAGCACAAAGCTCTGAGTACCTGTGGCT
 CCCACATTGGCATCATCCTGGTTTTCTACATCCCTGCCTTCTTCTCCTTCTCACCACCGC
 TTTGGTCACCAAGTCCCCAAGCATGTGCACATCTTCTGGCTAATCTCTATGTGCTGG
 TGCCTCCTGTACTCAATCCTATTCTCTATGGAGCTAGAACCAAGGAGATTTCGGAGTCGACT
 35 TCTAAAACTGCTTCACCTGGGGAAGACTTCAATATGA (SEQ ID NO: 102)

AOLFR57 sequences:

MSFQVTYMFYLHWTMEKSNNSTLFILLGFSQNKIEVLCFVLFVFCYIAIWMGNLLIMISITCTQ
 LIHQPMYFFLNYSLSLDCYTSTVTPKLMVDLLAERKTISYNNCMIQLFTTHFFGGIEFILTGM
 40 AYDRYVAICKPLHYTIIMSROKCNTHIVCCTGGFIHSASQFLLTIFVPFCGPNEIDHYFCDVYPLL
 KLACSNHIMIGLLVIANSGLIALVTFVLLLSYVFILYTIIRAYSERRSKALATCSSHVIVVVLFF
 APALFIYIRPVTTFSEDKV FALFYTHAPMFNPLIYTLRNTMKNAMRKVWCCQILLKRNQLF
 (SEQ ID NO: 103)

ATGTCATTTTCAGGTGACTTATATGTTCTATCTACACTGGACCATGGAAAAAAGCAATAATA
 GCACTTTGTTTATTCTCTTGGGGTTTTCCCAAAATAAGAACATTGAAGTCTCTGCTTTGTA
 TTATTTTTGTTTTGCTACATTGCTATTTGGATGGGAACTTACTCATAATGATTTCTATCAC
 GTGCACCCAGCTCATTACCAACCCATGTATTTCTTCTCAATTACCTCTCACTCTCCGACC
 TTTGCTACACATCCACAGTGACCCCCAAATTAATGGTTGACTTACTGGCAGAAAGAAAGAC
 50 CATTTCCCTATAATACTGTATGATACAACTCTTTACCACCCATTTTTTTGGAGGCATAGAGA
 TCTTCATTCTCACAGGGATGGCCTATGACCGCTATGTGGCCATTGCAAGCCCCCTGCCTA
 CACCATTATTATGAGCAGGCAAAAGTGTAACACAATCATCATAGTTTGTGTGCTGGGGA
 TTTATACATTCTGCCAGTCAGTTTCTTCTCACCATCTTTGTACCATTTTGTGGCCCAAATGA
 GATAGATCACTACTTCTGTGATGTGTATCCTTTGCTGAAATTGGCCTGTTCTAATATACACA
 55 TGATAGGTCTCTTAGTCATTGCTAATTCAGGCTTAATTGCTTTGGTGACATTTGTTGCTTG
 TTGTTGTCTTATGTTTTTATATTGTATACCATCAGAGCATACTCTGCAGAGAGACGCAGCA

5 AAGCTCTTGCCACTTGTAGTTCTCATGTAATTGTTGTGGTCCTGTTTTTGGCTCCTGCATTG
TTCATTTACATTAGACCGGTCAACATTCTCAGAAGATAAAGTGTTGCCCTTTTTTATAC
CATCATTGCTCCCATGTTCAACCTCTCATATACACGCTGAGAAACACAGAGATGAAGAAC
GCCATGAGGAAAAGTGTGGTGTGTCAAATACTCCTGAAAAGAAATCAACTTTTCTGA (SEQ
ID NO: 104)

AOLFR58 sequences:

10 MFSMTTEALNNFALGCTNLLMTMPQIDLKQIFLCPNCRLYMPVGAFIFSLGNMQNQSFVTEF
VLLGLSQPNVQEIVFVFLFVYIATVGGNMLIVVTILSSPALLVSPMYFFLGFLSFLDACFSSVI
TPKMIVDSL YVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRL
CGILMGVAWTGGLLHSMIQLFTFQLPFCGPNVINHFMC DLYPLLELACTDTHIFGLMVVINS
FICINFSLLLVS YAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA
AIFYILNPLLNPLIYTRNKEVKQAMRRIWNRLMVVSDEKENIKL (SEQ ID NO: 105)

15 ATGTTCTCAATGACAACAGAAGCACTCAATAATTTTGCACTTGGATGTACCAACTTGTTAA
TGACTATGATACCACAAATTGATCTGAAGCAAATTTTCCTTTGTCTTAATTGCAGACTATA
CATGATCCCTGTTGGAGCTTTCATCTTTTCCTTGGGAAACATGCAAAACCAAAGCTTTGTA
ACTGAGTTTGTCTCCTGGGACTTTCACAGAATCCAAATGTTTCAGGAAATAGTATTTGTTG
TATTTTTGTTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCATTCCTC
20 AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTA CTCTTCTTGGGCTTCCTGTCCTTCCTGGA
TGCCTGCTTCTCATCTGTCTATCAACCCAAAGATGATTGTAGACTCCCTCTATGTGACAAAA
ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTTCTTTGCTGGGGTGG
AGGTGATTGTCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTTGCAAGCCCTTGCA
TTACTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG
25 GGCCTCTTGCAATCCATGATACAAATTC TTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA
TGTCATCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCCTGCACTGATACTC
ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG
TTGCTTGTCTCCTATGCTGTCTATCTTGTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG
GAAAGCTCTCTCCACCTGTGGATCTCCAGTTGCTGTTGTGATTTTGTCTTTGTGCCATGCA
30 TATTTGTATATACACGACCTCCATCTGCTTTTTCCCTTGACAAAATGGCGGCAATATTTTAT
ATCATCTTAAATCCCTTGCTCAATCCTTTGATTTACACTTTCAGGAATAAGGAAGTAAAC
AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTA
AACTTTAA (SEQ ID NO: 106)

35 **AOLFR59 sequences:**

MGDWNNSDAVEPIFILRGFPGL EYVHWSLSILFCLAYLVAFMGNVTILSVIWISSLHQPMYYFI
SILAVNDLGMSTLPTMLAVLW L D APEIQASACYAQLFFHTFTFLESSVLLAMAFDRFVAICH
PLHYPTILTNSVIGKIGLACLLRSLGVVLP TPLLLRH YHYCHGNALSHAFCLHQDVLRLSCTDA
RTNSIYGLCVVIATLGVD SIFILLSYVLILNTVLDIASREEQLKALNTCVSHICVVLFFVPIGV S
40 MVHRFGKHLSPIVHILMADIYLLPVLNPIVYSVR TKQIRLGILHKFVLRRRF (SEQ ID NO:
107)

ATGGGAGACTGGAATAACAGTGATGCTGTGGAGCCCATATTTATCCTGAGGGGTTTTCTCTG
GACTGGAGTATGTTCACTTCTGGCTCTCCATCCTCTTCTGTCTTG CATATTTGGTAGCATT
45 ATGGGTAATGTTACCATCCTGTCTGTCACTTGGATAGAATCCTCTCTCCATCAGCCCATGTA
TTACTTTATTTCCATCTTAGCAGTGAATGACCTGGGGATGTCCCTGTCTACACTTCCACCA
TGCTTGCTGTGTTATGTTGGATGCTCCAGAGATCCAGGCAAGTGCTTGCTATGCTCAGCT
GTTCTTCATCCACACATTCAATTCCTGGAGTCCCTCAGTGTTGCTGGCCATGGCCTTTGACC
GTTTTGTTGCTATCTGCCATCCACTGCACTACCCACCATCCTCACCACAGTGTAATTGGC
50 AAAATTGGTTTGGCCTGTTTGCTACGAAGCTTGGGAGTTGTA CTCTCCACACCTTTGCTACT
GAGACACTATCACTACTGCCATGGCAATGCCCTCTCTCACGCCTTCTGTTTGCAACAGGAT
GTTCTAAGATTATCCTGTACAGATGCCAGGACCAACAGTATTTATGGGCTTTGTGTAGTCA
TTGCCACACTAGGTGTGGATTCAATCTTCATACTTCTTTCTTATGTTCTGATTCTTAATACT
GTGCTGGATATTGCATCTCGTGAAGAGCAGCTAAAGGCACTCAACACATGTGTATCCATA
55 TCTGTGTGGTGCTTATCTTCTTTGTGCCAGTTATTGGGGTGTCAATGGTCCATCGCTTTGGG
AAGCATCTGTCTCCCATAGTCCACATCCTCATGGCAGACATCTACCTTCTTCTCCCCCAGT

CCTTAACCCTATTGTCTATAGTGTGAGAACAAAGCAGATTTCGTCTAGGAATTCTCCACAAG
TTTGTCTAAGGAGGAGGTTTAA (SEQ ID NO: 108)

AOLFR60 sequences:

5 MFLPNDTQFHPSSFLLLGIPGLETLHIWIGFPFCVYMIALIGNFTILLVIKTDSSLHQPMFYFLA
MLATTDVGLSTATIPKMLGIFWINLRGIFEAQLTQMFFIHNFTLMESAFLVAMAYDSYVAJCN
PLQYSAILTNKVSVIGLGVFVRALIFVIPSILLILRLPFCGNHVIPHTYCEHMGHLAHLSCASIKINI
IYGLCAICNLVFDITVIALSYVHILCAVFRLPHEPRLKSLSTCGSHVCVILAFYTPALFSFMTHC
FGRNVPRYIHILLANLYVVVPPMLNPVIYGVRTKQIYKCVKKILLQEQGMEKEEYLIHTRF
10 (SEQ ID NO: 109)

ATGTTCCCTTCCCAATGACACCCAGTTTCACCCCTCCTCCTTCTGTTGCTGGGGATCCCAGG
ACTAGAAACACTTCACATCTGGATCGGCTTTCCCTTCTGTGCTGTGTACATGATCGCACTC
ATAGGGAACCTTCACTATTCTACTTGTGATCAAGACTGACAGCAGCCTACACCAGCCCATGT
15 TCTACTTCTGGCCATGTTGGCCACCACTGATGTGGGTCTCTCAACAGCTACCATCCCTAA
GATGCTTGGAAATCTTCTGGATCAACCTCAGAGGGATCATCTTTGAAGCCTGCCTCACCCAG
ATGTTTTTTATCCACAACCTTCACTTATGGAGTCAGCAGTCCTTGTGGCAATGGCTTATG
ACAGCTATGTGGCCATCTGCAATCCACTCCAATATAGCGCCATCCTCACCAACAAGGTTGT
TTCGTGATTGGTCTTGGTGTGTTTGTGAGGGCTTAAATTTTCGTCAATCCCTCTATACTTC
20 TTATATTGCGGTTGCCCTTCTGTGGGAATCATGTAATTCCCCACACCTACTGTGAGCACAT
GGGTCTTGCTCATCTATCTTGTGCCAGCATCAAAATCAATATTATTTATGGTTTATGTGCCA
TTTGTAAATCTGGTGTGTTGACATCACAGTCATTGCCCTCTCTTATGTGCATATTCTTTGTGCT
GTTTTCCGTCTTCTACTCATGAGCCCCGACTCAAGTCCCTCAGCACATGTGGTTACATGT
GTGTGTAATCCTTGCTTCTATACACCAGCCCTCTTTTCTTTATGACTCATGTGTTGGCC
25 GAAATGTGCCCCGCTATATCCATATACTCCTAGCCAATCTCTATGTTGTGGTGCCACCAAT
GCTCAATCCTGTCTATATATGGAGTCAGAACCAAGCAGATCTATAAATGTGTAAAGAAAAAT
ATTATTGCAGGAACAAGGAATGGAAGAGTACCTAATACATACGAGGTTCTGA
(SEQ ID NO: 110)

AOLFR61 sequences:

30 MSIINTSYVEITTFVLVGMPLGLEYAHIWISIPICSMYLIAILNGNTILFNIKTEPSLHGPMPYYFLSML
AMSDLGLSLSSLPTVLSIFLNPAPETSSSACFAQEFFIHGFSVLESSVLLIMSFDRFLAIHNPLRYT
SILTTVRVAQIGIVFSFKSMMLVLPFPFTLRSLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY
GFFGALCLMVDFILIAVSYTLILKTVPGIASKKEELKALNTCVSHICAVIIFYLPIINLAVVHRFAG
35 HVSPLINVLMANVLLVPPLMKPIVYCVKTKQIRVRVVAKLCQWKI (SEQ ID NO: 111)

ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTTGGTTGGGATGCCAG
GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT
40 CTAGGAAATGGCACCATTCTTTTATCATCAAGACAGAGCCCTCCTTGCATGGGCCCCATGT
ACTATTTTCTTCCATGTTGGCTATGTCAGACTTGGGTTTGTCTTTATCATCTCTGCCCACT
GTGTTAAGCATCTTCTGTTCAATGCCCCGAAACTTCTTCTAGTGCCTGCTTTGCCAGGA
ATTCTTCATTATCATGGATTCTCAGTACTGGAGTCTCAGTCCCTCCTGATCATGTCAATTTGATA
GATTCCCTAGCCATCCACAATCCTCTGAGATACACCTCAATCCTGACAACTGTCAGAGTTGC
CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT
45 TAAGAAGCTTGAGATATTGCAAGAAAAACCAATTATCCCATTCTACTGTCTCCACCAGGA
TGTCATGAAGTTGGCCTGTTCTGACAACAGAAATTGATGTTATCTATGGCTTTTTTGGAGCA
CTCTGCCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCCTGATCCTCAAGACTGT
ACCGGGAATTGCATCCAAAAAGGAGGAGCTTAAGGCTCTCAATACTTGTGTTTACACATC
TGTCAGTGATCATCTTCTACCTGCCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCGG
50 GCATGTCTCTCCCTCATTAAATGTTCTCATGGCAATGTTCTCCTACTGTACCTCCGCTGA
TGAAACCAATTGTTTATTGTGTAAAACTAAACAGATTAGAGTGAGAGTTGTAGCAAAAT
GTGTCAATGGAAGATTTAA (SEQ ID NO: 112)

AOLFR62 sequences:

55 MFYHNKSIHFPVTFFLIGIPGLEDFHWMISGPFCSVYLVALLGNATILLVIKVEQTLREPMFYFL
AILSTIDLALSATSVPRLMLGIFWFDAAHEINYGACVAQMFLIHAFTGMEAEVLLAMAFDRYVAIC

APLHYATILTSLVLVGISMCTVRPVLLTLPVYLYRLPFCQAHIIAHSYCEHMGIAKLSCGNIRI
 NGIYGLFVVSFFVLNLVLIGISYVYILRAVFRLP SHDAQLKALSTCGAHVGVICVFYIPSVFSFLT
 HRFQGHQIPGYIHLVANLYLIIPPSLNPITYGVRTKQIRERVLYVFTKK (SEQ ID NO: 113)

5 ATGTTTTATCACAACAAGAGCATATTTACCCAGTCACATTTTTCTCATTGGAATCCCAGG
 TCTGGAAGACTTCCACATGTGGATCTCCGGGCCTTTCTGCTCTGTTTACCTTGTGGCTTTGC
 TGGGCAATGCCACCATTCTGCTAGTCATCAAGGTAGAACAGACTCTCCGGGAGCCCCATGTT
 CTACTTCCTGGCCATTCTTTCCACTATTGATTTGGCCCTTTCTGCAACCTCTGTGCCTCGCA
 TGGTGGGTATCTTCTGGTTTGATGCTCACGAGATTAACTATGGAGCTTGTGTGGCCAGAT
 10 GTTCTGATCCATGCCTTCACTGGCATGGAGGCTGAGGTCTTACTGGCTATGGCTTTTGAC
 CGTTATGTGGCCATCTGTGCTCCACTACATTACGCAACCATTCTGACATCCCTAGTGTGGT
 GGGCATTAGCATGTGCATTGTAATTCGTCCCGTTTTACTTACACTTCCCATTGGTCTATCTTA
 TCTACCGCCTACCTTTTGTGAGGCTCACATAATAGCCCATTCCTACTGTGAGCACATGGG
 CATTGCAAAAATTGTCTGTGAAACATTTCGTATCAATGGTATCTATGGGCTTTTTGTAGTTT
 15 CTTTCTTTGTTCTGAACCTGGTGTCTATTGGCATCTCGTATGTTTACATTCTCCGTGCTGTC
 TTCCGCCTCCCATCACATGATGCTCAGCTAAAAGCCCTAAGCACGTGTGGCGCTCATGTTG
 GAGTCATCTGTGTTTTCTATATCCCTTCAGTCTTCTCTTTCTTACTCATCGATTTGGACAC
 CAAATACCAGGTTACATTACATTCTTGTGCAATCTCTATTTGATTATCCCACCTCTCT
 CAACCCCATCATTTATGGGGTGAGGACCAACAGATTGAGAGCGAGTGCTCTATGTTTTT
 20 ACTAAAAAATAA (SEQ ID NO: 114)

AOLFR63 sequences:

MSINTSYVEITTFVLVGMPLGEYAHIWISIPICSMYLIAILGNGTILFIKTEPSLHEPMYFYLSML
 AMSDLGLSLSSLPTVLSIFLNAPEISSNACFAQEFFIHGFSVLESSVLLIMSFDRLAIHNPLRYTS
 25 ILTTVRVAQIGIVFSFKSMMLVLPFPFTLRNLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY
 GFFGALCLMVDFILAVSYTLILKTVLGIASKKEQLKALNTCVSHICAVIIFYLPINLAVVHRFAR
 HVSPLINVLMANVLLLVPPLTNPIVYCVKTKQIRVRVVAKLCQRKI (SEQ ID NO: 115)

ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTTGGTTGGGATGCCAG
 30 GGCTAGAAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT
 CTAGGAAATGGCACCATTCTTTTTATCATCAAGACAGAGCCCTCCTTGCATGAGCCCATGT
 ACTATTTTCTTTCCATGTTGGCTATGTCAGACTTGGGTTTGTCTTTATCATCTCTGCCCACT
 GTGTTAAGCATCTTCTGTCAATGCTCCTGAAATTTTCATCCAATGCCTGCTTTTGCCAGGA
 ATTCTTCATTCAATGATTCTCAGTACTGGAGTCCTCAGTCCTCCTGATCATGTCAATTTGATA
 35 GATTCTAGCCATCCACAACCCTCTGAGATACACCTCAATCCTGACAACTGTCAGAGTTGC
 CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT
 TAAGAACTTGAGATATTGCAAGAAAAACCAATTATCCCATTCCTACTGTCTCCACCAGGA
 TGTCAATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTTTGGAGCA
 CTCTGCCTTATGGTAGACTTATTCTCATTGCTGTGCTTACACCCTGATCCTCAAGACTGT
 40 ACTGGGAATTGCATCCAAAAAGGAGCAGCTTAAGGCTCTCAATACTTGTGTTTACACATC
 TGTGCAGTGATCATCTTCTACCTGCCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCCG
 GCATGTCTCTCCCTCATTAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCACTGA
 CGAACCAATTGTTTATTGTGTAAAACTAAACAGATTAGAGTGAGAGTTGTAGCAAAATT
 GTGTCAACGGAAGATTAA (SEQ ID NO: 116)

45

AOLFR64 sequences:

MTILLNSSLQRAFFLTGFQGLEGLHGWISIPFCFIYLTIVLGNLTILHVICTDATLHGPMYYFLG
 MLAVTDLGLCLSTLPTVLGIFWFDTREIGIPACFTQLFFIHTLSSMESSVLLSMSIDRSVAVCNPL
 HDSTVLTPACIVKMGLSSVLSALLILPLPFLLRKFQYCHSHVLAHAYCLHLEIMKLACSSIIVN
 50 HIYGLFVVACTVGVDSLLIFLSYALILRTVLSIASHQERLRALNTCVSHICAVLLFYPMIGLSLV
 HRFGEHLPRVVHLFMSYVYLLVPLMNPPIYSIKTKQIRQRIKKFQFIKSLRCFWKD (SEQ ID
 NO: 117)

ATGACAATTCTTCTTAATAGCAGCCTCCAAAGAGCCACTTTCTTCTGACGGGCTTCCAAG
 55 GTCTAGAAGGTCTCCATGGCTGGATCTCTATTCCCTTCTGCTTCATCTACCTGACAGTTATC
 TTGGGGAACCTCACCATTCTCCACGTCATTGTACTGATGCCACTCTCCATGGACCCATGT

ACTATTTCTTGGGCATGCTAGCTGTCACAGACTTAGGCCTTTGCCTTTCCACACTGCCCCACT
 GTGCTGGGCATTTTCTGGTTTGATACCAGAGAGATTGGCATCCCTGCCTGTTTCACTCAGC
 TCTTCTCATCCACACCTTGTCTTCAATGGAGTCATCAGTTCTGTTATCCATGTCCATTGAC
 CGCTCCGTGGCCGTCTGCAACCCACTGCATGACTCCACCGTCTGACACCTGCATGTATTG
 5 TCAAGATGGGGCTAAGCTCAGTGCTTAGAAGTGCTCTCCTCATCCTCCCCCTGCCATTCCCTC
 CTGAAGCGCTTCCAATACTGCCACTCCCATGTGCTGGCTCATGCTTATTGTCTTCACCTGGA
 GATCATGAAGCTGGCCTGCTCTAGCATCATTGTCAATCACATCTATGGGCTCTTTGTTGTG
 GCCTGCACCGTGGGTGTGGACTCCCTGCTCATCTTTCTCTCATACGCCCTCATCCTTCGCAC
 CGTGCTCAGCATTGCCTCCCACCAGGAGCGACTCCGAGCCCTCAACACCTGTGTCTCTCAT
 10 ATCTGTGCTGTACTGCTCTTCTACATCCCCATGATTGGCTTGTCTCTTGTGCATCGCTTTGG
 TGAACATCTGCCCCGCGTTGTACACCTCTTCATGTCCCTATGTGTATCTGCTGGTACCACCCC
 TTATGAACCCCATCATCTACAGCATCAAGACCAAGCAAAATTCGCCAGCGCATCATTAAGAA
 GTTTCAGTTTATAAAGTCACTTAGGTGTTTTTGAAGGATTAA (SEQ ID NO: 118)

15 **AOLFR65 sequences:**

MAGRMSTSNHTQFHPSSFLLLGIPGLEDVHIWIGVPFFVYLVALLGNTALLFVIQTEQSLHEPM
 YYFLAMLDSIDLGLSTATIPKMLGIFWNTKEISFGGCLSHMFFIHFHTAMESIVLVAMAFDRYI
 AICKPLRYTMILTSKIISLIAGIAVLRSLYMVVPLVFLLLRLPFCGHRIPHTYCEHMGRIARLACAS
 KVNIRFGLGNISLLLDVILILSYVRILYAVFCLPSWEARLKALNTCGSHIGVILAFFTPAFFSFL
 20 THRFHGNIPQYIHILANLYVVPALNPVIYGVRTKQIRERVLRIFLKTNH (SEQ ID NO: 119)

ATGGCAGGAAGAATGTCTACGTCTAATCACACCCAGTTCATCCTTCTTCATTCTCTACTGCT
 GGGTATCCCAAGGCTAGAAGATGTGCACATTTGGATTGGAGTCCCTTTTTCTTTGTGTAT
 CTTGTTGCACTCCTGGGAAACACTGCTCTCTTGTGTTGTGATCCAGACTGAGCAGAGTCTCC
 25 ATGAGCCTATGTACTACTTCTGGCCATGTTGGATTCCATTGACCTGGGCTTGTCTACAGC
 CACCATCCCCAAAATGTTGGGCATCTTCTGGTTCATACCAAAGAAATATCTTTGGAGGC
 TGCCTTTCTCACATGTTCTTCATCCATTTCTTCACTGCTATGGAGAGCATTTGTTGGTGGC
 CATGGCCTTTGACCGCTACATTGCCATTGCAAACCTCTTCGGTACACCATGATGCTCAGCA
 GCAAATCATCAGCCTCATTGCAGGCATTGCTGTCCTGAGGAGCCTGTACATGGTTGTTCC
 30 ACTGGTGTCTCTCTTCTGAGGCTGCCCTTCTGTGGGCATCGTATCATCCCTCATACTTATT
 GTGAGCACATGGGCATTGCCCGTCTGGCCTGTGCCAGCATCAAAGTCAACATTAGGTTTGG
 CCTTGGCAACATATCTCTCTTGTACTGGATGTTATCCTTATTATTCTCTCCTATGTCAGGA
 TCCTGTATGCTGTCTTCTGCCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGT
 GGTCTCATATTGGTGTATCTTAGCCTTTTTTACACCAGCATTTTTTTCATTCTTGACACA
 35 TCGTTTTGGCCATAATATCCACAGTATATACATATTATATTAGCCAACCTGTATGTGGTTG
 TCCCACCAGCCCTCAATCCTGTAATCTATGGAGTCAGGACAAAGCAGATTCGAGAGAGAG
 TGCTGAGGATTTTTCTCAAGACCAATCACTAA (SEQ ID NO: 120)

AOLFR66 sequences:

40 MSFLNGTSLTPASFILNGIPGLEDVHLWISFPLCTMYSIAITGNFGLMYLIYCDEALHRPMYVFL
 ALLSFTDVLMTSTLPNTLFLWNLKEIDFKACLAQMFFVHTFTGMESGVMLMALDHCVAI
 CFPLRYATILTNSVIAKAGFLTFLRGVMLVIPSTFLTKRLPYCKGNVIPHTYCDHMSVAKISCGN
 VRVNAIYGLIVALLIGGFIDILCTISYTMILQAVVSLSSADARQKAFSTCTAHFCAIVLTYVPAFF
 TFFTHHFGGHTIPLHHIIMANLYLLMPPTMNPVYGVKTRQVRESVIRFFLKGDNSHNF (SEQ
 45 ID NO: 121)

ATGTCATTTCTAAATGGCACCAGCCTAACTCCAGCTTCATTTCATCCTAAATGGCATCCCTG
 GTTTGGAAGATGTGCATTTGTGGATCTCCTTCCCACTGTGTACCATGTACAGCATTTGCTATT
 ACAGGGAACCTTCGGCCTTATGTACCTCATCTACTGTGATGAGGCCTTACACAGACCTATGT
 50 ATGCTTCTCCTTGGCCTTCTTTCTTTCACAGATGTGCTCATGTGCCACCAGCACCTTCCCAAC
 ACTCTCTCATATTGTGGTTAATCTCAAGGAGATTGATTTTAAAGCCTGCCTCGCCCAAGAT
 GTTCTTTGTGCACACCTTCAAGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGAC
 CACTGTGTGGCCATCTGCTTCCCTCTGCGTTATGCCACCATCCTCACTAATTCAGTCATTGC
 TAAAGCTGGGTTCCTCACTTTTCTTAGGGGTGTGATGCTTGTATCCCTTCCACTTTCCTCA
 55 CCAAGCGCCTTCCATACTGCAAGGGCAACGTATACCCACACCTACTGTGACCACATGTC
 TGTGGCCAAGATATCTTGTGTAATGTCAGGGTTAACGCCATCTATGGTTTGATAGTTGCC

CTGCTGATTGGGGGCTTTGATATCCTGTGCATTACAATCTCCTACACTATGATTCTTCAAGC
 AGTTGTGAGTCTATCATCAGCAGATGCTCGACAGAAGGCCTTCAGCACCTGCACTGCCCAC
 TTCTGTGCCATAGTCCTCACCTATGTTCCAGCCTTCTTTACCTTCTTTACACACCATTTTGG
 GGGACACACCATTCCTCTACACATACATATTATTATGGCTAATCTCTACCTACTAATGCCTC
 5 CCACAATGAACCTATTGTGTATGGGGTGAAAACACAGGCAGGTACGAGAAAGTGTCTTA
 GGTCTTTCTTAAGGGAAAGGACAATTCTCATAACTTTTAA (SEQ ID NO: 122)

AOLFR67 sequences:

MSGDNSSSLTPGFFILNGVPGLEATHIWISLPFCFMYIIA VVGNCGLICLISHEEALHRPMYYFLA
 10 LLSFTDVTLCCTMVPNMLCIFWFNLKEIDFNACLAQMFFVHMLTGMESGVMLMLALDRYVAI
 CYPLRYATILTNPVIKAGLATFLRNVMLIPFTLLTKRLPYCRGNFIPHTYCDHMSVAKVSCGN
 FKVNAIYGLMVALLIGVFDICISVSYTMLQAVMSLSSADARHKAFSTCTSHMCSIVITYVAAF
 FTFFTHRFVGHNPNIHIIIVANLYLLLPTMNPVYGVKTKIQEGVIKFLGDKVSFTYDK
 (SEQ ID NO: 123)

15 ATGTCTGGGGACAACAGCTCCAGCCTGACCCAGGATTCTTTATCTTGAATGGCGTTCCTG
 GGCTGGAAGCCACACACATCTGGATCTCCCTGCCATTCTGCTTTATGTACATCATTGTCTGC
 GTGGGGAACGTGGGGCTCATCTGCCTCATCAGCCATGAGGAGGCCCTGCACCGGCCCATGT
 ACTACTTCCTGGCCCTGCTCTCCTTCACTGATGTCACCTTGTGCACCACCATGGTACCTAAT
 20 ATGCTGTGCATATTCTGGTTCAACCTCAAGGAGATTGACTTTAACGCCTGCCTGGCCCA
 TGTTTTTTGTCCATATGCTGACAGGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGA
 CCGCTATGTGGCCATCTGCTACCCCTTACGCTATGCCACCATCCTTACCAACCCTGTCATCG
 CCAAGGCTGGTCTTGCCACCTTCTTGAGGAATGTGATGCTCATCATCCCATCACTCTCCTC
 ACCAAGCGCCTGCCCTATTGCCGGGGGAACCTTCATCCCCACACCTACTGTGACCATATGT
 25 CTGTGGCCAAGGTATCCTGTGGCAATTTCAAGGTCAATGCTATTTATGGTCTGATGGTTGC
 TCTCCTGATTGGTGTGTTTGATATCTGCTGTATCTCTGTATCTTACACTATGATTTTGCAGG
 CTGTTATGAGCCTGTCATCAGCAGATGCTCGTCACAAAGCCTTCAGCACCTGCACATCTCA
 CATGTGTTCCATTGTGATCACCTATGTTGCTGCTTTTTTCACTTTTTTCACTCATCGTTTGT
 AGGACACAATATCCCAAACCACATACACATCATCGTGGCCAACCTTTATCTGCTACTGCTCCT
 30 CCTACCATGAACCCAATTGTTTATGGAGTCAAGACCAAGCAGATTGAGGAAGGTGTAATTA
 AATTTTTACTTGGAGACAAGGTAGTTTTTACCTATGACAAATGA (SEQ ID NO: 124)

AOLFR68 sequences:

MTTHRNDTLSTEASDFLLNCFVRSPSWQHWLSLPLSLLFLLAVGANNTLLMTIWLEASLHQPL
 35 YYLLSLLSLLDIVLCLTVIPKVLTFWFDLRPISFPACFLQMYIMNCF LAMESCTFMVMAYDRY
 VAILPLRYPSTIDHFVVKAAAMFILTRNVLMTLPILSAQLRYCGRNVIENCIFANMSVSRISC
 DDVTINHL YQFAGGWTL LGSDDLIFLSYTFILRAVLR LKAEGA VAKALSTCGSHFMLILFFSTIL
 LVFVLTHVAKKKVSPDVPVLLNVLHHVIPALNPIYGVRTQEI KQGMQRLLKKG C (SEQ ID
 NO: 125)

40 ATGACAACACACCGAAATGACACCTCTCCACTGAAGCTTCAGACTTCCTCTTGAATTGTT
 TTGTCAGATCCCCCAGCTGGCAGCACTGGCTGTCCCTGCCCTCAGCCTCCTTTTCTCTTG
 GCCGTAGGGGCCAACACCACCCTCCTGATGACCATCTGGCTGGAGGCCTCTCTGCACCAGC
 CCCTGTACTACCTGCTCAGCCTCCTCTCCCTGCTGGACATCGTGCTCTGCCTCACTGTCATC
 45 CCAAGGTCTGACCATCTTCTGGTTTGACCTCAGGCCCATCAGCTTCCCTGCCTGCTTCTCCT
 CCAGATGTACATCATGAATTGTTTCTAGCCATGGAGTCTTGACATTTCATGGTCATGGCC
 TATGATCGTTATGTAGCCATCTGCCACCCACTGAGATATCCATCAATCATCACTGATCACTT
 TGTAAGTCAAGGCTGCCATGTTTATTTTGACCAGAAATGTGCTTATGACTCTGCCCATCCCC
 ATCCTTTTACGACAACTCCGTTATTGTGGAAGAAATGTCAATTGAGAACTGCATCTGTGCCA
 50 ATATGCTGTGTTCCAGACTCTCCTGCGATGATGTCACCATCAATCACCTTTACCAATTTGCT
 GGAGGCTGGACTCTGCTAGGATCTGACCTCATCCTTATCTTCTCTCTACACCTTCATTCT
 GCGAGCTGTGCTGAGACTCAAGGCAGAGGTGCGGTGGCAAAGGCCCTTAAGCACATGTGG
 CTCCCACTTCATGCTCATCCTCTTCTTACGACCATCCTTCTGGTTTTTGTCTCACACATGT
 GGCTAAGAAGAAAGTCTCCCTGATGTGCCAGTCTTGCTCAATGTTCTCCACCATGTCATT
 55 CCTGCAGCCCTTAACCCCATCATTTACGGGGTGAGAACCAAGAAATTAAGCAGGGAATG
 CAGAGGTTGTTGAAGAAAGGGTGCTAA (SEQ ID NO: 126)

AOLFR69 sequences:

- MSYSIYKSTVNPLSHGVVHSFCHNMNCNFMHIFKFVLDFNMKNVTEVTLFVLKGFTDNLELQ
 TIFFFLFLAIYLF TLMGNLGLILVVIRDSQLHKPMYYFLSMLSSVDACYSSVITPNMLVDFTTKN
 5 KVISFLGCVAQVFLACSFGTTECFLLAAMAYDRYVAIYNPLLYSVSMSPRVYMPNLINASYVAGI
 LHATHTVATFSLSFCGANEIRRVFC DIPLLAISYSDTHTNQLLLFYFVGSIELVTILVLISYGLIL
 LAILKMYSAEGRRKVFSTCGAHLTGVSIIYGTILFMYVRPSSSYASDHDMIVSIFYTIVIPLLNPV
 IYSLRNKDVKDSMKKMF GKNQVINKVYFHTKK (SEQ ID NO: 127)
- 10 ATGTCGTACAGTATATACAAGAGCACAGTTAACATCCCCTTGAGTCATGGTGTGTTTCATT
 CTTTTGTGCATAATATGAACTGTAACCTTATGTCATATCTTCAAGTTTGTTCTAGATTTCAAC
 ATGAAGAATGTCACCTGAAGTTACCTTATTTGTAAGGAGGCTTCACAGACAATCTTGAAC
 TGCAGACTATCTTCTTCTCCTGTTTCTAGCAATCTACCTCTTCACTCTCATGGGAAATTTA
 GGACTGATTTTAGTGGTCATTAGGGATTCCCAGCTCCACAAACCCATGTACTATTTTCTGA
 15 GTATGTTGTCTTCTGTGGATGCCTGCTATTCCTCAGTTATTACCCCAAATATGTTAGTAGAT
 TTTACGACAAAGAATAAAGTCATTTTCATTCCTTGGATGTGTAGCACAGGTGTTTCTTGCTT
 GTAGTTTGGAAACCACAGAATGCTTTCTCTTGGCTGCAATGGCTTATGATCGCTATGTAGC
 CATCTACAACCTCTCCTGTATTCACTGAGCATGTACCCAGAGTCTACATGCCACTCATC
 AATGCTTCTATGTTGCTGGCATTTTACATGCTACTATACATACAGTGGCTACATTTAGCCT
 20 ATCCTTCTGTGGAGCCAATGAAATTAGGCGTGTCTTTGTGATATCCCTCCTCTCCTTGCTA
 TTTCTTATTCTGACACTCACACAAACAGCTTCTACTCTTCTACTTTGTGGGCTCTATCGAG
 CTGGTCACTATCCTGATTGTTCTGATCTCCTATGGTTGATTCTGTTGGCCATTCTGAAGAT
 GTATTCTGCTGAAGGGAGGAGAAAAGTCTTCTCCACATGTGGAGCTCACCTAACTGGAGT
 GTCATTTATTATGGGACAATCCTCTTCATGTATGTGAGACCAAGTTCAGCTATGCTTCG
 25 GACCATGACATGATAGTGTCAATATTTACACCATTGTGATTCCCTTGCTGAATCCCGTCAT
 CTACAGTTTGAGGAACAAAGATGTAAAAGACTCAATGAAAAAATGTTTGGGAAAAATCA
 GGTTATCAATAAAGTATATTTTCATACTAAAAAATAA (SEQ ID NO: 128)

AOLFR70 sequences:

- MDSTFTGYNLNQLVKTEMDKLSSGLDIYRNPLKNKTEVTMFILTGFTDDFELQVFLFLFFAI
 YLFTLIGNLGLVVLVIEDSWLHNPMMYYFLSVLSFLDACYSTVVPKMLVNFLAKNKSISFIGCA
 TQMLLFVTFGTTECFLLAAMAYDHYVAIYNPLLYSVSMSPRVYVPLITASYVAGILHATIHIVA
 TFSLSFCGSNEIRHVFC DMPPLLAISCSDTHTNQLLLFYFVGSIEIVTILVLISCFILL SILKMHSA
 KGRQKAFSTCGSHLTGVTIYHGTLVSYMRPSSSYASDHDIIVSIFYTIVIPKLNPIIYSLRNKEVK
 35 KAVKMKMLVYK (SEQ ID NO: 129)
- ATGGACTCCACTTTCACAGGCTATAACCTTTATAACCTGCAAGTAAAAACTGAAATGGACA
 AGTTGTCTACAGGTTTGGATATATACAGGAATCCACTGAAGAACAAGACTGAAGTCAACCA
 TGTATATTGACAGGCTTCACAGATGATTTTGAGCTGCAAGTCTTCTATTTTTACTATTT
 40 TTTGCAATCTATCTCTTTACCTTGATAGGCAATTTAGGGCTGGTTGTGTTGGTCATTGAGG
 ATTCCTGGCTCCACAACCCCATGTATTATTTCTTAGTGTGTTTATCATTCCTTGGATGCTTGC
 TATTCTACAGTTGTCACTCCAAAAATGTTGGTCAATTTCTGGCAAAAAATAAATCCATTT
 CATTTATCGGATGTGCAACACAGATGCTTCTTTTGTGTTACTTTTGGAACTACAGAATGTTT
 CTCTGGCTGCAATGGCTTATGATCACTATGTAGCCATCTACAACCTCTCCTGTATTCACT
 45 GAGCATGTACCCAGAGTCTATGTGCCACTCATCACTGCTTCTACGTTGCTGGCATTTTAC
 ATGCTACTATACATATAGTGGCTACATTTAGCCTGTCTTCTGTGGATCCAATGAAATTAG
 GCATGTCTTTGTGATATGCCTCCTCTCCTTGCTATTTCTTGTCTGACACTCACACAAACC
 AGCTTCTACTCTTCTACTTTGTGGGTTCTATTGAGATAGTCACTATCCTGATTGTCTCATT
 TCCTGTGATTTTCACTTCTGTTGCCATTCTGAAGATGCATTCTGCTAAGGGAAGGCAAAAGG
 50 CCTTCTCATATGTGGCTCTCACTAAGTGAAGTGACAATTTATCATGGAACAATCTCGTC
 AGTTATATGAGACCAAGTTCAGCTATGCTTCAGACCATGACATCATAGTGTCAATATTTT
 ACACAATTGTGATTCCCAAGTTGAATCCCATCATCTATAGTTTGAGGAACAAAGAAGTAAA
 AAAGGCAGTGAAGAAAATGTTGAAATTGGTTTACAAATGA (SEQ ID NO: 130)

AOLFR71 sequences:

MGRRNNTNVPDFILTGLSDSEEVQMALFILLLIYLTMLGNVGMILIRLDLQLHTPMYFFLTH
 LSFIDLSYSTVITPKTLANLLTSNYISFMGCFAQMFFVFLGAAECFLSSMAYDRYVAICSPRLRY
 PVIMSKRLCCALVTGPYVISFINSEFVNVVWMSRLHFCDSNVVRHFFCDTSPILALSCMDTYDIEI
 5 MIHILAGSTLMVSLITISASYVSILSTILKINSTSGKQKALSTCASHLLGVTFYGTMIFTYLKPRK
 SYSLGRDQVASVFYTTIVPMLNPLIYSLRNKEVKNALIRVMQRRQDSR (SEQ ID NO: 131)

ATGGGTTAGAAGAAATAACACAAATGTGCCTGACTTCATCCTTACGGGACTGTCAGATTCTG
 AAGAGGTCCAGATGGCCCTCTTTATACTATTTCTCCTGATATACCTAATTACTATGCTGGGG
 10 AATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTATTTT
 TCCTTACTCACTTGTCAATTTATTGACCTCAGTTACTCAACTGTCATCACACCTAAAACCTTA
 GCGAACTTACTGACTTCCAATAATTTCTTCTCATGGGCTGCTTTGCCAGATGTTCTTTTT
 TGTCTTCTTGGGAGCTGCTGAATGTTTTCTTCTCTCATCAATGGCCTATGATCGCTACGTTAG
 CTATCTGCAGTCCTCTACGTTACCCAGTTATTATGTCCAAAAGGCTGTGTTGCGCTCTTGTG
 15 ACTGGGCCCTATGTGATTAGCTTTATCAACTCCTTTGTCAATGTGGTTTGGATGAGCAGAC
 TGCATTTCTGCGACTCAAATGTAGTTCGTCACTTTTTCTGCGACACGTCTCCAATTTTAGCT
 CTGTCTGTCATGGACACATACGACATTGAAATCATGATACACATTTTAGCTGGTTCCACCC
 TGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTTACCATCCTGAAA
 ATTAATTCCACTTCAGGAAAGCAGAAAGCTTTGTCTACTTGTGCTCTCATCTCTTGGGAG
 20 TCACCATCTTTTATGGAATATGATTTTTACTTATTTAAAACCAAGAAAGTCTTATTCTTTG
 GGAAGGGATCAAGTGGCTTCTGTTTTTATACTATTGTGATTCCCATGCTGAATCCACTCAT
 TTATAGTCTTAGAAACAAAGAAGTTAAAAATGCTCTCATTAGAGTCATGCAGAGAAGACA
 GGACTCCAGGTAA (SEQ ID NO: 132)

25 **AOLFR72 sequences:**

MAPENFTRVTEFILTVGVSSPELQIPLFLVFLVLYGLTMAGNLGIITLTSVDSRLQTPMYFFLQHL
 ALINLGNSTVIAPKMLINFLVKKKTTSFYECATQLGGFLFFIVSEVIMLALMACDRYVAICNPLL
 YMVVVSRRLLCLLVSLTYLYGFSTAIVVSSYVFSVSYCSSNINHFYCDNVPLALSCSDTYLPE
 TVVFISAATNVVGSLLIIVLSYFNIVLSILKICSSEGRKKAFSTCASHMMAVTIFYGTLLFMYVQP
 30 RSNHSLDITDDKMASVFYTLVIPMLNPLIYSLRNKDVKTALQRFMNLCYSFKTM (SEQ ID NO:
 133)

ATGGCTCCTGAAAATTTACCCAGGGTCACTGAGTTTATTCTTACAGGTGTCTCTAGCTGTC
 CAGAGCTCCAGATTCCCCTCTTCTGGTCTTTCTGGTGCTCTATGGGCTGAGCTGGCAGG
 35 GAACCTGGGCATCATCACCTCACCAGTGTGACTCTCGACTTCAAACCCCATGTACTTTT
 TCCTGCAACATCTGGCTCTCATTAATCTGGTAACTCTACTGTCAATTGCCCTAAAAGTCTG
 ATTAACTTTTTAGTAAAGAAGAAACTACCTCATTCTATGAATGTGCCACCCAACTGGGAG
 GGTCTTGTCTTTTATTGTATCGGAGGTAATCATGCTGGCTTTGATGGCCTGTGACCGCTAT
 GTGGCTATTTGTAACCTCTGCTGTACATGGTGGTGGTGTCTCGGCGGCTCTGCCTCCTGCT
 40 GGTCTCCCTCACATACCTCTATGGCTTTTCTACAGCTATTGTGGTTTCATCTTATGTATTCT
 CTGTGTCTTATTGCTCTTCTAATATAATCAATCATTTTTACTGTGATAATGTTCTCTGTTA
 GCATTATCTTGTCTGATACTTACTTACCAGAAACAGTTGTCTTTATATCTGCAGCAACAA
 ATGTGGTTGGTTCCTTGATTATAGTTCTAGTATCTTATTTCAATATTGTTTTGTCTATTTTA
 AAAATATGTTTCATCAGAAGGAAGGAAAAAGCCTTTTCTACCTGTGCTTCACATATGATGG
 45 CAGTCACAATTTTTATGGGACATTGCTATTCTATGTATGTGCAGCCCCGAAGTAACCATTCT
 ATGGATACTGATGATAAGATGGCTTCTGTGTTTTACACGTTGGTAATTCTCATGCTGAAT
 CCCTTGATCTACAGCCTGAGGAATAAGGATGTGAAGACTGCTCTACAGAGATTTCATGACA
 AATCTGTGCTATTCTTTAAACAATGTAA (SEQ ID NO: 134)

50 **AOLFR73 sequences:**

MNHVVKHNHTAVTKVTEFILMGITDNPGLQAPLFGFLIITYLTVIGNLGMVILTYLDSKLHTP
 MYFFLRHLSITDLGYSTVIAPKMLVNFIVHKNTISYNWYATQLAFFEIFISELFILSAMAYDRYV
 AICKPLLYVIMAEKVLWVLVIVPYLYSTFVSLFTIKLFKLSFCGSNIISYFYCDCIPLMSILCSDT
 NELELILIFSGCNLLFSLSIVLISYMFILVAILRMNSRKGRYKAFSTCSSHLTVVIMFYGTLLFYFL
 55 QPKSSHTLAIDKMASVFYTLIPMLNPLIYSLRNKEVKDALKRTLNRFKIPI (SEQ ID NO: 135)

ATGAATCATGTGGTAAAACACAATCACACGGCAGTGACCAAGGTGACTGAATTTATTCTCA
 TGGGGATTACAGACAACCCTGGGCTGCAGGCTCCACTGTTTGGACTCTTCCTCATCATATA
 TCTGGTCACAGTGATAGGCAATCTGGGCATGGTTATCTTGACCTACTTGGACTCCAAGATA
 CACACCCCATGTACTTTTTCTTAGACATTTGTCAATCACTGATCTTGGTTACTCCACTGT
 5 CATTGCCCCGAAGATGTTAGTAACTTCATAGTGCACAAAAACACAATTTCTTACAATTGG
 TATGCCACTCAGCTAGCATTCTTTGAGATTTTCATCATCTCTGAGCTCTTTATTCTATCAGC
 AATGGCCTATGATCGCTACGTAGCCATCTGTAAACCTCTTCTGTACGTGATCATCATGGCA
 GAGAAAGTACTTTGGGTGCTGGTAATTGTTCCCTATCTCTATAGCACGTTTGTGTCACTATT
 TCTCACAATTAAGTTATTTAAACTGTCCTTCTGTGGCTCAAACATAATCAGCTATTTTACT
 10 GTGACTGTATCCCTCTGATGTCCATACTCTGTTCTGACACAAATGAATTAGAATTAATAAT
 TTTGATCTTCTCAGGCTGTAATTTGCTCTTCTCCCTCTCAATTGTTCTCATATCCTACATGTT
 TATTCTAGTGGCCATTCTCAGAATGAACTCAAGGAAAGGGAGGTACAAAGCCTTCTCCACC
 TGTAGCTCTCATCTGACAGTGGTGATCATGTTCTATGGGACATTGTTATTTATTTACTTGCA
 ACCCAAGTCCAGTCATACTTTGGCTATTGATAAAATGGCCTCAGTGTTTTATACCCTGTTG
 15 ATTCCTATGCTGAATCCGTTGATCTACAGCCTAAGGAACAAAGAAGTAAAAGATGCTCTAA
 AGAGAACTTTAACCAATCGATTCAAAATCCCATTAA (SEQ ID NO: 136)

AOLFR74 sequences:

MEQHNLTTVNEFILTGITDIAELQAPLFALFLMIYVISVMGNLGMIVLTKLDSRLQTPMYFFLRH
 20 LAFMDLGYSTTVGPKMLVNFVVDKNIISYFCAATQLAFFLVFIGSELFILSAMSVDLYVAICNPL
 LYTVIMSRRVCQVLVAIPYLYCTFISLLVTIKIFLSFCGYNVISHFYCDLPLPLCSNTHIELI
 ILIFAAIDLISLLIVLLSYLLILVAILRMNSAGRQKAFSTCGAHLTVVIVFYGTLLFMVYQPKSSH
 SFDTDKVASIFYTLVIPMLNPLIYSLRNKDVKYALRRTWNNLCNIFV (SEQ ID NO: 137)

25 ATGGAACAACACAATCTAACAACGGTGAATGAATTCATTCTTACGGGAATCACAGATATC
 GCTGAGCTGCAGGCACCATTATTTGCATTGTTCCCTCATGATCTATGTGATCTCAGTGATGG
 GCAATTTGGCATGATTGTCTCCACCAAGTTGGACTCCAGGTTGCAAACCCCTATGTACTT
 TTTTCTCAGACATCTGGCTTTCATGGATCTTGGTTATTCAACAACCTGTGGGACCCAAAATG
 TTAGTAAATTTTGTGTGGATAAGAATATAATTTCTTATTATTTTGTGCAACACAGCTAGC
 30 TTTCTTTCTTGTGTTCAATTGGTAGTGAACCTTTTTATTCTCTCAGCCATGTCCTACGACCTCT
 ATGTGGCCATCTGTAACCCTCTGCTATACACAGTAATCATGTACGAAGGGTATGTCAGGT
 GCTGGTAGCAATCCCTTACCTCTATTGCACATTCAATTTCTCTTCTAGTCACCATAAAGATTT
 TTACTTTATCCTTCTGTGGCTACAACGTCATTAGTCATTTCTACTGTGACAGTCTCCCTTG
 TTACCTTTGCTTTGTTCAAATACACATGAAATTGAATTGATAATTCTGATCTTTGCAGCTAT
 35 TGATTTGATTTCACTCTTCTGATAGTTCTTTTATCTTACCTGCTCATCCTTGATGCCATTCT
 CAGGATGAATTCTGCTGGCAGACAAAAGGCTTTTTCTACCTGTGGAGCCCACCTGACAGTG
 GTCATAGTGTTCTATGGGACTTTGCTTTTCATGTACGTGCAGCCCAAGTCCAGTCATTCCCT
 TGACACTGATAAAGTGGCTTCCATATTTTACACCCTGGTTATCCCCATGTTGAATCCCTTGA
 TCTATAGTTTACGAAACAAAGATGTAATAATGCCCTACGAAGGACATGGAATAACTTATG
 40 TAATATTTTTGTTTAA (SEQ ID NO: 138)

AOLFR75 sequences:

MEGKNQTNISEFLLGFSSWQQQVLLFALFLCLYLTLGLFGNLLILLAIGSDHCLHTPMYFFLA
 NLSLVDLCLPSATVPKMLLNITQTQTISYPGCLAQMYFCMMFANMDNFLTVMAYDRYVAI
 45 CHPLHYSTIMALRLCASLVAAPWVIAILNPLLHTLMMMAHLHFCSDNVIIHFFCDINSLPLSCSD
 TSLNQLSVLATVGLIFVPSVCILVSYILIVSAVMKVPSAQGKLKAFSTCGSHLALVILFYGANT
 GVYMSPLSNHSTEKDSAASVIFMVVAPVLNPFYSLRNNELKGTLLKTLRPGAVAHACNPSTL
 GGRGGWIMRSGDRDHPG (SEQ ID NO: 139)

50 ATGGAAGGGAAAAATCAAACCAATATCTCTGAATTTCTCCTCCTGGGCTTCTCAAGTTGGC
 AACAACAGCAGGTGCTACTCTTTGCACTTTTCTGTGTCTCTATTAAACAGGGCTGTTTGGAA
 AACTTACTCATCTTGCTGGCCATTGGCTCGGATCACTGCCTTCACACACCCATGTATTTCTT
 CCTTGCCAATCTGTCTTGGTAGACCTCTGCCTTCCCTCAGCCACAGTCCCCAAGATGCTAC
 TGAACATCCAAACCCAAACCCAAACCATCTCCTATCCCGGCTGCCTGGCTCAGATGTATTT
 55 CTGTATGATGTTTGCCAATATGGACAATTTTCTTCTCACAGTGATGGCATATGACCGTTAC
 GTGGCCATCTGTCACCCTTACATTACTCCACCATTATGGCCCTGCGCCTCTGTGCCTCTCT

GGTAGCTGCACCTTGGGTCAATTGCCATTTTGAACCCTCTCTTGACACTCTTATGATGGCCC
 ATCTGCACTTCTGCTCTGATAATGTTATCCACCATTTCTTCTGTGATATCAACTCTCTCCTC
 CCTCTGTCCTGTTCCGACACCAGTCTTAATCAGTTGAGTGTCTGGCTACGGTGGGGCTGA
 TCTTTGGGTACCTTCAGTGTGTATCCTGGTATCCTATATCCTCATTTGTTCTGCTGTGATG
 5 AAAGTCCCTTCTGCCCAAGGAAAACCTCAAGGCTTTCTCTACCTGTGGATCTCACCTTGCCTT
 GGTCACTTCTTTTCTATGGAGCAAAACAGGGGTCTATATGAGCCCCCTATCCAATCACTCT
 ACTGAAAAAGACTCAGCCGCATCAGTCATTTTATGGTTGTAGCACCTGTGTTGAATCCAT
 TCATTTACAGTTTAAGAAACAATGAAGTGAAGGGGACTTTAAAAAAGACCCTAAGCCGGC
 CGGGCGGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA
 10 TGAGGTCAGGAGATCGAGACCATCCTGGCTAA (SEQ ID NO: 140)

AOLFR76 sequences:

MENNTEVSEFILLGLTNAPELQVPLFIMFTLYLITLTGNLGMILLILDSHLHTPMYFFLSNLSLA
 GIGYSSAVTPKVLTLIEDKAISYSACAAQMFFCAVFATVENYLLSSMAYDRYAAVCNPLHY
 15 TTTMTTRVCACLAIGCYVIGFLNASIQIGDTFRLSFCMSNVHHFFCDKPAVITLTCSEKHISELIL
 VLISFNVFFALLVTLISYLFILITLKRHTGKGQKPLSTCGSHLIAIFLYITVIIMYIRPSSSHSM
 DTDKIASVFYTMIPMLSPIVYTLRNKDVKNFMKVVEKAKYSLDSVF (SEQ ID NO: 141)

ATGGAGAATAATACAGAGGTGAGTGAATTCATCCTGCTTGGTCTAACCAATGCCCCAGAA
 20 CTACAGGTTCCCCTCTTTATCATGTTTACCCTCATCTACCTCATCACTCTGACTGGGAACCT
 GGGGATGATCATATTAATCCTGCTGGACTCTCATCTCCACACTCCCATGTACTTTTTCTCA
 GTAACCTGTCTCTTGACAGGCATTGGTTACTCCTCAGCTGTCACTCCAAAGGTTTAACTGG
 GTTGCTTATAGAAGACAAAGCCATCTCCTACAGTGCCTGTGCTGCTCAGATGTTCTTTGT
 GCAGTCTTTGCCACTGTGGAAAATTACCTCTTGCTCAATGGCCTATGACCGCTACGCAG
 25 CAGTGTGTAACCCCTACATTATACCACCACCATGACAACACGTGTGTGTGCTTGTCTGGC
 TATAGGCTGTTATGTCATTGGTTTTCTGAATGCTTCTATCCAAATTGGAGATACATTTCCGC
 TCTCTTTCTGCATGTCCAATGTGATTCATCACTTTTTCTGTGACAAACCAGCAGTCACTTACT
 CTGACCTGCTCTGAGAAACACATTAGTGAGTTGATTCTTGTTCTTATATCAAGTTTAAATGT
 CTTTTTGCACCTCTTGTTACCTTGATTTCCATCTGTTTCATATTGATCACCATTCTTAAGAG
 30 GCACACAGGTAAGGGATACCAGAAGCCTTTATCTACCTGTGGTTCTCACCTCATTGCCATT
 TTCTTATTTTATATAACTGTCATCATCATGTACATACGACCAAGTTCCAGTCATTCCATGGA
 CACAGACAAAATTGCATCTGTGTTCTACACTATGATCATCCCCATGCTCAGTCCTATAGTCT
 ATACCCTGAGGAACAAAGACGTGAAGAATGCATTTCATGAAGGTTGTTGAGAAGGCAAAAT
 ATTCTCTAGATTCAGTCTTTTAA (SEQ ID NO: 142)

35

AOLFR77 sequences:

MGDVNQSVASDFILVGLFSHSGSRQLLFSLVAVMVFVIGLLGNTVLLFLIRVDSRLHTPMYFLLS
 QLSLFDIGCPMVTIPKMASDFLRGEGATSYGGGAAQIFFLTLMGVAEGVLLVMSYDRYVAVC
 QPLQYPVLMRRQVCLLMGSSWVVGVLNASIQTSITLHFPYCASRIVDHFCEVPALLKLSCA
 40 DTCAYEMALSTSGVLILMLPLSLIATSYGHVLQAVLSMRSEEARHKAVTTCSSHITVVGIFYGA
 AVFMYMVPYAHSPQQDNVVSFLYSLVPTLNPLIYSLRNPEVWMALVKVLSRAGLRQMC
 (SEQ ID NO: 143)

ATGGGGGATGTGAATCAGTCGGTGGCCTCAGACTTCATTCTGGTGGGCCTCTTCAGTCACT
 45 CAGGATCACGCCAGCTCCTCTTCTCCCTGGTGGCTGTCATGTTTGTGATAGGCCTTCTGGGC
 AACACCGTTCTTCTCTTCTTGATCCGTGTGGACTCCCGGCTCCACACACCCATGTACTTCT
 GCTCAGCCAGCTCTCCCTGTTTGACATTGGCTGTCCCATGGTCACCATCCCCAAGATGGCA
 TCAGACTTTCTGCGGGGAGAAGGTGCCACCTCCTATGGAGGTGGTGCAGCTCAAATATTCT
 TCCTCACACTGATGGGTGTGGCTGAGGGCGTCTGTTGGTCTCATGTCTTATGACCGTTA
 50 TGTTGCTGTGTGCCAGCCCTGCAGTATCCTGTACTTATGAGACGCCAGGTATGTCTGTG
 ATGATGGGCTCCTCCTGGGTGGTAGGTGTGCTCAACGCCCTCCATCCAGACTCCATCACCC
 TGCATTTTCCCTACTGTGCCTCCCGTATTGTGGATCACTTCTTCTGTGAGGTGCCAGCCCTA
 CTGAAGCTCTCCTGTGCAGATACCTGTGCCTACGAGATGGCGCTGTCCACCTCAGGGGTGC
 TGATCCTAATGCTCCCTCTTTCCCTCATCGCCACCTCCTACGGCCACGTGTTGCAGGCTGTT
 55 CTAAGCATGCGCTCAGAGGAGGCCAGACACAAGGCTGTCAACACCTGCTCCTCGCACATCA
 CGGTAGTGGGGCTCTTTATGGTGCCGCGGTGTTTCATGTACATGGTGCCTTGCCTACCA

CAGTCCACAGCAGGATAACGTGGTTTCCCTCTTCTATAGCCTTGTCACCCCTACACTCAAC .
 CCCCTTATCTACAGTCTGAGGAATCCGGAGGTGTGGATGGCTTTGGTCAAAGTGCTTAGCA
 GAGCTGGACTCAGGCAAATGTGCTGA (SEQ ID NO: 144)

5 **AOLFR78 sequences:**

MSPDGNHSSDPTEFVLAGLPNLNSARVELFSVFLVYLLNLTGNVLIVGVVRADTRLQTPMYF
 FLGNLSCLEILLTSVIIPKMLSNFLSRQHTISFAACITQFYFYFFLGASEFLLAVMSADRYLAICH
 PLRYPLLMGAVCFRVALACWVGGLVPVLGPTVAVALLPFCKQGAVVQHFFCDSGPLRLAC
 10 TNTKKLEETDFVLASLVIVSSLLITAVSYGLIVLAVLSIPSASGRQKAFSTCTSHLIVVTLFYGSAI
 FLYVRPSQSGSVDTNWAVTVITTFVTPLLNPFYIALRNEQVKEALKDMFRKVVAGVLGNLLLD
 KCLSEKAVK (SEQ ID NO: 145)

ATGAGTCCTGATGGGAACACAGTAGTGATCCAACAGAGTTCGTCCTGGCAGGGCTCCCA
 AATCTCAACAGCGCAAGAGTGGAATTATTTTCTGTGTTTCTTCTGTCTATCTCCTGAATCT
 15 GACAGGCAATGTGTTGATTGTGGGGGTGGTAAGGGCTGATACTCGACTACAGACCCCTAT
 GTACTTCTTTCTGGGTAACCTGTCCTGCCTAGAGATACTGCTCACTTCTGTCTATCTCCAA
 AGATGCTGAGCAATTCCTCTCAAGGCAACACACTATTTCTTTGCTGCTATCATCCACCA
 ATTCTATTTCTACTTCTTTCTCGGGGCTCCGAGTTCCTACTGTTGGCTGTCTGTCGGG
 ATCGCTACCTGGCCATCTGTCACTCCTCTGCGCTACCCCTTGCTCATGAGTGGGCTGTGTG
 20 CTTTCGTGTGGCCTTGGCCTGCTGGGTGGGGGACTCGTCCCTGTGCTTGGTCCACAGTG
 GCTGTGGCCTTGCTTCTTTCTGTAAGCAGGGTGCTGTGGTACAGCACTTCTTCTGCGACA
 GTGGCCCACTGCTCCGCTGGCTTGACCAACACCAAGAAGCTGGAGGAGACTGACTTTGT
 CCTGGCCTCCCTCGTCATTGTATCTTCTTGTGATCACTGCTGTGCTTACGGCCTCATTG
 TGCTGGCAGTCTGAGCATCCCTCTGCTTCAGGCCGTCAGAAGGCCTTCTCTACCTGTAC
 25 CTCCCACTTGATAGTGGTGACCCTCTTCTATGGAAGTGCCATTTTTCTCTATGTGCGGCCAT
 CGCAGAGTGGTCTGTGGACACTAACTGGGCAGTGACAGTAATAACGACATTTGTGACAC
 CACTGTTGAATCCATTCTATGCTTACGTAATGAGCAAGTCAAGGAAGCTTTGAAGGA
 CATGTTTAGGAAGGTAGTGGCAGGCGTTTTAGGGAATCTTTTACTTGATAAATGTCTCAGT
 GAGAAAGCAGTAAAGTAA (SEQ ID NO: 146)

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AOLFR79 sequences:

MTPGELALASGNHTPVTKFILQGFSNYPDLQELLFGAILLIYAITVVGNLGMMLIFTDSHLQSP
 MYFFLNVL SFLDICYSSVVPKLLVNFLVSDKSISFEGCVVQLAFFVVHVTAESFLLASMAFYDR
 FLAICQPLHYGSIMTRGTCLQLVAVSYAFGGANSIAIQTNVFPALPFCGPNQLTHYYCDIPLLH
 35 LACANTATARVVLYVFSALVTLPAAVILTSYCLVLVAGRMRSVAGREKDLSTCASHFLAIAI
 FYGTVVFTYVQPHGSTNNTNGQVVSFYTIIIPMLNPFYSLRNKEVKGALQRLQVNIFFP
 (SEQ ID NO: 147)

ATGACACCTGGAGAACTAGCCCTTGCCAGTGGCAACCACACCCAGTCACCAAGTTCATCT
 40 TGCAGGGATTCTCCAATTATCCAGACCTCCAGGAGCTTCTCTCGGAGCCATCCTGCTCAT
 CTATGCCATAACAGTGGTGGGCAACTTGGGAATGATGGCACTCATCTTCACAGACTCCCAT
 CTCCAAAGCCCAATGTATTTCTTCTCAATGTCTCTCGTTTCTTGATATTTGTTACTCTTCT
 GTGGTCACACCTAAGCTCTTGGTCAACTTCTGCTCTGACAAGTCCATCTCTTTTGAGG
 GCTGTGTGGTCCAGCTCGCCTTCTTTGTAGTGCATGTGACAGCTGAGAGCTTCTGCTGGC
 45 CTCCATGGCCTATGACCGCTTCTTAGCCATCTGTCAACCCCTCCATTATGGTTCTATCATGA
 CCAGGGGGACCTGTCTCCAGCTGGTAGCTGTGTCTATGCATTTGGTGGAGCCAACTCCGC
 TATCCAGACTGGAAATGTCTTTGCCCTGCCTTCTGTGGGCCCCAACAGCTAACACACTAC
 TACTGTGACATAACACCCCTTCTCCACCTGGCTTGTGCCAACACAGCCACAGCAAGAGTGG
 TCCTCTATGTCTTTTCTGCTCTGGTCACCTTCTGCCTGCTGCAGTCATTCTCACCTCCTACT
 50 GCTTGGTCTTGGTGGCCATTGGGAGGATGCGCTCAGTAGCAGGGAGGGAGAAGGACCTCT
 CCACTTGTGCCTCCCACTTCTGGCCATTGCCATTTCTATGGCACTGTGGTTTCACTAT
 GTTCAGCCCCATGGATCTACTAACAATAACCAATGGCCAAGTAGTGTCCGCTTCTACACCA
 TCATAATCCCATGCTCAATCCCTTCACTATAGCCTCCGCAACAAGGAGGTGAAGGGCGC
 TCTGCAGAGGAAGCTTCAGGTCAACATCTTTCCCGGCTGA (SEQ ID NO: 148)

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AOLFR80 sequences:

MEGINKTAKMQFFRPFSPDPEVQMLIFVVFLMMYLTSLGGNATIAVIVQINHSHTPMYFFLA
 NLAVLEIFYTSSITPLALANLLSMGKTPVSITGCGTQMFFVFLGGADCVLLVVMAYDRFIAICH
 PLRYRLMSWSLVCVELLVGSLVLGFLSLPLTLIFHLPFCHNDEIFYHFYCDMPAVMRLACADTR
 5 VHKTALYIISFIVLSIPLSLISISYVFIVVAILRIRSAEGRQQAYSTCSSHILVLLQYGCTSFYILSPS
 SSSYPEMGRVVSVAYTFTIPILNPLIYSLRNKELKDALKALRKF (SEQ ID NO: 149)

ATGGAAGGAATAAATAAAACTGCAAAGATGCAGTTTTTCTTTCGTCCATTCTCACCTGACC
 CTGAGGTCCAGATGCTGATTTTTGTGGTCTTCCTGATGATGTATCTGACCAGCCTCGGTGG
 10 AAATGCTACAATTGCAGTCATTGTTTCAGATCAATCATTCCCTCCACACCCCATGTACTTTT
 TCCTGGCTAATCTGGCAGTTCTAGAAATCTTCTATACATCTTCCATCACCCATTGGCCTTG
 GCAAACCTCCTTTCAATGGGCAAACTCCTGTTTCCATCACGGGATGTGGCACCCAGATGT
 TTTTCTTTGCTCTTCTGGGTGGGGCTGATTGTGCTCTGCTGGTAGTCATGGCTTATGACCGG
 TTTATAGCGATCTGTCACCCCTGCGGATACAGGCTCATCATGAGCTGGTCTGTGTGTGG
 15 AGCTGCTGGTAGGCTCCTTGGTGCTGGGGTTCCTGTTGTCACTGCCACTCACCATTTTAATC
 TTCCATCTCCCATTTCTGCCACAATGATGAGATCTACCACTTCTACTGTGACATGCCTGCAGT
 CATGCGCCTGGCTTGTGCAGACACACGCGTTCACAAGACTGCTCTGTATATCATCAGCTTC
 ATCGTCCTTAGCATCCCCCTCTCATTGATCTCCATCTCCTATGTCTTCATCGTGGTAGCCAT
 TTTACGGATCCGGTCAGCAGAAGGGCGCCAGCAAGCCTACTCTACCTGCTCTTCTCACATC
 20 TTAGTGGTCTCCTGCAGTATGGCTGCACCAGCTTTATATACTTGTCCCCCAGTCCAGCTA
 CTCTCCTGAGATGGGCCGGGTGGTATCTGTGGCCTACACATTTATCACTCCCATTTTAAAC
 CCCTTGATCTATAGTTTGAGGAACAAGGAAGTCAAAGATGCCCTAAGGAAAGCATTGAGA
 AAATTCTAG (SEQ ID NO: 150)

AOLFR81 sequences:

MGVKNHSTVTEFLLSGLTEQAEQLPLFCLFLGIYTVTVVGNLSMISIIRLNRLHTPMYYFLSS
 LSFLDFCYSSVITPKMMKLWMESHLPETRPSRPMMSNQTLVTEFILQGFSEHPEYRVFLFSCF
 LFLYSGALTGNVLITLITFNPGLHAPMYFFLLNLATMDIICTSSIMPKALASLVSEESSISYGGC
 MAQLYFLTWAASSELLLLTVMAYDRYAAICHPLHYSSMMSKVFCGLATAVWLLCAVNTAIIH
 30 TGLMLRLDFCGPNVHHFFCEVPPLLLSCSSTYVNGVMIVLADAFYGIVNFMITIASYGFIVSSI
 LKVKTAWGRQKAFSTCSSHLTVVCMYYTAVFYAYISPVSGYSAGKSKLAGLLYTVLSPTLNPL
 IYTLRNKEVKAALRKLFPFFRN (SEQ ID NO: 151)

ATGAAGCTGTGGATGGAGAGTCACCTGATAGTCCCAGAAACCCGTCCCAGCCCAAGGATG
 35 ATGAGTAACCAGACGTTGGTAACCGAGTTCATCCTGCAGGGCTTTTCGGAGCACCCAGAAT
 ACCGGGTGTTCTTATTCAGCTGTTTCCTCTCTCTACTCTGGGGCCCTCACAGGTAATGTC
 CACATCACCTTGCCATCACGTTCAACCCCTGGGCTCCACGCTCCTATGTACTTTTCTTACT
 CCAACTGGCTACTATGGACATTATCTGCACCTCTTCCATCATGCCCAAGCGCTGGCCAGT
 CTGGTGTGCGAAGAGAGCTCCATCTCCTACGGGGGCTGCATGGCCCAGCTCTATTTCTCA
 40 CGTGGGCTGCATCCTCAGAGCTGCTGCTCCTCACGGTCATGGCCTATGACCGGTACGCAGC
 CATCTGCCACCCGCTGCATTACAGCAGCATGATGAGCAAGGTGTTCTGCAGCGGGCTGGCC
 ACAGCCGTGTGGCTGCTCTGCGCCGTCAACACGGCCATCCACACGGGGCTGATGCTGCGCT
 TGGATTTCTGTGGCCCCAATGTCATTATCCATTTCTTCTGCGAGGTCCCTCCCCTGCTGCTT
 CTCTCCTGCAGCTCCACCTACGTCAACGGTGTGATGATTGTCCTGGCGGATGCTTTCTACG
 45 GCATAGTGAACCTTCTGATGACCATCGCGTCTATGGCTTCATCGTCTCCAGCATCCTGAA
 GGTGAAGACTGCCTGGGGGAGGCAGAAAGCCTTCTCCACCTGCTCTTCCCACCTCACCGTG
 GTGTGCATGTATTACACCGCTGTCTTCTACGCCTACATAAGCCCGGTCTCTGGCTACAGCG
 CAGGGAAGAGCAAGTTGGCTGGCCTGCTGTACACTGTGCTGAGTCTACCTCAACCCCT
 CATCTATACTTTGAGAAACAAGGAGGTCAAAGCAGCCCTCAGGAAGCTTTTCCCTTTCTTC
 50 AGAAATTAA (SEQ ID NO: 152)

AOLFR82 sequences:

MQLNNNVTEFILLGLTQDPFWKKIVFVIFLRLYLGTLLGNLLIISVKASQALKNPMFFFLFYLSL
 SDTCLSTSIAPRMIVDALLKKTTSFSECMIQVFSSHVFGCLEIFILITAVDRYVDICKPLHYMTII
 55 SQWVCGVLMVAWVWGVHSLVQIFLALSLPFCGPNVINHCFLDLQPLLKQACSETYVVNLL

VSNSGAICAVSYVMLIFSIVIFLHSLRNHSAEVIKKALSTCVSHIIVVILFFGPCIFMYTCPATVFP
MDKMIADVFTVGTSTFLNPVIYTLKNTEVKSAMRKLWSKKLITDDKR (SEQ ID NO: 153)

5 ATGCAACTGAATAATAATGTGACTGAGTTCATTCTGCTTGGATTGACACAGGATCCTTTTT
GGAAGAAAATAGTGTGTTTATTTTTTTCGCTCTCTACTTGGGAACACTGTTGGGTAATTT
GCTAATCATTATTAGTGTCAAGGCCAGCCAGGCACTTAAGAACCCAATGTTCTTCTTCCTT
TTCTACTTATCTTTATCTGATACTTGCCTCTCTACTTCCATAGCCCCTAGAATGATTGTGGA
TGCCCTTTTGAAGAAGACAACTATCTCCTTCAGCGAGTGCATGATCCAAGTCTTTTCATCC
10 CATGTCTTTGGCTGCCTGGAGATCTTCATCCTCATCCTCACGGCTGTTGACCGCTATGTGGA
CATCTGTAAGCCCCTGCACTACATGACCATCATAAGCCAGTGGGTCTGTGGTGTGTTTATGATG
GCTGTGGCCTGGGTGGGATCCTGTGTGCATTCTTTAGTTCAGATTTTCTTGGCCTGAGTTT
GCCATTCTGTGGCCCCAATGTGATCAATCACTGTTTCTGTGACTTGCAGCCCTGTTGAAA
CAAGCCTGTTGAGAAACCTATGTGGTTAACTACTCCTGGTTTCCAATAGTGGGGCCATTT
GTGCAGTGAGTTATGTCATGCTAATATTCTCCTATGTCATCTTCTTGCATTCTCTGAGAAAC
15 CACAGTGCTGAAGTGATAAAGAAAGCACTTCCACATGTGTCTCCACATCATTGTGGTCA
TCTTGTCTTTGGACCTTGCAATTTATGTACACATGCCCTGCAACCGTATTCCCATGGAT
AAGATGATAGCTGTATTTTATACAGTTGGAACATCTTTTCTCAACCCTGTGATTTACACGCT
GAAGAATACAGAAGTGAAAAGTGCCATGAGGAAGCTTTGGAGCAAGAAATTGATCACAGA
TGACAAAAGATAA (SEQ ID NO: 154)

20

AOLFR83 sequences:

MGNWTAADVTEFVLLGFSLREVELLLLVLPTFLLTLLGNLLIISTVLSRSLHTPMYFFLCNL
SILDILFTSVISPKVLANLGSRDKTISFAGCITQCYFYFFLGTVEFLLLTVMYSYDRYATICPLRYT
TIMRPSVCIGTVVFSWVGFLSVLPFTILISQLPFCGSNIINHFFCDSPLLALACADTTAELMDF
25 MLSSMVILCCIVLVAYSYTYIILTIVRIPSASGRKKAFTNCASHLTIVIIPSGITVFIYVTPSQKEYL
EINKIPLVLSSVTPFLNPFITYTLRNDTVQGVLRDVWVRVRGVFEKRMRAVLRSLSSNKDQH
GRACSSPPCVYSVKLQC (SEQ ID NO: 155)

30 ATGGGTAAGTGGACTGCAGCGGTGACTGAGTTTGTCTGCTGGGGTTTTCCCTGAGCAGGG
AGGTGGAGCTGCTGCTCCTGGTGCTCCTGCTGCCACGTTCTGCTGACTCTTCTGGGGAA
CCTGCTCATCATCTCCACTGTGCTGTCTGCTCCCGCTCCACACCCCCATGTACTTCTTCT
TGTGCAACCTCTCTATCCTGGACATCCTCTTACCTCAGTCATCTCTCCAAAAGTGTGGCC
AACTTAGGATCTAGGGATAAAACCATCTCCTTTGCCGGATGTATCACCCAGTGCTATTTCT
ACTTTTTCTTGGGCACAGTTGAGTTCCTCCTGCTGACGGTCATGTCCTATGACCGTTATGCC
35 ACCATCTGCTGCCCCCTGCGGTACACCACCATCATGAGACCTTCTGTCTGCATTGGGACCG
TTGTATTCTCTTGGGTGGGAGGCTTCTGTCTGTGCTCTTTCCAACCATCCTCATCTCCAG
CTGCCCTTCTGTGGCTCCAATATCATTAACCACTTCTTCTGTGACAGTGAGCCCTTGCTGGC
CCTGGCCTGTGCAGACCACTGCCATCGAGCTGATGGATTTTATGCTTTCTTCCATGGTC
ATCCTCTGCTGCATAGTCTCGTGGCCTATTCTATACGTACATCATCTTGACCATAGTGCG
40 CATTCTTCTGCAAGTGGAAGGAAGAAGGCCTTTAATACCTGTGCTTCCCACCTGACCATA
GTCATCATTCCTAGTGCCATCACTGTGTTATCTATGTGACTCCCTCCCAGAAAGAATATCT
GGAGATCAACAAGATCCCTTTGGTTCTGAGCAGTGTGGTGACTCCATTCTCAACCCCTTT
ATATATACTCTGAGGAATGACACAGTGCAGGGAGTCTCAGGGATGTGTGGGTGAGGGTT
CGAGGAGTTTTTGAAGAAGAGGATGAGGGCAGTGTGAGAAGCAGATTATCCTCCAACAAA
45 GACCACCAAGGAAGGCTTGTCTTCTCCACCATGTGTCTATTCTGTAAAGCTCCAGTGTT
AG (SEQ ID NO: 156)

AOLFR85 sequences:

MGAKNNVTEFVFLGFESREMQHTCFVFFLFHVLTVLGNLLVIITINARKTLKSPMYFFLSQL
50 SFADICYPSTTIPKMIADTFVEHKIISFNGCMTQLFSAHFFGGTEIFLLTAMAYDRYVAICRPLHY
TAIMDCRKCGLLAGASWLAGFLHSILQTLTVQLPFCGPNEIDNFFCDVHPLLKLACADTYMV
GLIVVANSGMISLASFFILHSYVILLNLRSSQSSDDRKA VSTCGSHVITVLLVLMPPMFMYIRPS
TTLAADKLILFNIVMPPLNPLIYTLRNDVKNAMRKLFRVKRSLGEK (SEQ ID NO: 157)

55 ATGGGTGCCAAGAACAATGTGACTGAGTTTGTGTTTTATTTGGCCTTTTTGAGAGCAGAGAGA
TGCAGCATACATGCTTTGTGGTATTCTTCTCTTTCATGTGCTCACTGTCTGGGGAACTT

CTGGTCATCATCACCATCAATGCTAGAAAGACCCTGAAGTCTCCCATGTATTTCTTCCTGA
 GCCAGTTGTCTTTTGTGACATATGTTATCCATCCACTACCATAACCAAGATGATTGCTGAC
 ACTTTTGTGGAGCATAAGATCATCTCCTTCAATGGCTGCATGACCCAGCTCTTTTCTGCCCA
 CTTCTTTGGTGGCACTGAGATCTTCCTCCTTACAGCCATGGCCTATGACCGCTATGTGGCC
 5 ATCTGTAGGCCCCCTGCACTACACAGCCATCATGGATTGCCGGAAGTGTGGCCTGCTAGCGG
 GGGCCTCCTGGTTAGCTGGCTTCCTGCATTCCATCCTGCAGACCCTCCTCACGGTTCAGCTG
 CCTTTTGTGGGCCCAATGAGATAGACAACCTTCTTCTGTGATGTTTCATCCCCTGCTCAAGTT
 GGCCTGTGCAGACACCTACATGGTAGGTCTCATCGTGGTGGCCAACAGCGGTATGATTCT
 TTAGCATCCTTTTTTATCCTTATCATTTTCCTATGTTATCATCTTACTGAACCTAAGAAGCCA
 10 GTCATCTGAGGACCGGCGTAAGGCTGTCTCCACATGTGGCTCACACGTAATCACTGTCTT
 TTGGTTCTCATGCCCCCATGTTTCATGTACATTTCGTCCTCCACCACCCTGGCTGCTGACAA
 ACTTATCATCCTCTTTAACATTGTGATGCCACCTTTGCTGAACCCCTTGATCTATACACTAA
 GGAACAACGATGTGAAAAATGCCATGAGGAAGCTGTTTAGGGTCAAGAGGAGCTTAGGGG
 AGAAGTGA (SEQ ID NO: 158)

15

AOLFR86 sequences:

MQLVLLLMFLLVFIGNTAPAFSVTLESMDIPQNITEFFMLGLSQNSEVQRVLFVVFLLIYVVTVC
 GNMLIVVTITSSPTLASPVYFFLANLSFIDTFYSSSMAPKLIADSLYEGRTISYECCMAQLFGAHF
 LGGVEIILLTVMAYDRYVAICKPLHNITIMTRHLCAMLVGVAVWLGGFLHSLVQLLLVLWLPC
 20 GPNVINHFACDLYPLLEVACTNTYVIGLLVVANSGLICLLNFLMLAASYIVILYSLRSHSADGRC
 KALSTCGAHFIVVALFFVPCIFTYVHPFSTLPIDKNMALFYGILTPMLNPLIYTLRNEEVKNAMR
 KLFTW (SEQ ID NO: 159)

ATGCAATTAGTTCTATTACTTATGTTTCTCCTTGTCTTTATAGGCAATACTGCACCTGCATT
 25 CTCAGTGACCTTGAATCTATGGACATACCACAAAATATCACAGAATTTTTCATGCTGGGG
 CTCTCACAGAACTCAGAGGTACAGAGAGTTCTCTTTGTGGTCTTTTGTGATCTATGTGG
 TCACGGTGTGTGGCAACATGCTCATTGTGGTCACTATCACCTCCAGCCCCACGCTGGCTTC
 CCCTGTGATTTTTTCTGGCCAACCTATCCTTTATTGACACCTTTATCTTCTTCTTATGGC
 TCCTAAACTCATTGCTGACTCATTGTATGAGGGGAGAACCATCTCTTATGAGTGTGCTGATG
 30 GCTCAGCTCTTTGGAGCTCATTTTTTGGGAGGTGTTGAGATCATTCTGCTCACAGTGATGG
 CTTATGACCGCTATGTGGCCATCTGTAAGCCCCTGCACAATACTACCATCATGACCAGGCA
 TCTCTGTGCCATGCTTGTAGGGGTGGCTTGGCTTGGGGGCTTCTGCATTCAATTGGTTCAG
 CTCCTCCTGGTCTTTGGTTGCCCTTCTGTGGGCCCAATGTGATCAATCACTTTGCCTGTGA
 CTTGTACCCTTTGCTGGAAGTTGCCTGCACCAATACGTATGTCAATTGGTCTGCTGGTGGTT
 35 GCCAACAGTGGTTTAATCTGCCTGTTGAACCTCCTCATGCTGGCTGCCTCCTACATTGTCAT
 CCTGTACTCCTTGAGGTCCCACAGTGCAGATGGGAGATGCAAAGCCCTCTCCACCTGTGGA
 GCCCACTTCATTGTTGTTGCCTTGTCTTTGTGCCCTGTATTTACTTATGTGCATCCATTT
 TCTACTTTACCTATAGACAAAAATATGGCATTATTTTATGGTATTCTGACACCTATGTTGAA
 TCCACTCATTATACCCTGAGAAATGAAGAGGTAAAAATGCCATGAGAAAGCTCTTTACA
 40 TGGTAA (SEQ ID NO: 160)

AOLFR87 sequences:

MNNIAQLSLGFDLGIPIVLQKIILTKIILLFKMYVSNCNPCAHRKINYPNTKLDPEQVNNITEFI
 LLGLTQNAEAQKLLFAVFTLIYFLTMVDNLIVVTITSPALDSPVYFFLSFFSFIDGCSSTMAP
 45 KMIFDLLTEKKTISFSGCMTQLFVEHFFGGVEIILLVVMAYDCYVAICKPLYLITMNRQVCG
 LVAMAWVGGFLHALIQMLLIVWLPFCGPNVIDHFICDLFPLKLSCTDTHVFGFLVAANSGLM
 CMLIFSILITSYVLILCSQRKALSTCAFHITVVVLFVPCILVYLRPMITFPIDKAVSVFYTVVTPM
 LNPLYTLRNTTEVKNAMKQLWSQIHWGNLDCD (SEQ ID NO: 161)

ATGAATAACATAGCTCAACTTAGTCTTGGGTTTATAGATTTAGGGATTCCATCAGTGTTAC
 AGAAAAATAATCCTGACCAAAATTATTTTATTGTTCAAATGTATGTGTCAAATTGCAATCC
 TTGTGCTATTACAGAAAAATCAATTATCCAAATACCAAACTGGATTTTCGAGCAAGTGAAC
 AACATAACGGAATTCATCTTGGCTTGGCCTGACACAGAACGCAGAGGCACAGAACTCTTGT
 TTGCTGTGTTTACACTCATCTACTTTCTCACCATGGTAGACAACCTAATCATTGTGGTGACA
 55 ATCACCACCAGCCCAGCCCTGGACTCCCCCGTGATTTTTTTCTGTCTTTCTTTCTTTCAT
 AGATGGCTGCTCCTCTTCTACCATGGCCCCCAAAATGATATTTGACTTACTCACTGAAAAG

AAAACTATTTCTTCAGTGGGTGCATGACCCAGCTCTTTGTAGAACATTTCTTTGGGGGAG
 TTGAGATCATTCTGCTCGTGGTGATGGCCATGACTGCTATGTGGCCATCTGCAAGCCCCT
 GTACTACCTGATCACAATGAACAGGCAGGTATGTGGCCTCCTGGTGGCCATGGCATGGGTC
 GGGGGATTTCTTCACGCTCTGATTCAAATGCTTTTAATAGTCTGGCTGCCCTTCTGTGGCCC
 5 CAATGTCAATTGACCATTTTCATCTGTGACCTTTTCCCTCTGCTAAAACTCTCCTGCACTGACA
 CTCACGTCTTTGGACTCTTTGTTGCCGCCAACAGTGGGCTGATGTGTATGCTCATTTTTTCT
 ATTCTTATTACCTCTTACGTCCTAATCCTCTGCTCACAGCGGAAGGCTCTCTACCTGCGC
 CTTCCATATCACTGTAGTCGTCCTATTCTTTGTTCCCTGTATATTGGTGTACCTTCGACCCA
 TGATCACCTTCCCTATTGATAAAGCTGTGTCTGTGTTTTATACTGTGGTAACACCCCATGTA
 10 AACCTTTAATCTACACCCTCAGAAACACAGAGGTGAAAAATGCCATGAAGCAGCTCTGG
 AGCCAAATAATCTGGGGTAACAATTTGTGTGATTAG (SEQ ID NO: 162)

AOLFR88 sequences:

MWQKNQTSIADFILEGLFDDSLTHLFLFSLTMVVFLIAVSGNTLTILLICIDPQLHTPMYFLLSQ
 15 LSLMDLMHVSTILKMATNYLSGKKSISFVGCATQHFLYLCLGGAECFLAVMSYDRYVAICH
 PLRYAVLMNKKVGLMMAVMSWLGA SVNSLIHMAILMHFPFCGPRKVYHFYCEFPVAVKLVC
 GDITVYETTVYISSILLPIFLISTSYVFILQSVIQMRSSGSKRNAFATCGSHLTVVSLWFGACIFS
 YMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVAKALRRVLRDVTQCIQRLQLWLP
 RV (SEQ ID NO: 163)
 20
 ATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGGGCTCTTCGATGACT
 CCCTTACCCACCTTTTCTTTTCTCCTTGACCATGGTGGTCTTCCTTATTGCGGTGAGTGGC
 AACACCCCTCACCATTCTCCTCATCTGCATTGATCCCCAGCTTCATACACCAATGTATTTCT
 GCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAATCATCCTGAAGATGGCT
 25 ACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCAACCCAGCACTTCC
 TCTATTTGTGTCTAGGTGGTGTGAATGTTTTCTCTTAGCTGTCTATGCTTACCCGCTAT
 GTTCCCATCTGTCTATCCACTGCGCTATGCTGTGCTCATGAACAAGAAGGTGGGACTGATGA
 TGGCTGTCTATGTCTATGGTTGGGGGCATCCGTGAACCTCCCTAATTCACATGGCGATCTTGAT
 GCACTTCCCTTTCTGTGGGCTCGGAAAGTCTACCCTTCTACTGTGAGTTCCCAGCTGTTG
 30 TGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTACATCAGCAGCATTCT
 CCTCCTCCTCCCATCTTCTGATTTCTACATCCTATGTCTTCATCCTTCAAAGTGTCAATCA
 GATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTTGTGGCTCCCACCTCACGGTG
 GTTCTCTTTGGTTTGGTGCCTGCATCTTCTCTACATGAGACCCAGGTCCAGTGCATCT
 ATTGCAGAACAAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCCACATTGAATTCTCTG
 35 ATTTATACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGTGTGAGGAGAGAT
 GTTATACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCCGAGTGTAG (SEQ ID NO:
 164)

AOLFR89 sequences:

MLDPSISSHTLYLHSLFPQGLRKGMWQKNQTSIADFILEGLFDDSLTHLFLFSLTMVVFLIAVS
 40 GNTLTILLICIDPQLHTPMYFLLSQLSLMDLMHVSTILKMATNYLSGKKSISFVGCATQHFLYL
 CLGGAECFLAVMSYDRYVAICHPLRYAVLMNKKVGLMMAVMSWLGA SVNSLIHMAILMHF
 PFCGPRKVYHFYCEFPVAVKLVC GDITVYETTVYISSILLPIFLISTSYVFILQSVIQMRSSGSK
 RNAFATCGSHLTVVSLWFGACIFS YMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVA
 45 KALRRVLRDVTQCIQRLQLWLP RV (SEQ ID NO: 165)
 ATGCTGGACCCAGTATTTCCAGTCACACTCTTTATCTCCACTCTCTGTTTCCTCAGGGATT
 GAGAAAGGGGACAATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGG
 GCTCTTCGATGACTCCCTTACCCACCTTTCTCTTTCTCCTTGACCATGGTGGTCTTCCTTAT
 50 TGCGGTGAGTGGCAACACCCTCACCATTCTCCTCATCTGCATTGATCCCCAGCTTCATACA
 CCAATGTATTTCTGCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAACCAT
 CCTGAAGATGGCTACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCA
 ACCCAGCACTTCTCTATTTGTGTCTAGGTGGTGTGAATGTTTTCTCTTAGCTGTCTATGTC
 CTATGACCGCTATGTTGCCATCTGTCTATCCACTGCGCTATGCTGTGCTCATGAACAAGAAG
 55 GTGGGACTGATGATGGCTGTCTATGCTGTTGGGGGCATCCGTGAACCTCCCTAATTCACA
 TGGCGATCTTGATGCACTTCCCTTTCTGTGGGCTCGGAAAGTCTACCCTTCTACTGTGA

GTTCCCAGCTGTTGTGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTAC
 ATCAGCAGCATTCTCCTCCTCCTCCCATCTTCTGATTTCTACATCCTATGTCTTCATCCTT
 CAAAGTGTCAATCAGATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTTGTGGCT
 CCCACCTCACGGTGGTTTCTCTTTGGTTTGGTGCCTGCATCTTCTCCTACATGAGACCCAGG
 5 TCCCAGTGCACCTCTATTGCAGAACAAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCCA
 CATTGAATTCTCTGATTTATACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGT
 GCTGAGGAGAGATGTTATCACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCCGAGTG
 TAG (SEQ ID NO: 166)

10 **AOLFR90 sequences:**

MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMPVGAIFISLGNMQNQSFVTEF
 VLLGLSQNPVQEI VVFLFVYIATVGGNMLIVVTILSSPALLVSPMYFFLGFLSFLDACFSSVI
 TPKMIVDSLYVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL
 CGILMGVAWTGGLLHSMIQLFTFQLPCGPNVINHFMC DLYPLLELACTDTHIFGLMVVINS
 15 FICIINFSLLLVSYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA
 AIFYIILNPLLNPLIYTFRNKEVKQAMRRIWNRLMVVSDEKENIKL (SEQ ID NO: 167)

ATGTTCTCAATGACAACAGAAGCACTCAATAATTTTGCCTTGGATGTACCAACTTGTTAA
 TGACTATGATACCACAAATTGATCTGAAGCAAATTTTCTTTGTCCTAATTGCAGACTATA
 20 CATGATCCCTGTTGGAGCTTTCATCTTTTCTTGGGAAACATGCAAAACCAAAGCTTTGTA
 ACTGAGTTTGTCTCCTGCGGACTTTCACAGAATCCAAATGTTTCAAGAAATAGTATTTGTTG
 TATTTTTGTTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCATCTC
 AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTTGGGCTTCTGCTTCTCCTGGA
 TGCGTGCTTCTCATCTGTCTATCAACCCAAAGATGATTGTAGACTCCCTCTATGTGACAAAA
 25 ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTTCTTTGCTGGGGTGG
 AGGTGATTGTCCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTGCAAGCCCTTGCA
 TTACTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG
 GGCCTCTTGCAATCCATGATACAAATCTTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA
 TGTCAATCAACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCCTGCACTGATACTC
 30 ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG
 TTGCTTGTCTCCTATGCTGTCTCTTGTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG
 GAAAGCTCTCTCCACCTGTGGATCTCACATTGCTGTTGTGATTTTGTCTTTGTCCCATGCA
 TATTTGTATATACACGACCTCCATCTGCTTTTCCCTTGACAAAATGGCGGCAATATTTTAT
 ATCATCTTAAATCCCTTGCTCAATCCTTTGATTTACACTTTCAGGAATAAGGAAGTAAAC
 35 AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTA
 AACTTTAA (SEQ ID NO: 168)

AOLFR91 sequences:

MGNWSTVTEITLIAFPALLEIRISLFVVLVVYTLTATGNITHISLIWIDHRLQTPMYFFLSNLSFL
 40 DILYTTVITPKLLACLLGEEKTISFAGCMIQTYFYFFLGTVEFILLAVMSFDRYMAICDPLHYTVI
 MNSRACLLLVLCWVGAFSLVLFPTIVVTRLPYCRKEINHFFCDIAPLLQVACINTHLIEKINFL
 SALVILSSLAFTTGSYVYIISTILRIPSTQGRQKAFSTCASHITVVSIAHGSNIFVYVRPNQNSSLD
 YDKVAAVLITVVTPLNPFYISLRNEKVQEVLRVTRNRMTLIQRKT (SEQ ID NO: 169)

ATGGGAAACTGGAGCACTGTGACTGAAATCACCTAATTGCCTTCCCAGCTCTCCTGGAGA
 TTCGAATATCTCTCTTCGTGGTTCTTGTGGTAACTTACACATTAACAGCAACAGGAAACAT
 CACCATCATCTCCCTGATATGGATTGATCATCGCCTGCAAACTCCAATGTACTTCTTCTCA
 GTAATTTGTCTTTCTGGATATCTTATACACCACTGTCATTACCCCAAAGTTGTTGGCCTGC
 CTCCTAGGAGAAGAGAAAACCATATCTTTGCTGGTTGCATGATCCAAACATATTTCTACT
 50 TCTTTCTGGGGACGGTGGAGTTTATCCTCTTGGCGGTGATGTCTTTGACCGCTACATGGC
 TATCTGCGACCCACTGCACTACACGGTCATCATGAACAGCAGGGCCTGCCTTCTGCTGGTT
 CTGGGATCTGGGTGGGAGCCTTCTGTCTGTGTTTCCAACCATTTGACACAGGC
 TACCTTACTGTAGGAAAGAAATTAATCATTTCTTCTGTGACATTGCCCTCTTCTTACAGGTG
 GCCTGTATAAAATACTCACCTCATTGAGAAGATAAACTTTCTCCTCTCTGCCCTTGTATCCT
 55 GAGCTCCCTGGCATTCACTACTGGGTCTACGTGTACATAATTTCTACCATCCTGCGTATCC
 CCTCCACCCAGGGCCGTCAGAAAGCTTTTTCTACCTGTGCTTCTCACATCACTGTTGTCTCC

ATTGCCACGGGAGCAACATCTTTGTGTATGTGAGACCCAATCAGAACTCCTCACTGGATT
 ATGACAAGGTGGCCGCTGTCCTCATCAGTGGTGACCCCTCTCCTGAACCCCTTTTATCTA
 CAGCTTGAGGAATGAGAAGGTACAGGAAGTGTTGAGAGAGACAGTGAACAGAATCATGAC
 CTTGATACAAAGGAAAACCTGA (SEQ ID NO: 170)

5

AOLFR92 sequences:

MRNGTVITEFILLGFPVIQGLQTPLFIAIFLTYILTLAGNGLIATVWAEPRILQIPMYFFLCNLSFLE
 IWYTTTTVIPKLLGTFVVARTVICMSCLLQAFFHFVGTTEFLILTIMSFDRYLTICNPLHHTIM
 TSKLCQLALSSWVVGFTIVFCQTMLLIQLPFCGNNVISHFYCDVGPLKAACIDTSILELLGVIA
 10 TILVIPGSLLFNMISYIYLSAILRIPSATGHQKTFSTCASHLTVVSLLYGAVLFMYLRPTAHSSFK
 INKVSVLNTILTPLLNPFIYTIRNKEVKGALRKAMTCPKTGHAK (SEQ ID NO: 171)

ATGAGAAATGGCACAGTAATCACAGAATTCATCCTGCTAGGCTTTCCTGTTATCCAAGGCC
 TACAAACACCTCTCTTTATTGCAATCTTTCTCACCTACATATTAACCCCTTGCAAGGCAATGGG
 15 CTTATTATTGCCACTGTGTGGGCTGAGCCCAGGCTACAAATTCCAATGTACTTCTTCCTTTG
 TAACTTGTCTTTCTTAGAAATCTGGTACACCACCACAGTCATCCCCAACTGCTAGGAACC
 TTTGTAGTGGCAAGAACAGTAATCTGCATGCTCCTGCTGCCTGCTGCAGGCTTCTTCCACT
 TCTTCGTGGGCACCAACCGAGTTCTTGATCCTCACTATCATGTCTTTTGACCCGCTACCTCAC
 ATCTGCAATCCCCCTTCAACACCCCAACCATCATGACCAGCAAACTCTGCCTGCAGCTGGCCC
 20 TGAGCTCCTGGGTGGTGGGCTTACCATTGTCTTTTGTGACGATGCTGCTCATCCAGTT
 GCCATTCTGTGGCAATAATGTTATCAGTCATTTCTACTGTGATGTTGGGCCAGTTTGAAA
 GCCGCTGCATAGACACCAGCATTTTGGAACTCCTGGGCGTCATAGCAACCATCCTTGTGA
 TCCCAGGGTCACTTCTCTTAATATGATTTCTTATATCTACATTCTGTCCGCAATCCTACGA
 ATTCCTTCAGCCACTGGCCACCAAAAGACTTTCTCTACCTGTGCCTCGCACCTGACAGTTGT
 25 CTCCCTGCTCTACGGGGCTGTTCTGTTTCATGTACCTAAGACCCACAGCACACTCCTCCTTA
 AGATTAATAAGGTGGTGTCTGTGCTAAATACTATCCTCACCCCCCTTCTGAATCCCTTTATT
 TATACTATTAGAAACAAGGAGGTGAAGGGAGCCTTAAGAAAGGCAATGACTTGCCCAAAG
 ACTGGTCATGCAAAGTAA (SEQ ID NO: 172)

30 **AOLFR93 sequences:**

MLMNYSSATEFYLLGFPGSEELHHILFAIFFFFYLVTLMGNTVIIMIVCVDKRIQSPMYFFLGHL
 SALEILVTIIVPVMWGLLLPGMQTIYLSACVVQLFLYLAVGTTEFALLGAMAVDRYVAVCN
 PLRYNIIMNRHTCNFVVLVSVVFGFLFIWVYVMFQLTYCKSNVNNFFCDRGQLKLSCN
 NTLFTEFILFLMAVFVLFGLIPTIVSNAYIISTILKIPSSSGRRKSFSTCASHFTCVVIGYGSCFLY
 35 VKPKQTQAADYNWVVSMLMVSVPFLNPFIFTLRNDKVIBALRDGVKRCCQLFRN (SEQ ID
 NO: 173)

ATGTTGATGAATTACTCTAGTGCCACTGAATTTTATCTCCTTGGCTTCCCTGGCTCTGAAGA
 ACTACATCATATCCTTTTTGCTATATTCTTTCTTTTCTACTTGGTGACATTAATGGGAAACA
 40 CAGTCATCATCATGATTGTCTGTGTGGATAAACGCTGTCAGTCCCCCATGTATTTCTTCCTC
 GGCCACCTCTCTGCCCTGGAGATCCTGGTACAAACCATAATCGTCCCCGTGATGCTTTGGG
 GATTGCTGCTCCCTGGGATGCAGACAATATATTTGTCTGCCTGTGTTGTCCAGCTCTTCTTG
 TACCTTGCTGTGGGGACAACAGAGTTTCGATTACTTGGAGCAATGGCTGTGGACCGTTATG
 TGGCTGTCTGTAAACCCTCTGAGGTACAACATCATTATGAACAGACACACCTGCAACTTTGT
 45 GGTCTTGTGTGTCATGGGTGTTTGGGTTTCTTTTTCAAATCTGGCCGGTCTATGTCATGTTT
 AGCTTACTTACTGCAAATCAAATGTGGTGAACAATTTTTTTGTGACCGAGGGCAATTGCT
 CAAACTATCCTGCAATAATACTCTTTTCACGGAGTTTATCCTCTTCTTAATGGCTGTTTTTG
 TTCTCTTTGGTTCTTTGATCCCTACAATTGTCTCCAACGCCTACATCATCTCCACCATCTC
 AAGATCCCGTCATCCTCTGGCCGGAGGAAATCCTTCTCCACTTGTGCCTCCCACTTCACCTG
 50 TGTGTGATTGGCTACGGCAGCTGCTTGTCTCTACGTGAAACCCAAGCAAACGCAGGCA
 GCTGATTACAATTGGGTAGTTTCCCTGATGGTTTTCAGTAGTAACCTCTTCTCAATCCTTT
 CATCTTCAACCTCCGGAATGATAAAGTCATAGAGGCCCTTCGGGATGGGGTGAAACGCTGC
 TGTCAACTATTACAGGAATTAG (SEQ ID NO: 174)

AOLFR94 sequences:

METWVNQSYTDGFFLLGIFSHSTADLVLFVSVMAVFTVALCGNVLLIFLIYMDPHLHTPMYFF
 LSQLSLMDLMLVCTNVPKMAANFLSGRKSISFVGCIGLQIGLVCLVGSEGLLLGLMAYDRYVA
 ISHPLHYPILMNQVRVCLQITGSSWAFGIIDGLIQMVVVMNFPYCGLRKVNHHFFCEMLSLLKLAC
 5 VDTSLFEKVIFACCVFMLLPFSIIVASYAHLGTVLQMHSQAQWKKALATCSSHLTAVTLFYG
 AAMFIYLRPHRYAPSHDKVASIFYTVLTPMLNPLIYSLRNREVMGALRKGLDRCRIGSQH
 (SEQ ID NO: 175)

ATGGAGACGTGGGTGAACAGTCCTACACAGATGGCTTCTTCCTCTTAGGCATCTTCTCCC
 10 ACAGTACTGCTGACCTTGTCTCTTCTCCGTGGTTATGGCGGTCTTCACAGTGGCCCTCTGT
 GGGAATGTCTCTCATCTTCTCATCTACATGGACCCTCACCTTCACACCCCCATGTA
 CTTCCTCAGCCAGCTCTCCCTCATGGACCTCATGTTGGTCTGTACCAATGTGCCAAAGATG
 GCAGCCAACTTCTGTCTGGCAGGAAGTCCATCTCCTTTGTGGGCTGTGGCATACAAATTG
 GCCTCTTTGTCTGTCTTGTGGGATCTGAGGGGCTCTTGTCTGGGACTCATGGCTTATGACCG
 15 CTATGTGGCCATTAGCCACCACTTCACTATCCCATCCTCATGAATCAGAGGGTCTGTCTCC
 AGATTACTGGGAGTCTCTGGGCCCTTTGGGATAATCGATGGCTTGATCCAGATGGTGGTAGT
 AATGAATTTCCCCTACTGTGGCTTGAGGAAGGTGAACCATTTCTTCTGTGAGATGCTATCC
 TTGTTGAAGCTGGCCTGTGTAGACACATCCCTGTTTGAGAAGGTGATATTTGCTTGCTGTG
 TCTTCATGCTTCTCTTCCCATTTCTCCATCATCGTGGCCTCCTATGCTCACATTCTAGGGACT
 20 GTGCTGCAAATGCACTCTGCTCAGGCCTGGAAAAAGGCCCTGGCCACCTGCTCCTCCCACC
 TGACAGCTGTCAACCTCTTCTATGGGGCAGCCATGTTTCTACCTGAGGCCTAGGCACTA
 CCGGGCCCCCAGCCATGACAAGGTGGCCTCTATCTTCTACACGGTCTTACTCCCATGCTC
 AACCCCTCATTTACAGCTTGAGGAACAGGGAGGTGATGGGGGCACTGAGGAAGGGGCTG
 GACCGCTGCAGGATCGGCAGCCAGCACTGA (SEQ ID NO: 176)

25

AOLFR95 sequences:

MLGSKPRVHLYILPCASQQVSTMGDRGTSNHSEMTDFILAGFRVRPELHILLFLLFLFVYAMILL
 GNVGMMTIIMTDPRLNTPMYFFLGNLSFIDLIFYSSVIEPKAMINFWSENKSISFAGCVAQLFLFA
 LLIVTEGFLAAMA YDRFAICNPLLYSVQMSTRCTQLVAGSYFCGCISSVIQTSMTFTLSFCAS
 30 RAVDHFYCDRPLQRLSCSDLFIHRMISFSLSCIILPTIIVTVSYMYIVSTVLKIHSTEGHKAFST
 CSSHLGVVSVLYGAVFFMYLTPDRFPESKVASLCYSLVTPMLNPLIYSLRNKDVQEALKKFLE
 KKNIL (SEQ ID NO: 177)

ATGCTAGGATCCAAACCAAGAGTTCATTTGTATATTTTGCCCTGTGCCTCTCAACAGGTTTC
 35 TACCATGGGTGACAGGGGAACAAGCAATCACTCAGAAATGACTGACTTCATTCTTGCAGG
 CTTACAGGGTACGCCAGAGCTCCACATTCTCCTCTTCTGCTATTTTTGTTTGTATGCCA
 TGATCCTTCTAGGGAATGTTGGGATGATGACCATTATTATGACTGATCCTCGGCTGAACAC
 ACCAATGTATTTTTCTAGGCAATCTCTCCTTATTGATCTTTTCTATTCTGTATTGA
 ACCCAAGGCTATGATCAACTTCTGGTCTGAAAACAAGTCTATCTCCTTGCAGGCTGTGTG
 40 GCCCAGCTCTTTCTCTTTGCCCTCCTATTGTGACTGAGGGATTTCTCCTGGCGGCCATGGC
 TTATGACCGCTTTATTGCCATCTGCAACCTCTGCTCTACTCTGTTCAAATGTCCACACGTC
 TGTGTACTCAGTTGGTGGCTGGTTCCTATTTTTGTGGCTGCATTAGCTCAGTTATTAGACT
 AGCATGACATTTACTTTATCTTTTGGCCTTCTCGGGCTGTTGACCACTTTTACTGTGATTC
 TCGCCCACTTCAGAGACTGTCTTGTCTGATCTCTTATCCATAGAATGATATCTTTTCTCCT
 45 TATCATGTATTATTATCTTGCCACTATCATAGTCATTATAGTATCTTACATGTATATTGTG
 TCCACAGTTCTAAAGATACATTCTACTGAGGGACATAAGAAGGCCTTCTCCACCTGCAGCT
 CTCACCTGGGAGTTGTGAGTGTGCTGTATGGTGTCTTTTTTATGTATCTCACTCCTGAC
 AGATTTCTGAGCTGAGTAAAGTGGCATCCTTATGTTACTCCCTAGTCACTCCCATGTTGA
 ATCCTTTGATTTACTCTCTGAGGAACAAAGATGTCCAAGAGGCTCTAAAAAATTTCTAGA
 50 GAAGAAAAATATTATTCTTTGA (SEQ ID NO: 178)

AOLFR96 sequences:

MICENHTRVTEFILLGFTNNPEMQVSLFIFFLAIYTVTLLGNFLIVTVTSVDLALQTPMYFFLQN
 55 LSLLEVCFTLVMVPKMLVDLVSPRKIISFVGCQTQMYFFFFGSSECFLLSMMA YDRFVAICNP
 LHYSVIMNRSCLWMAIGSWMSGVPVSMQLTAWMMALPFCGPNAVDFHFFCDGPPVLKLVTV
 DTTMYEMQALASTLLFIMFPFCLLVS YTRIITILRMSSATGRQKAFSTCSSHLIVVSLFYGTASL

TYLRPKSNQSPESKKLVSLSYTVITPMLNPIIYGLRNNEVKGAVKRITITQKVLQKLDVF (SEQ ID NO: 179)

5 ATGATCTGTGAAAATCACACCAGAGTCACTGAATTTATTCTTCTTGGTTTTACAAACAACC
CCGAGATGCAAGTTTCCCTCTTTATTTTTTTCCTGGCCATTATACAGTCACTTTGTTGGGC
AACTTTCTTATTGTACAGTTACCAGTGTGGATCTCGCACTTCAAACACCCATGTACTTCTT
TCTTCAAATCTGTCACTTCTTGAAGTATGTTTCACCTTGGTTATGGTGCCAAAAATGCTTG
TAGATCTAGTGTCCCAAGGAAAATTATCTCTTTTGTGGGCTGTGGTACCCAGATGTACTT
CTTCTTCTTCTTTGGCAGTTCTGAATGTTTCCTTCTCTCCATGATGGCTTATGATCGCTTTGT
10 GGCCATCTGTAAACCTCTCCATTATTCAGTCATAATGAACAGGTCCCTATGCTTGTGGATG
GCCATAGGCTCTTGGATGTCCGGTGTTCCTGTGTCTATGCTACAGACAGCTTGGATGATGG
CCCTTCTTTCTGTGGACCAATGCCGTGGACCACTTTTTCTGTGATGGTCCCCCAGTGTTA
AAACTAGTCACAGTGGATAACAACCATGTATGAAATGCAAGCACTTGCCTCCACACTCCTGT
TTATCATGTTTCCCTTTTGTCTCATTTTGGTTTCTACACCCGCATTATCATAACAATTCTG
15 AGGATGTCCTCTGCCACTGGCCGCCAGAAGGCATTTTCTACTTGTTCCTCACACCTCATTGT
GGTGTCCCTCTTCTACGGAACAGCCAGTCTGACCTACCTGCGGCCAAATCAAACAGTCC
CCTGAGAGCAAGAAGCTAGTGTCTTGTCTACACTGTCTACACCTATGCTAAACCCCA
TCATCTACGGCCTGAGGAACAATGAAGTGAAAGGGGCTGTCAAGAGGACAATCACTCAAA
AAGTCTTACAGAAGTTAGATGTGTTTTGA (SEQ ID NO: 180)

20

AOLFR97 sequences:

MTEFHLQSQMPSIRLIFRRLSLGRIKPSQSPRCSTSMVVPVSFSIAEHWRMKGANLSQGMFEL
LGLTTDPQLQRLLFVFLGMYTATLLGNLVMFLIHVSATLHTPMYSLLKSLSFLDFCYSTVV
PQTLVNFLAKRKVISYFGCMTQMFFYAGFATSECYLIAAMAYDRYAAICNPLLYSTIMSPEVC
25 ASLIVGSYSAGFLNSLIHTGCFSLKFCGAHVVTTHFFCDGPPLSLSCVDTSLCEILLFIFAGFNLLS
CTLTILISYFLILNTILKMSSAQGRFKAFTCASHLTAICLFFGTTLFMYLRPRSSYSLTQDRTVA
VIYTVVIPVLNPLMYSLRNKDVKKALIKVWGRKTME (SEQ ID NO: 181)

30 ATGACAGAGTTTCATCTGCAAAGCCAAATGCCCTCAATAAGACTCATCTTCAGAAGGCTGT
CCTTAGGCAGAAATTAACCCAGTCAGAGCCCCAGGTGTTCAACCTCATTTATGGTGGTGCC
TTCTTTCTCCATCGCAGAGCACTGGAGAAGGATGAAAGGGGCAAACCTGAGCCAAGGGAT
GGAGTTTGAGCTCTTGGGCCTCACCAGTCAACCCAGCTCCAGAGGCTGCTCTTCTCGTGGTG
TTCTGTGGCATGTACACAGCCACTCTGCTGGGGAACCTGGTCATGTTCTCTCTGATCCATG
TGAGTGCCACCCCTGCACACACCCATGTACTCCCTCCTGAAGAGCCTCTCCTTCTTGATTTT
35 TGCTACTCCTCCACGGTTGTGCCCCAGACCCTGGTGAACCTTCTTGCCAAGAGGAAAGTGA
TCTCTTATTTTGGCTGCATGACTCAGATGTTCTTCTATGCGGGTTTTGCCACCACTGAGTGC
TATCTCATCGCTGCCATGGCCTATGACCGCTATGCCGCTATTTGTAACCCCTGCTCTACTC
AACCATCATGTCTCCTGAGGTCTGTGCCTCGCTGATTGTGGGCTCCTACAGTGCAGGATTC
CTCAATTCTCTTATCCACACTGGCTGTATCTTTAGTCTGAAATTCTGCGGTGCTCATGTCTG
40 CACTCACTTCTTCTGTGATGGGCCACCCATCCTGTCTTGTCTTGTGTAGACACCTCACTGT
GTGAGATCCTGCTCTTCAATTTTGTGTTTCAACCTTTTGTGCTGCACCTCACCATCTTG
ATCTCCTACTTCTTAATTCTCAACACCATCCTGAAAATGAGCTCGGCCAGGGCAGGTTTA
AGGCATTTTCCACCTGTGCATCCACCTCACTGCCATCTGCCTCTTCTTTGGCACAACACTT
TTTATGTACCTGCGCCCCAGGTCCAGCTACTCCTTGACCCAGGACCGCACAGTTGCTGTCA
45 TCTACACAGTGGTGATCCAGTGCTGAACCCCTCATGTACTCTTTGAGAAACAAGGATGT
GAAGAAAGCTTTAATAAAGGTTTGGGGTAGGAAAACAATGGAATGA (SEQ ID NO: 182)

AOLFR98 sequences:

MRGFNKTTVVTQFILVGFSSLGELQLLLFVIFLLLYLTILVANVTIMAVIRFSWTLHTPMYGFLLI
50 LSFSESCYTFVVIPLLVHLLSDTKTISFMACATQLFFLGFACNTCLLIAMGYDRYVAICHPLR
YTLINKRLGLELISLGATGFFIALVATNLICDMRFGPNRVNHYFCDMAPVKLACTDTHVKE
LALFSLVIMVFPFLILISYGFIVNTILKIPSAEGKKAFTVCASHLTVVVFHYGCASITYLRPKSK
SASDKDQLVAVTYTVVTPLLNPLVYSLRNKEVKTALKRVLGMPVATKMS (SEQ ID NO: 183)

55 ATGCGAGGTTTCAACAAAACCACTGTGGTTACACAGTTCATCCTGGTGGGTTTCTCCAGCC
TGGGGGAGCTCCAGCTGCTGCTTTTTGTCTCTTCTCTCTTACTTGACAATCCTGGTG

GCCAATGTGACCATCATGGCCGTTATTTCGCTTCAGCTGGACTCTCCACACTCCCATGTATG
 GCTTTCTATTTCATCCTTTTCATTTTCTGAGTCCTGCTACACTTTTGTTCATCATCCCTCAGCTGC
 TGGTCCACCTGCTCTCAGACACCAAGACCATCCTTCATGGCCTGTGCCACCCAGCTGTT
 CTTTTCTTGGCTTTGCTTGCACCAACTGCCTCCTCATTGCTGTGATGGGATATGATCGCT
 5 ATGTAGCAATTTGTACCCCTCTGAGGTACACACTCATCATAAAACAAAAGGCTGGGGTTGGA
 GTTGATTTCTCTCTCAGGAGCCACAGGTTTCTTTATTGCTTTGGTGGCCACCAACCTCATTT
 GTGACATGCGTTTTTGTGGCCCCAACAGGGTTAACCCTATTTCTGTGACATGGCACCTGT
 TATCAAGTTAGCCTGCACTGACACCCATGTGAAAGAGCTGGCTTTATTTAGCCTCAGCATC
 10 CTGGTAATTATGGTGCCTTTTCTGTTAATTCTCATATCCTATGGCTTCATAGTTAACACCAT
 CCTGAAGATCCCCTCAGCTGAGGGCAAGAAGGCCTTTGTACCTGTGCCTCACATCTCACT
 GTGGTCTTTGTCCACTATGGCTGTGCCTCTATCATCTATCTGCGGCCCAAGTCCAAGTCTGC
 CTCAGACAAGGATCAGTTGGTGGCAGTGACCTACACAGTGGTTACTCCCTTACTTAATCCT
 CTTGTCTACAGTCTGAGGAACAAAGAGGTAAAACTGCATTGAAAAGAGTTCTTGGAATG
 CCTGTGGCAACCAAGATGAGCTAA (SEQ ID NO: 184)

15

AOLFR99 sequences:

MERVNETVVREVIFLGFSSSLARLQQLLFVIFLLLYLFTLGTNAIISTIVLDRALHIPMYFFLAILSC
 SEICYTFIIVPKMLVDLLSQKKTISFLGCAIQMFSFLFLGCSHSFLLAVMGYDRYIAICNPLRYSV
 LMGHGVCMLVAAAACACGFTVAQIITSLVFHLPFYSSNQLHHFFCDIAPVLKLASHHNFHSQIV
 20 IFMLCTLVLAIPLLLLVSYVHLSAILQFPSTLGRCKAFSTCVSHLIIVTVHYGCASFYILRPQSNY
 SSSQDALISVSYTHITPLFNPMIYSLRNKEFKSALCKIVRRITISLL (SEQ ID NO: 185)

ATGGAGCGGGTCAATGAGACTGTGGTGAGAGAGGTCATCTTCCTCGGCTTCTCATCCCTGG
 CCAGGCTGCAGCAGCTGCTCTTTGTTATCTTCCTGCTCCTCTACCTGTTCACTCTGGGCACC
 25 AATGCAATCATCATTTCCACCATTTGCTCTGGACAGGGCCCTTCATATCCCCATGTACTTCTT
 CCTTGCCATCCTCTCTTGTCTGTGAGATTGCTACACCTTCATCATTGTACCCAAAGATGCTGG
 TTGACCTGCTGTCCCAGAAGAAGACCATTTCTTTCTCGGGCTGTGCCAATGTTTCTCC
 TTCCTCTTCCTTGGCTGCTCTCACTCCTTTCTGCTGGCAGTCATGGGTTATGATCGTTACAT
 AGCCATCTGTAACCCACTGCGCTACTCAGTGCTAATGGGACATGGGGTGTGTATGGGACTA
 30 GTGGCTGCTGCCTGTGCCTGTGGCTTCACTGTTGCACAGATCATCACATCCTTGGTATTTCA
 CCTGCCTTTTTTATTCTCCAATCAACTACATCACTTCTTCTGTGACATTGCTCCTGTCTCA
 AGCTGGCATCTCACCATAACCACTTTAGTCAGATTGTCATCTTCATGCTCTGTACATTGGTC
 CTGGCTATCCCCTTATTGTTGATCTTGGTGTCTATGTTACATCCTCTCTGCCATACTTCA
 GTTTCCTTCCACACTGGGTAGGTGCAAAGCTTTTCTACCTGTGTATCTCACCTCATTATTG
 35 TCACTGTCCACTATGGCTGTGCCTCCTTTATCTACTTAAGGCCTCAGTCCAATACTCCTCA
 AGCCAGGATGCTCTAATATCAGTATCCTACACTATTATAACTCCATTGTTCAACCCAATGA
 TTTATAGCTTGAGAAATAAAGAGTTCAAATCAGCTCTTTGTAATAATTGTGAGAAGAACAAT
 TTCCCTGTTGTAA (SEQ ID NO: 186)

40 **AOLFR101 sequences:**

MDTGNWSQVAEFILGFPHLQGVQIYFLLLLLLIYLMTVLGNLLIFLVVCLDSRLHTPMYHFVSI
 LSFSELGYTAATIPKMLANLLSEKKTISFSGCLLQIYFFHSLGATECYLLTAMAYDRYLAICRPL
 HYPTLMTPTLCAEIAIGCWLGGLAGPVVEISLISRLPFCGPNRIQHVFCDPFPVLSLACTDTSINV
 LVDFVINSCKILATFLLILCSYVQIICTVLRIPSAAGKRKAISTCASHFTVVLIFYGSILSMYVQLK
 45 KSYSLDYDQALAVVYSVLTPLNPFYISLRNKEIKEAVRRQLKRIGILA (SEQ ID NO: 187)

ATGGACACAGGGAAGTGGAGCCAGGTAGCAGAATTCATCATCTTGGGCTTCCCCCATCTCC
 AGGGTGTCCAGATTTATCTTCTCTTGTGCTTCTCATTTACCTCATGACTGTGTTGGGA
 AACCTGCTGATATTCTTGGTGGTCTGCCTGGACTCCCGGCTTCACACACCCATGTACCACT
 50 TTGTCAGATTCTCTCTTCTCAGAGCTTGGCTATACAGCTGCCACCATCCCTAAGATGCTG
 GCAAACCTTGCTCAGTGAGAAAAAGACCATTTCTATTCTCTGGGTGTCTCCTGCAGATCTATT
 TCTTTCACTCCCTTGGAGCGACTGAGTGCTATCTCCTGACAGCTATGGCCTACGATAGGTA
 TTTAGCCATCTGCCGGCCCCCTCCACTACCAACCCTCATGACCCCAACACTTTGTGCAGAG
 ATTGCCATTGGCTGTTGGTGGGAGGCTTGGCTGGGCCAGTAGTTGAAATTTCTTGTATTT
 55 CACGCCTCCCATTCTGTGGCCCCAATCGCATTACAGCACGTCTTTTGTGACTTCCCTCCTGTG
 CTGAGTTTGGCTTGCCTGATACGTCTATAAATGTCCTAGTAGATTTTGTATAAATTCCTG

5 CAAGATCCTAGCCACCTTCCTGCTGATCCTCTGCTCCTATGTGCAGATCATCTGCACAGTGC
TCAGAATTCCTCAGCTGCCGGCAAGAGGAAGGCCATCTCCACGTGTGCCTCCCACTTCAC
TGTGGTTCTCATCTTCTATGGGAGCATCCTTTCCATGTATGTGCAGCTGAAGAAGAGCTAC
TCACTGGACTATGCCAGGCCCTGGCAGTGGTCTACTCAGTGCTCACACCCCTTCCTCAACC
CCTTCACTACAGCTTGGCGCAACAAGGAGATCAAGGAGGCTGTGAGGAGGCAGCTAAAGA
GAATTGGGATATTGGCATGA (SEQ ID NO: 188)

AOLFR102 sequences:

10 MPVGKLVFNQSEPTFVFRAFTTATEFQVLLFLLFLLLYLMILCGNTAIIWVVVCTHSTLRTPMYF
FLSNLSFLELCYTTVVVPLMLSNI LGAQKPISLAGCGAQMFFVTLGSTDCFLLAIMAYDRYVAI
CHPLHYTLIMTRELCTQMLGGALGLALFPSSLQLTALIFTL PFCGHHQEINHF LCDVPPVLR LACA
DIRVHQAVLYVVSILVLTIPFL LICVSYVFITCAILSIRSAEGRRRAFSTCSFHLTVVLLQYGCCSL
VYLRPRSSTSEDEDSQIALVYTFVTPLLNPLLYSLRNKDVKGALRSAIRKAASDAN (SEQ ID
NO: 189)

[illegible]

AOLFR103 sequences:

35 MAEMNLTIVTEFLLIATFEYPEWALPLFLLLLFMYLITVLGNLEMILILMDHQLHAPMYFLLSH
LAFMDVTCYSSITVPQMLAVLLEHGAALSYTRCAAQFFLFTFFGSIDCYLLALMAYDRYLAVCQ
PLLVTILTQQARLSLVAGAVVAGLISALVRTVSAFTLSFCGTSEIDFIFCDLPPLLKLTGSEYT
QEVLIIMFAIFVIPASMVVLVSYLFIIVAIMGPAGSKAFCTSTCTSHLTAVSLFFGTILFMYLRG
NSDQSSEKNRVVSVLYTEVIPMLNPLIYSLRNKEVKALRKILNRKALS (SEQ ID NO: 191)

40 ATGGCAGAGATGAACCTCACCTTGGTGACCGAGTTCTCTCTTATTGCATTCACTGAATATC
CTGAATGGGCACTCCCTCTCTTCTCTTGTATTATTTATGTATCTCATCACCGTATTGGGG
AACTTAGAGATGATTATTCTGATCCTCATGGATCACCGCTCCACGCTCCAATGTATTTCTT
TCTGAGTCACCTCGCTTTTCATGGACGCTGCTACTCATCTATCACTGTCCCCCAGATGCTGG
45 CAGTGCTGCTGGAGCATGGGGCAGCTTTATCTTACACACGCTGTGCTGCTCAGTTCTTTCT
GTTACACCTTCTTTGGTTCCATCGACTGCTACCTCTTGGCCCTCATGGCCTATGACCGCTACT
TGGCTGTGTGCCAGCCCTGCTTTATGTACCATCCTGACACAGCAGGCCCGCTTGAGTCT
TGTGGCTGGGGCTTACGTTGCTGGTCTCATCAGTGCTTGGTGCGGACAGTCTCAGCCTTC
ACTCTCTCCTTCTGTGGAACCAAGTGAGATTGACTTTATTTTCTGTGACCTCCCTCCTCTGTT
AAAGTTGACCTGTGGGGAGAGCTACACTCAAGAAGTGCTGATTATTATGTTTGCCATTTTT
50 GTCATCCCTGCTTCCATGGTGGTGATCTTGGTGTCTACCTGTTTATCATCGTGGCCATCAT
GGGATCCCTGCTTCCATGGTGGTGATCTTGGTGTCTACCTGTTTATCATCGTGGCCATCAT
GTGTCACTCTTCTTTGGTACCCTCATCTTCATGTTGACTTGAGAGGTAAGTCACTGCTTC
GGAGAAGAATCGGGTAGTGTCTGTGCTTTACACAGAGGTCATCCCCATGTTGAATCCCTC
ATCTACAGCCTGAGGAACAAGGAAGTGAAGGAGGCCCTGAGAAAAATTCTCAATAGAGCC
55 AAGTTGTCCTAA (SEQ ID NO: 192)

AOLFR105 sequences:

MQGLNHTSVSEFILVGFSAPHLQLMLFLLFLLMYLFTLLGNLLIMATVWSESLHMPMYLFLC
 ALSITEILYTVAIIPRMLADLLSTQRSIAFLACASQMFFSFSFGFTHSFLLTVMGYDRYVAICHPL
 RYNVLMSLRGCTCRVGCSSWAGGLVMGMVVTSAIFHLAFCGHEIHHFFCHVPPLLKLACGDD
 5 VLVAAGVGLVCTALLGCFLILLSYAFIVAAILKIPSAEGRNKAFTSCASHLTVVVVHYGFAS
 VIYLPKPGPQSPGDTLMGITVTLTPFLSPIFSLRNKELKVAMKKTCTKLFPQNC (SEQ ID
 NO: 193)

ATGCAGGGGCTAAACCACACCTCCGTGTCTGAATTCATCCTCGTTGGCTTCTCTGCCTTCCC
 10 CCACCTCCAGCTGATGCTCTTCTGCTGTTCTGCTGATGTACCTGTTACGCTGCTGGGCA
 ACCTGCTCATCATGGCCACTGTCTGGAGCGAGCGCAGCCTCCACATGCCCATGTACCTCTT
 CCTGTGTGCCCTCTCCATCACCGAGATCCTCTACACCGTGGCCATCATCCCGCGCATGCTT
 GCCGACCTGCTGTCCACCCAGCGCTCCATCGCCTTCTGCGCTGTGCCAGTCAGATGTTCTT
 CTCCTTCAGCTTCGGGTTCAACCACTCCTTCTGCTCACTGTCATGGGCTACGACCGCTACG
 15 TGGCCATCTGCCACCCCTGCGTTACAACGTGCTCATGAGCCTGCGGGGCTGCACCTGCCG
 GGTGGGCTGCTCCTGGGCTGGTGGCTTGGTCATGGGGATGGTGGTGACCTCGGCCATTTTC
 CACCTCGCCTTCTGTGGACACAAGGAGATCCACCATTTCTTCTGCCACGTGCCACCTCTGTT
 GAAGTTGGCCTGTGGAGATGATGTGCTGGTGGTGGCCAAAGGCGTGGGCTTGGTGTGTAT
 CACGGCCCTGCTGGGCTGTTTTCTCCTCATCCTCCTCTCCTATGCCTTCATCGTGGCCGCCA
 20 TCTTGAAGATCCCTTCTGCTGAAGGTCGGAACAAGGCCTTCTCCACCTGTGCCTCTCACCT
 CACTGTGGTGGTCTGCACTATGGCTTTGCCTCCGTCACTTACCTGAAGCCCAAAGGTCCC
 CAGTCTCCGGAAGGAGACACCTTGATGGGCATCACCTACACGGTCTCACACCTTCTCA
 GCCCCATCATCTTCAGCTCAGGAACAAGGAGCTGAAGGTCGCCATGAAGAAGACTTGCTT
 CACCAAACCTCTTCCACAGAACTGCTGA (SEQ ID NO: 194)

25

AOLFR106 sequences:

METANYTKVTEFVLTLGLSQTPEVQLVLFVIFLSFYLFILPGNLIICTISLDPHLLTSPMYFLLANLA
 FLDIYSSITAPEMLIDFFVERKIIISFDGCIQLFFLHFAGASEMFLLTVMAFDLYTAICRPLHYA
 TIMNQRLLCILVALSWRGGFIHSIIQVALIVRLPFCGPNELDSYFCDITQVVRACANTFPEELVM
 30 ICSSGLISVVCILALLMSYAFLLALFKKLSGSGENTNRAMSTCYSHITIVLVMFGPSIYIYARFDD
 SFSLDKVVSVFNTLIFPLRNPIIYTLRNKEVKAAMRKLVTKYILCKEK (SEQ ID NO: 195)

ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC
 CAGAGGTCCAAGTATCCTATTTGTTATATTTCTATCCTTCTATTTGTTTCATCCTACCAGGA
 35 AATATCCTTATCATTTGCACCATCAGTCTAGACCCTCATCTGACCTCTCCTATGTATTTCTT
 GTTGGCTAATCTGGCCTTCTTGATATTTGGTACTCTTCCATTACAGCCCTGAAATGCTCA
 TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTTGATGGATGCATTGCACAGCTCTTCTT
 CTTACACTTTGCTGGGGCTTCGGAGATGTTCTTGCTCACAGTGATGGCCTTTGACCTCTACA
 CTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCAACGTCTCTGCTGTATCCTG
 40 GTGGCTCTCTCCTGGAGGGGGGGCTTCATTCTATCATACAGGTGGCTCTCATTGTTT
 GACTTCTTTCTGTGGGCCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTTGT
 CCGGATTGCCTGTGCCAACACCTTCCCAGAGGAGTTAGTGATGATCTGTAGTAGTGGTCTG
 ATCTCTGTGGTGTGTTGATTGCTCTGTTAATGTCTATGCCTTCTTCTGGCCTTGTTCAA
 GAAACTTTTCAGGCTCAGGTGAGAATACCAACAGGGCCATGTCCACCTGCTATTCCCACATT
 45 ACCATTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCATTGACTCGTT
 TTCCCTAGATAAAGTGGTGTCTGTGTTCAATACTTTAATATTCCCTTTACGTAATCCCATTA
 TTTACACATTGAGAAACAAGGAAGTAAAGGCACCCATGAGGAAGTTGGTCACCAAATATA
 TTTTGTGTAAAGAGAAAGTGA (SEQ ID NO: 196)

AOLFR107 sequences:

MELWNFTLGSFILVGLNDSGSPELLCATITILYLLALISNGLLLAITMEARLHMPMYLLLGQ
 LSLMDLLFTSVVTPKALADFLRRENTISFGGCAQMFLALTMGGAEDLLAFMAYDRYVAICH
 PLTYMTLMSSRACWLMVATSWILASLSALIYTVYTMHYPCRAQEIRHLLCEPHLLKVACAD
 TSTRYELMVYVMGVTFILPSLAAILASYTQILLTVLHMPNSNEGRKKALVTCSSHLTVVGMFYGA
 55 ATFMVYLPSSFHSTRQDNIIISVFYITVTPALNPLIYSLRNKEVMRALRRVLGKYMLPAHSTL
 (SEQ ID NO: 197)

5 ATGGAGCTCTGGAACCTCACCTTGGGAAGTGGCTTCATTTTGGTGGGGATTCTGAATGACA
 GTGGGTCTCCTGAACTGCTCTGTGCTACAATTACAATCCTATACTTGTGGCCCTGATCAG
 CAATGGCCTACTGCTCCTGGCTATCACCATGGAAGCCCGGCTCCACATGCCCATGTACCTC
 10 CTGCTTGGGCAGCTCTCTCATGGACCTCCTGTTCACATCTGTTGTCACTCCCAAGGCCCT
 TGGGACTTTCTGCGCAGAGAAAACACCATCTCCTTTGGAGGCTGTGCCCTTCAGATGTTT
 CTGGCACTGACAATGGGTGGTGTGAGGACCTCCTACTGGCCTTCATGGCCTATGACAGGT
 ATGTGGCCATTTGTCATCCTCTGACATACATGACCCTCATGAGCTCAAGAGCCTGCTGGCT
 CATGGTGGCCACGTCCTGGATCCTGGCATCCCTAAGTGCCCTAATATATACCGTGTATACC
 15 ATGCACTATCCCTTCTGCAGGGCCCAGGAGATCAGGCATCTTCTCTGTGAGATCCCACACT
 TGCTGAAGGTGGCCTGTGCTGATACCTCCAGATATGAGCTCATGGTATATGTGATGGGTGT
 GACCTTCCTGATTCCCTCTCTTGTGCTATACTGGCCTCCTATACACAAATTCTACTCACTG
 TGCTCCATATGCCATCAAATGAGGGGAGGAAGAAAGCCCTTGTACCTGCTCTTCCACCT
 GACTGTGGTTGGGATGTTCTATGGAGCTGCCACATTCATGTATGTCTTGCCCAGTTCCTTCC
 20 ACAGCACCAGACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAA
 TCCACTCATCTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCTGGG
 AAAATACATGCTGCCAGCACACTCCACGCTCTAG (SEQ ID NO: 198)

AOLFR108 sequences:

20 MCSFFLCQTGKQAKISMGEENQTFVSKFIFLGLSQDLQTOILLFILFLIYLLTVLGNQLIILIFLD
 SRLHTPMYFFLRNLSFADLCFSTSIVPQVLVHFLVKRKTISFYGCMTQIUVFLVGCTECALLAV
 MSYDRYVAVCKPLYYSTIMTQRVCLWLSFRSWASGALVSLVDTSFTFHLPHYWGQNINHYFCE
 PPALLKLASIDTYSTEMAIFSMGVVILLAPVSLILGSYWNIISTVIQMOSGEGRLKAFSTCGSHLI
 25 VVVLFGSGIFTYMRPNSKTTKELDKMISVFYTA VTPMLNPIIYSLRNKDVKGALRKLVGKRC
 FSHRQ (SEQ ID NO: 199)

30 ATGTGTTCTTTTTTCTTGTGCCAAACAGGTAAACAGGCAAAAATATCAATGGGAGAAGAAA
 ACCAAACCTTTGTGTCCAAGTTTATCTTCTGGGTCTTTCACAGGACTTGCAGACCCAGAT
 CCTGCTATTTATCCTTTTCTCATCTTATCTGCTGACCGTGCTTGAAACCAGCTCATCA
 TCATTCTCATCTTCTGGATTCTCGCCTTCACACTCCCATGTATTTTTTTCTAGAAATCTCT
 CCTTTCAGATCTCTGTTTCTCTACTAGCATTGTCCCTCAAGTGTGGTTCACTTCTTGGTA
 AAGAGGAAAACCATTTCTTTTTATGGGTGTATGACACAGATAATTGTCTTTCTTCTGGTTG
 GGTGTACAGAGTGTGCGCTGCTGGCAGTGATGTCCTATGACCGGTATGTGGCTGTCTGCAA
 35 GCCCCTGTACTACTCTACCATCATGACACAACGGGTGTGTCTCTGGCTGTCTTCAGGTCTT
 GGGCCAGTGGGGCACTAGTGTCTTTAGTAGATACCAGCTTTACTTTCCATCTTCCCTACTG
 GGGACAGAATATAATCAATCACTACTTTTGTGAACCTCCTGCCCTCCTGAAGCTGGCTTCC
 ATAGACACTTACAGCACAGAAATGGCCATCTTTTCAATGGGCGTGGTAATCTCTGGCCC
 CTGTCTCCCTGATTCTTGGTTCTTATTGGAATATTATCTCCACTGTTATCCAGATGCAGTCT
 GGGGAAGGGAGACTCAAGGCTTTTCCACCTGTGGCTCCCATCTTATTGTTGTCTCTCTT
 40 CTATGGGTGAGGAATATTACCTACATGACGACCAAACTCCAAGACTACAAAGAACTGGA
 TAAAATGATATCTGTGTTCTATACAGCGGTGACTCCAATGTTGAACCCCATATTTATAGC
 TTGAGGAACAAAGATGTCAAAGGGGCTCTCAGGAACTAGTTGGGAGAAAGTGCTTCTCT
 CATAGGCAGTGA (SEQ ID NO: 200)

AOLFR109 sequences:

45 MLRNGSIVTEFILVGFQSSSTSTRALLFALFLALYSLTMAMNGLIIFITSWTDPKLNSPMYFFLG
 HLSLLDVCFTTTTIPQMLIHLVVRDHVSVVCCMTQMYFVFCVGVAECLLAFMAYDRYVAICY
 PLNYVPISQKVCVRLVGTAWFFGLINGIFLEYISFREPRRDNHIESFFCEAPIVIGLSCGDPQFSL
 50 WAFADAIVVILSPMVLTVTSYVHLATILSKASSSGRGKTFSTCASHLTVVFLYTSAMFSYMN
 PHSTHGPDKDKPFSLLYTIITPMCNPIIYSFRNKEIKEAMVRALGRTRLAQPQSV (SEQ ID NO:
 201)

55 ATGCTAAGGAATGGCAGCATAGTGACGGAATTTATCCTCGTGGGCTTTTCAGCAGAGCTCCA
 CTTCCACACGAGCATTGCTCTTTGCCCTCTTCTTGGCCCTCTACAGCCTCACCATGGCCATG
 AATGGCCTCATCATCTTTATCACCTCCTGGACAGACCCCAAGCTCAACAGCCCCATGTACT
 TCTTCTCGGCCATCTGTCTCTCTGATGTCTGCTTCATCACCCTACCATCCCACAGATG

TTGATCCACCTCGTGGTCAGGGACCACATTGTCTCCTTTGTATGTTGCATGACCCAGATGT
 ACITTTGTCTTCTGTGTGGTGTGGCCGAGTGCATCCTCTTGGCTTTCATGGCCTATGACCGT
 TATGTTGCTATCTGCTACCCACTTAACTATGTCCGATCATAAGCCAGAAGGTCTGTGTCA
 GGCTTGTGGGAACTGCCTGGTTCITTTGGGCTGATCAATGGCATCTTTCTCGAGTATATTTC
 5 ATTCCGAGAGCCCTTCCGAGAGACAACCACATAGAAAGCTTCTTCTGTGAGGCCCCCATA
 GTGATTGGCCTCTCTTGTGGGGACCCCTCAGTTTAGTCTGTGGGCAATCTTTGCCGATGCCA
 TCGTGGTAATTCTCAGCCCCATGGTGCTCACTGTCACTTCCTATGTGCACATCCTGGCCACC
 ATCCTCAGCAAAGCCTCCTCCTCAGGTGCGGGGAAGACTTCTCTACTTGTGCCTCTCACC
 TGA CTGTGGTCATCTTTCTCTACACTTCAGCTATGTTCTCTTACATGAACCCCCACAGCACA
 10 CATGGGCCTGACAAAGACAAACCTTTCTCCCTCCTGTACACCATCATTACCCCCATGTGCA
 ACCCCATCATTTATAGTTTCCGCAACAAGGAAATTAAGGAGGCCATGGTGAGGGCACTTG
 GAAGAACCAGGCTGGCCCAGCCACAGTCTGTCTAG (SEQ ID NO: 202)

AOLFR110 sequences:

15 MKIANNTVVTEFILLGLTQSQDIQLLVFVLILIFYLILPGNFLIIFTIRSDPGLTAPLYLFLGNLAFL
 DASYSFIVAPRMLVDFLSEKKVISYRGCTQLFFLHFLGGGEGLLLVVMAFDRIAICRPLHCST
 VMNPRACYAMMLALWLGGFVHSIIQVVLILRLPFCGPNQLDNFFCDVRQVIKLA CTDMFVVVEL
 LMVFNSGLMTLLCFLGLLASYAVILCHVRRASEGKNKAMSTCTTRVILLMFPGAIFTYMCPP
 20 RALPADKMSVSLFHTVIFPLMNPMTYTLRNQEVKTSMKRLLSRHVVCQVDFIIRN (SEQ ID NO:
 203)

ATGAAGATAGCAAACAACACAGTAGTGACAGAATTTATCCTCCTTGGTCTGACTCAGTCTC
 AAGATATTCAGCTCTTGGTCTTTGTGCTGATCTTAATTTTCTACCTTATCATCCTCCCTGGA
 AATTTTCTCATTATTTTACCATAAAGGTGAGCCCTGGGCTCACAGCCCCCTCTATTTATT
 25 TCTGGGCAACTTGGCCTTCTGGATGCATCCTACTCCTTCACTTGTGGCTCCCAGGATGTTGG
 TGGACTTCCTCTCTGAGAAAAAGGTAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTTT
 CITGCACTTCCTTGGAGGAGGGGAGGATTACTCCTTGTGTGATGGCCTTTGACCGCTAC
 ATCGCCATCTGCCGGCCTCTGCACTGTTCAACTGTCATGAACCCTAGAGCCTGCTATGCAA
 TGATGTTGGCTCTGTGGCTTGGGGGTTTTGTCCACTCCATTATCCAGGTGGTCTCATCCTC
 30 CGCTTGCCCTTTTTGTGGCCCAAACCAGCTGGACAACCTTCTTCTGTGATGTCCGACAGGTCA
 TCAAGCTGGCTTGCACCGACATGTTTGTGGTGGAGCTTCTAATGGTCTTCAACAGTGGCCT
 GATGACACTCCTGTGCTTCTTGGGGCTTCTGGCTTCCTATGCAGTCATCCTCTGCCATGTTT
 GTAGGGCAGCTTCTGAAGGGAAGAACAAGGCCATGTCCACGTGCACCACTCGTGTCAATTA
 TTATACTTCTTATGTTTGGACCTGCTATCTTCACTACATGTGCCCTTTCAGGGCCTTACCA
 35 GCTGACAAGATGGTTTCTCTTTTACACAGTGATCTTTCCATTGATGAATCCTATGATTTA
 TACCCTTCGCAACCAGGAAGTGAAAACCTCCATGAAGAGGTTATTGAGTCGACATGTAGTC
 TGTCAAGTGGATTTTATAATAAGAACTGA (SEQ ID NO: 204)

AOLFR111 sequences:

40 MCYIYLIFKEWTLIFYFSLLLFLQITPAIMANLTIVTEFILMGEFSTNKNMCLHSILFLIYL CALM
 GNVLIIMITTL DHHLHTPVYFFLKNLSFLDLCLISVTAPKSIANS LIHNNSISFLGCVS QVFLLLSS
 ASAE LLLTVMSFDRYTAICHPLHYDVIMDRSTCVQRATVSWLYGG LIAVMHTAGTFSLSYCG
 SNMVHQFFCDIPQLLAISCSEN LIREIALILINVLD FCCFIVIIITYVHV FSTVKKIPSTEGQSKAY
 45 SICLP HLLVVLSTGFIA YLKPASESPSILDAVISVFY TMLPPTFNPIIYSLRNKA I KVALGMLIKG
 KLTKK (SEQ ID NO: 205)

ATGTGTTATATATATTTAATATTTAAAGAGTGGACATTGATATTTTACTTCAGTCTTCTCCT
 TTTCTGCAGATTACTCCTGCAATAATGGCAAATCTCACAATCGTGACTGAATTTATCCTTA
 TGGGGTTTTCTACCAATAAAAAATATGTCATTTTGCATTTCGATTCTCTTCTTGTGATTTAT
 50 TTGTGTGCCCTGATGGGGAATGTCCTCATTATCATGATCACAACCTTGGACCATCATCTCC
 ACACCCCGTGATTTTCTTCTTGAAGAATCTATCTTTCTTGGATCTCTGCCTTATTTTCAGTC
 ACGGCTCCCAAATCTATCGCCAATTCTTTGATACACAACAACCTCCATTTCATTCTTGGCTG
 TGTTTCCCAGGTCTTTTTGTGCTTTCTTCAGCATCTGCAGAGCTGCTCCTCCTCACGGTGA
 TGTCTTTGACCGCTATACTGCTATATGTCACCTCTGCACTATGATGTCATCATGGACAGG
 55 AGCACCTGTGTCCAAAGAGCCACTGTGTCTTGGCTGTATGGGGTCTGATTGCTGTGATGC
 ACACAGCTGGCACCTTCTCCTTATCCTACTGTGGGTCCAACATGGTCCATCAGTTCTTCTGT

GACATTCCCCAGTTATTAGCTATTTCTTGCTCAGAAAATTTAATAAGAGAAATTGCACTCA
 TCCTTATTAATGTAGTTTTGGATTTCTGCTGTTTTATTGTCATCATCATTACCTATGTCCAC
 GTCTTCTCTACAGTCAAGAAGATCCCTTCCACAGAAGGCCAGTCAAAAGCCTACTCTATTT
 GCCTTCCACACTTGCTGGTTGTGTTATTTCTTTCCACTGGATTCAATTGCTTATCTGAAGCCA
 5 GCTTCAGAGTCTCCTTCTATTTTGGATGCTGTAATTTCTGTGTTCTACACTATGCTGCCCCC
 AACCTTTAATCCCATTATATACAGTTTGAGAAACAAGGCCATAAAGGTGGCTCTGGGGATG
 TTGATAAAGGGAAAGCTCACCAAAAAGTAA (SEQ ID NO: 206)

AOLFR113 sequences:

10 MKFWHGFSSHLNPMFSSFLLYLSLPWINTTIQAWLNLCALPVMWMSGAGFLSCCYWHTCSP
 SVVTCSSSQSSDWMQLCTHLCTTSLVFFPSWSCGQLPLSLRCLIFSRRKPFLLQDASFRPTSS
 TPWGACECYLLTAMAYDRYLAICRPLHYPIIMTTTLCAKMAAACWTCGFLCPISEVILASQLPF
 CAYNEIQHFCDPPLSLACKDTSANILVDFAINAFILITFFIMISYARIIGAVLKIKTASGRKK
 AFSTCASHLAVVLIFGSIIFMYVRLKSYSLLDRTLAIVYSVLTPMVNPIIYSLRNKEIKAIKR
 15 TIFQKGDKASLAHL (SEQ ID NO: 207)

ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTTGTGCATTAACAGGA
 AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC
 CTTCTCTCTGTGGGTATCCAGGACTGCAATCTTACATCTTTGGCTGGCTATCTCACTGA
 20 GTGCCATGTACATCATAGCCCTGTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA
 TTCCACTCGGCATGAGCCCATGTATTGCTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTA
 TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG
 CTTTAGTGCTTGTTCCTCACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG
 CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA
 25 GAATTCTCACGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT
 AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT
 GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA
 GCAGTCTCTACAGTCTGATTGGTTCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT
 GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA
 30 AGCATTAAAGCACATGTGGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATG
 GCATCCATCTATGCGGCCTGGTTGGGGCAGGATGTAAGTCCCTTGACACCCCAAGTCTGCTG
 TAGCTGACCTGTACGTGATCATCCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC
 CAAACAAGTGGGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATTCCAAC
 CTGGGTTTCATGA (SEQ ID NO: 208)

35

AOLFR114 sequences:

MERINHTSSVSEFILLGLSSRPEDQKTLFVLFLIVYLVTITGNLLILAIRFNPHLQTPMYFFLSFLS
 LTDICFTTSVVPKMLMNFLEKKTISYAGCLTQMYFLYALGNSDSCLLAVMAFDTRYVAVCDPF
 HYVTMTSHHHCVLLVAFSCSFPHLHSLHLLNRLTFCDNSVHHFLCDLSPVLKLSGSSIFVN
 40 EIVQMTEAPIVLVTRFLCIAFSYIRILTVLKIPSTSGKRKAFSTCGFYLTVVTLFYGSIFCVYLQP
 PSTYAVKDHVATIVYTVLSSMLNPFYISLRNKDLKQLRKLMSKRS (SEQ ID NO: 209)

ATGGAAAGAATCAACCACACCAGCAGTGTCTCCGAGTTTATCCTCCTGGGACTCTCCTCCC
 GGCCTGAGGACCAAAAGACACTCTTTGTTCTCTTCTCATCGTGACCTGGTCACCATAAC
 45 AGGGAACCTGCTCATCATCCTGGCCATTGCTTCAACCCCATCTTACAGACCCCTATGTATT
 TCTTCTTGAGTTTTCTGTCTCTCACTGATATTTGCTTTACAACAAGCGTTGTCCCAAGATG
 CTGATGAACTTCTGTGAGAAAAGAAGACCATCTCCTATGCTGGGTGTCTGACACAGATGT
 ATTTTCTCTATGCCTTGGGCAACAGTGACAGCTGCCTTCTGGCAGTCATGGCCTTTGACCG
 CTATGTGGCCGTCTGTGACCTTTCCACTATGTACACCACCATGAGCCACCACTGTGTGCTG
 50 TGCTGGTGGCCTTCTCCTGCTCATTTCTCCTCACTCCACTCACTCCTGCACACACTTCTGCTG
 AATCGTCTCACTTCTGTGACTCCAATGTTATCCACCACCTTTCTCTGTGACCTCAGCCCTGT
 GCTGAAATTGTCTGCTCTTCCATATTTGTCAATGAAATTGTGCAGATGACAGAAGCACCT
 ATTGTTTTGGTGACTCGTTTTCTCTGCATTGCTTTCTCTTATATACGAATCCTCACTACAGT
 TCTCAAGATTCCCTCTACTTCTGGGAAACGCAAAGCCTTCTCCACCTGTGGTTTTACCTCA
 55 CCGTGGTGACGCTCTTTATGGAAGCATCTTCTGTGTCTATTTACAGCCCCCATCCACCTAC
 GCTGTCAAGGACCACGTGGCAACAATTGTTTACACAGTTTTGTGTCATCCATGCTCAATCCTT

TTATCTACAGCCTGAGAAACAAAGACCTGAAACAGGGCCTGAGGAAGCTTATGAGCAAGA
GATCCTAG (SEQ ID NO: 210)

AOLFR115 sequences:

5 MEGFYLRSSHQLQGMGKPRVNTTVSDFLLGLSEWPPEQPLLFGIFLGMVLTVMVGNLLII
LAISSDPHLHTPMYFFLANLSLTDACFTSASIPKMLANIHTQSQIISYSGCLAQLYFLLMFGGLD
NCLLAVMAYDRYVAICQPLHYSTSMSPQLCALMLGVCWVLTNCPALMHTLLLTRVAFCAQK
AIPHFYCDPSALLKLACSDTHVNELMIITMGLLFLTVPLLIVFSYVRIFWAVFVISSPGGRWKA
10 FSTCGSHLTVVLLFYGSLMGVYLLPPSTYSTERESRAAVLYMVIPTLNPFIYSLNRDMKEALG
KLFVSGKTFFL (SEQ ID NO: 211)

ATGGAAGGTTTTTATCTGCGCAGATCACACGAACTACAAGGGATGGGAAAACCAGGCAGA
GTGAACCAAAACCACTGTTTCAGACTTCCTCCTTCTAGGACTCTCTGAGTGGCCAGAGGAGC
AGCCTCTTCTGTTTGGCATCTTCCTTGGCATGTACCTGGTCACCATGGTGGGGAACCTGCTC
15 ATTATCTTGGCCATCAGCTCTGACCCACACCTCCATACTCCCATGTACTTCTTTCTGGCCAA
CTGTCTATTAACTGATGCCTGTTTCACTTCTGCCTCCATCCCCAAAATGCTGGCCCAACATTC
ATACCCAGAGTCAGATCATCTCGTATTCTGGGTGTCTTGACACAGCTATATTTCTCCTTATG
TTTGGTGGCCTTGACAACTGCCTGCTGGCTGTGATGGCATATGACCGCTATGTGGCCATCT
GCCAACCCTCCATTACAGCACATCTATGAGTCCCCAGCTCTGTGCACTAATGCTGGGTGT
20 GTGCTGGGTGCTAACCAACTGTCCTGCCCTGATGCACACACTGTTGCTGACCCGCGTGGCT
TTCTGTGCCAGAAAGCCATCCCTCATTCTATTGTGATCCTAGTGCTCTCCTGAAGCTTGC
CTGCTCAGATACCCATGTAAACGAGCTGATGATCATCACCATGGGCTTGCTGTTCTCTACT
GTTCCCCTCCTGCTGATCGTCTTCTCCTATGTCCGCATTTTCTGGGCTGTGTTTGTATCTC
ATCTCCTGGAGGGAGATGGAAGGCCTTCTCTACCTGTGGTTCTCATCTCACGGTGGTTCTG
25 CTCTTCTATGGGTCTCTTATGGGTGTGATTTACTTCTCCATCAACTTACTCTACAGAGAG
GGAAAGTAGGGCTGCTGTTCTCTATATGGTGATTATTTCCACGCTAAACCCATTCTTTAT
AGCTTGAGGAACAGAGACATGAAGGAGGCTTTGGGTAAACTTTTGTGTCAGTGAAAAACA
TTCTTTTATGA (SEQ ID NO: 212)

AOLFR116 sequences:

30 MDEANHSVSEFVFLGLSDSRKIQLLLFFSVFYVSSLMGNLLIVLTVTSDPRLQSPMYFFLAN
LSIINLVFCSSTAPKMIYDLFRKHKTISFGGCVVQIFFIHAVGGTEMVLLIAMAFDRYVAICKPLH
YLTIMNPQRCLFLVISWIIHHSVIQLAFVVDLLFCGPNELDSFFCDLPRFIKLACIETYTLGFMV
TANSFGISLASFLIISIYIFILVTVQKKSSGGIFKAFSMLSAHVIVVVLVFGPLIFFYIFPPTSHLD
35 KFLAIFDAVITPVLPVNIYTFRNKEMMVAMRRRCSSQFVNYSKIF (SEQ ID NO: 213)

ATGGATGAAGCCAATCACTCTGTGGTCTCTGAGTTTGTGTTCTCTGGGACTCTCTGACTCGC
GGAAGATCCAGCTCCTCCTCTCTCTCTTTTCTCAGTGTTCTATGTATCAAGCCTGATGGGA
AATCTCCTCATTGTGCTAACTGTGACCTCTGACCCTCGTTTACAGTCCCCCATGTACTTCT
40 GCTGGCCAACCTTTCCATCATCAATTTGGTATTTTGTCTCTCCACAGCTCCCAAGATGATTT
ATGACCTTTTTCAGGAAGCACAAGACCATCTCTTTTGGGGGCTGTGTAGTTCAGATCTTCTT
TATCCATGCAGTTGGGGGAAGTGAAGTGGTGTGCTCATAGCCATGGCTTTTGACCGATAT
GTGGCCATATGTAAGCCTCTCCACTACCTGACCATCATGAACCCACAAAGGTGCATTTTGT
TTTTAGTCATTTCTGGATTATAGGTATTATTCACTCAGTGATTGAGTTGGCTTTTGTGTA
45 GACCTGCTGTTCTGTGGCCCTAATGAATTAGATAGTTTCTTTTGTGATCTTCTCGATTAT
CAAACCTGGCTTGATAGAGACCTACACATTGGGATTTCATGGTTACTGCCAATAGTGGATTT
ATTTCTCTGGCTTCTTTTTTAATTTCTCATAATCTCTTACATCTTTATTTTGGTGACTGTTCAG
AAAAATCTTCAGGTGGTATATTCAAGGCTTTCTCTATGCTGTGAGCTCATGTCATTGTGG
TGGTTTGGTCTTTGGGCCATTAATCTTTTCTATATTTTCCATTTCCACATCATCATCTTG
50 ATAAATTCCTTGCCATCTTTGATGACGTTATCACTCCCGTTTGAATCCAGTCATCTATACT
TTTAGAAATAAAGAGATGATGGTGGCAATGAGAAGACGATGCTCTCAGTTTGTGAATTAC
AGTAAAATCTTTTAA (SEQ ID NO: 214)

AOLFR117 sequences:

55 MNNTIVFVIKIQIEKSDLKYRAISLQEISKISLLFWVLLVISRLLAMTLGNSTEVTEFYLLGFGA
QHEFWCILFIVFLLIYVTSIMGNSGILLINTDSRFQTLTYFFLQHLAFVDICYTSAITPKMLQSFT

EEKNLILFQGCVIQFLVYATFATSDCYLLAMMAVDPYVAICKPLHYTVMSRTVCIRLVAGSYI
MGSINASVQTGFTCSLSFCKSNSINHHFCDVPPILALSCSNVDINIMLLVVFVGSNLIFTGLVVIFS
YIYIMATILKMSSSAGRKKSFSTCASHLTAVTIFYGTLSYMYLQSHSNNSQENMKVAFIFYGTVI
PMLNPLIYSLRNKEVKEALKVIGKKLF (SEQ ID NO: 215).

5

ATGAATAACACTATTGTATTTGTCATAAAAATACAAATAGAAAAAAGTGACTTGAAATATA
GAGCCATTTTCATTGCAAGAAATCTCAAAGATTTCCCTTCTTTTCTGGGTCTTCTCTTGGTC
ATTTCTAGACTTTTACTAGCCATGACACTAGGAAACAGCACTGAAGTCACTGAATTCTATC
TTCTGGGATTTGGTGCCCGCATGAGTTTTGGTGTATCCTCTTCATTGTATTCCTTCTCATC
10 TATGTGACCTCCATAATGGGTAATAGTGAATAATCTTACTCATCAACACAGATTCCAGAT
TTCAAACACTCACGTACTTTTTCTACAACATTTGGCTTTTGTGATATCTGTTACACTTCT
GCTATCACTCCCAAGATGCTCCAAAGCTTCACAGAAGAAAAGAATTTGATATTATTTTCAGG
GCTGTGTGATACAATTCTTAGTTTATGCAACATTTGCAACCAGTGACTGTTATCTCCTGGCT
ATGATGGCAGTGGATCCTTATGTTGCCATCTGTAAGCCCCTTCACTATACTGTAATCATGT
15 CCCGAACAGTCTGCATCCGTTTGGTAGCTGGTTCATACATCATGGGCTCAATAAATGCCTC
TGTACAAACAGGTTTACATGTTCACTGTCCTTCTGCAAGTCCAATAGCATCAATCACTTTT
TCTGTGATGTTCCCCCTATTCTTGCTCTTTCATGCTCCAATGTTGACATCAACATCATGCTA
CTTGTGTTCTTTGTGGGATCTAACTTGATATCTCACTGGGTTGGTCGTCATCTTTTCTTACAT
CTACATCATGGCCACCATCCTGAAAATGTCTTCTAGTGCAGGAAGGAAAAAATCTTCTCA
20 ACATGTGCTTCCACCTGACCGCAGTCACCATTTTCTATGGGACACTCTCTTACATGTATTT
GCAGTCTCATTCTAATAATTCCAGGAAAATATGAAAGTGGCCTTTATATTTTATGGCACA
GTTATTTCCCATGTTAAATCCTTTAATCTATAGCTTGAGAAATAAGGAAGTAAAAGAAGCTT
TAAAAGTGATAGGGAAAAAGTTATTTTAA (SEQ ID NO: 216)

25 **AOLFR118 sequences:**

MNHMSASLKISNSSKFQVSEFILLGFPGIHSWQHWLSLPLALLYLSALAANTLILIIWQNPSLQQ
PMYIFLILCMVDMGLATTIIPKILAFWFDKVISLPECFAQIYAIHFFVGMESGILLCMAFDRY
VAICHPLRPSIVTSSLILKATLFMVLNRNGLFVTPVPVLAAQRDYCSKNBIEHCLCSNLGVTSLA
CDDRRPNSICQLVLAWLGMGSDLSLILSYLILYSVLRNLSAEAAKALSTCSSHLTLILFFYTIV
30 VVISVTHLTEMKATLIPVLLNVLHNIIPPSLNPTVYALQTKELRAAFQKVLFALTKEIRS (SEQ ID
NO: 217)

ATGAATCATATGTCTGCATCTCTCAAAATCTCCAATAGCTCCAAATTCCAGGTCTCTGAGTT
CATCCTGCTGGGATTCCCGGGCATTACAGCTGGCAACACTGGCTATCTCTGCCCCCTGGCA
35 CTACTGTATCTCTCAGCACTTGCTGCAAACACCCTCATCCTCATCATCTGGCAGAACCC
TTCTTTACAGCAGCCCATGTATATTTTCTTGGCATCCTCTGTATGGTAGACATGGGTCTGG
CCACTACTATCATCCCTAAGATCCTGGCCATCTTCTGGTTTGATGCCAAGGTTATTAGCCTC
CCTGAGTGCTTTGCTCAGATTTATGCCATTCACTTCTTTGTGGGCATGGAGTCTGGTATCCT
ACTCTGCATGGCTTTTGATAGATATGTGGCTATTTGTCACCCTCTTCGCTATCCATCAATTG
40 TCACCAGTTCCTTAATCTTAAAGCTACCCTGTTTCATGGTGCTGAGAAATGGCTTATTTGTC
ACTCCAGTGCCTGTGCTTGCAGCACAGCGTGATTATTGCTCCAAGAATGAAATTGAACACT
GCCTGTGCTCTAACCTTGGGGTCACAAGCCTGGCTTGATGACAGGAGGCCAAACAGCAT
TTGCCAGTTGGTTCTGGCATGGCTTGGAAATGGGGAGTGATCTAAGTCTTATTATACTGTCA
TATATTTTGATTCTGTACTCTGTACTTAGACTGAACTCAGCTGAAGCTGCAGCCAAAGGCC
45 TGAGCACTTGATGTTACATCTCACCTCATCCTTTTCTTTTACACTATTGTTGTAGTGATT
TCAGTGACTCATCTGACAGAGATGAAGGCTACTTTGATTCCAGTCTACTTAATGTGTTGC
ACAACATCATCCCCCTTCCCTCAACCCTACAGTTTATGCACTTCAGACCAAAGAAGCTTAG
GGCAGCCTTCCAAAAGGTGCTGTTTGCCCTTACAAAAGAAATAAGATCTTAG (SEQ ID NO:
218)

50

AOLFR119 sequences:

MPLFNSLCWFPTIHVTPPSFILNGIPGLERVHVWISLPLCTMYIIFLVGNLGLVYLIYYEESLHHP
MYFFFGHALSLDLLTCTTLPNALCIFWFSLEKINFNACLAQMFFVHGFTGVESGVLMLMALD
RYIAICYPLRYATTLTNPIAKAELATFLRGVLLMIPFPFLVKRLPFCQSNISHTYCDHMSVVKL
55 SCASIKVNVITYGLMVALLIGVFDICCSLSYTLILKAAISLSSSDARQKAFSTCTAHISAIITYVPA

FFTFFAHREFGGHTIPPSLHIIVANLYLLPPTLNPIVYGVKTKQIRKSVIKFFQGDKGAG (SEQ ID NO: 219)

5 ATGCCTCTATTTAATTCATTATGCTGGTTTCCAACAATTCATGTGACTCCTCCATCTTTTAT
TCTTAATGGAATACCTGGTCTGGAAAGAGTACATGTATGGATCTCCCTCCCACTCTGCACA
ATGTACATCATCTTCCTTGTGGGGAATCTTGGTCTTGTGTACCTCATTTATTATGAGGAGTC
CTTACATCATCCGATGTATTTTTTTTTTGGCCATGCTCTCTCCCTCATTGACCTCCTTACCTG
CACCACCACTCTACCCAATGCACTCTGCATCTTCTGGTTCAGTCTCAAAGAAATTAACCTCA
ATGCTTGCTTGGCCCAGATGTTCTTTGTTCATGGGTTACAGGTGTGGAGTCTGGGGTGTCT
10 CATGCTCATGGCTCTAGACCGCTATATAGCCATTTGCTACCCTTTGCGTTATGCTACCACAC
TCACCAACCCTATCATTGCCAAGGCTGAGCTTGCCACCTTCTGAGGGGTGTATTGCTGAT
GATTCCTTTCCCATTTCTTGGTTAAGCGTTTGCCTTTCTGCCAAAGCAATATTATCTCCATA
CGTACTGCGACCACATGTCTGTAGTAAAGCTATCTTGTGCCAGCATCAAGGTCAATGTAAT
CTATGGTCTAATGGTTGCTCTCCTGATTGGAGTGTITGACATTTGTTGTATATCTTTGTCTT
15 ACACTTTGATCCTCAAGGCAGCGATCAGCCTCTCTTCATCAGATGCTCGGCAGAAGGCTTT
CAGCACCTGCACTGCCCATATATCTGCCATCATCATCACCTATGTTCCAGCATTCTTCACTT
TCTTTGCCACCGTTTTTGGGGGACACACAATCCCCCTTCTCTTCACATCATTGTGGCTAAT
CTTTATCTTCTTCTCCCCCAACTCTAAACCCTATTGTTTATGGAGTAAAGACAAAACAGAT
ACGCAAGAGTGTCTATAAAGTTCTTCCAGGGTGATAAGGGTGCAGGTTGA (SEQ ID NO: 220)

20

AOLFR120 sequences:

MQPYTKNWTQVTEFVMMGFAGIHEAHLFFILFTMYLFTLVENLAHLVVGLDHRLRRPMYF
FLTHLSCLEIWYTSVTPKMLAGFIGVDGKNISYAGCLSQLFIFLFGATECFLLAAMAYDRY
VAICMPLHYGAFVSWGTCIRLAAACWLVGFLTPILPIYLLSQLTCGPNVIDHFSCDASPLLALS
25 CSDVTWKETVDFLVSLAVLLASSMVIAVSYGNIVWTLHIRSAAERWKAFTCAHLTVVSLF
YGTLLFFMYVQTKVTSSINFNKVVSVFYSVTPMLNPLIYSLRNKEVKGALGRVFSLNFWKGG
(SEQ ID NO: 221)

30 ATGCAACCATATACCAAAAACCTGGACCCAGGTAACCTGAATTTGTCATGATGGGCTTTGCTG
GCATCCATGAAGCACACCTCCTCTTCTCATACTCTTCCTCACCATGTACCTGTTACCTTG
GTGGAGAAATTTGGCCATCATTTTAGTGGTGGGTTTGGACCACCGACTACGGAGACCCATGT
ATTTCTTCTGACACACTTGTCTGCCTTGAAATCTGGTACACTTCTGTTACAGTGCCCAAG
ATGCTGGCTGGTTTTATTGGGGTGGATGGTGGCAAGAATATCTCTTATGCTGGTTGCCTAT
CCCAGCTCTTCATCTTCACCTTTCTTGGGGCAACTGAGTGTTTCTACTGGCTGCCATGGCC
35 TATGATCGTTATGTGGCCATTTGTATGCCTCTCCACTATGGGGCTTTTGTGTCTGGGGCAC
CTGCATCCGTCTGGCAGCTGCCTGTTGGCTGGTAGGTTTCTCACACCCATCTTGCCAATCT
ACCTCTTGTCTCAGCTAACATTTTGTGGCCCAAATGTCATTGACCATTTCTCCTGTGATGCC
TCACCCTTGCTAGCCTTGTCTGCTCAGATGTCACTTGGAAGGAGACTGTGGATTCTCTGG
TGTCTCTGGCTGTGCTACTGGCCTCCTCTATGGTCATTGCTGTGTCCTATGGCAACATCGTC
40 TGGACACTGCTGCACATCCGCTCAGCTGCTGAGCGCTGGAAGGCCTTCTCTACCTGTGCAG
CTCACCTGACTGTGGTGAGCCTCTTCTATGGCACTCTTTTCTTTATGTATGTCCAGACCAAG
GTGACCTCCTCCATCAACTTCAACAAGGTGGTATCTGTCTTCTACTCTGTTGTACGCCCCAT
GCTCAATCCTCTCATCTACAGTCTTAGGAACAAGGAAGTGAAGGGAGCTCTGGGTGCGAGTC
TTTTCTCTCAACTTTTGGGAAGGGACAGTGA (SEQ ID NO: 222)

45

AOLFR121 sequences:

MKRKNFTEVSEFIFLGFSSFGKHQITLFVVFLTVYILTLVANIIIVTIIICIDHHLHTPMYFFLSMLA
SSETVYTLVIVPRMLLSLIFHNQPISLAGCATQMFFVILATNNCFLLTAMGYDRYVAICRPLRY
TVIMSKGLCAQLVCGSFGIGLTMVAVLHVTFAMFNLPCGTVVDHFFCDIYPVMKLSCIDTTINEII
50 NYGVSSFVIFVPIGLIFISYVLVISSILQIASAEGRKKTFATCVSHLTVVIVHCGCASIAYLKPSES
SIEKDLVLSVTYTHITPLLNPVVYSLRNKEVKDALCRVVGRNIS (SEQ ID NO: 223)

55 ATGAAGAGAAAGAACTTCACAGAAGTGTGAGAATTCATTTTCTTGGGATTTTCTAGCTTTG
GAAAGCATCAGATAACCCTCTTTGTGGTTTTCCTAACTGTCTACATTTAACTCTGGTTGCT
AACATCATCATTGTGACTATCATCTGCATTGACCATCATCTCCACACTCCCATGTATTCTT
CCTAAGCATGCTGGCTAGTTCAGAGACGGTGACACACTGGTCATTGTGCCACGAATGCTT

TTGAGCCTCATTTTTTCATAACCAACCTATCTCCTTGGCAGGCTGTGCTACACAAATGTTCTT
 TTTTGTATCTTGGCCACTAATAATTGCTTCTGCTTACTGCAATGGGGTATGACCGCTATG
 TGGCCATCTGCAGACCCCTGAGATACACTGTGCATCATGAGCAAGGGACTATGTGCCAGCT
 GGTGTGTGGGTCTTTGGCATTGGTCTGACTATGGCAGTTCTCCATGTGACAGCCATGTTT
 5 AATTTGCCGTTCTGTGGCACAGTGGTAGACCATTCTTTTGTGACATTTACCCAGTCATGA
 AACTTTCTTGCAATTGATACCACTATCAATGAGATAATAAATTATGGTGTAAAGTTCATTTGT
 GATTTTTGTGCCCATAGGCCTGATATTTATCTCCTATGTCCTTGTGCATCTCTTCCATCCTTC
 AAATTGCCCTCAGCTGAGGGCCGGAAGAAGACCTTTGCCACCTGTGTCTCCACCTCACTGT
 GGTATTGTCCACTGTGGCTGTGCCTCCATTGCCTACCTCAAGCCGAAGTCAGAAAGTTCA
 10 ATAGAAAAAGACCTTGTTCTCTCAGTGACGTACACCATCATCACTCCCTTGCTGAACCCTG
 TTGTTTACAGTCTGAGAAACAAGGAGGTAAAGGATGCCCTATGCAGAGTTGTGGGCAGAA
 ATATTTCTTAA (SEQ ID NO: 224)

AOLFR122 sequences:

15 MEWENQTLVEFFLKGHSVHPRLELLFFVLIFMYVILLGNGTLILISILDPHLHTPMYFFLGNL
 SFLDICYTTTSPSTLVSFLSERKTISFSGCAVQMFLGLAMGTTECVLLGMMAFDYVAICNPLR
 YPIIMSKNAYVPMAGVSWFAGIVNSAVQTTFFVQLPFCRKNVINHFSCEILAVMKLACADISGN
 EFLMLVATILFTLMPLLLVISYSLIISILKIHSSSEGRSKAFSTCSAHLTVVIIFYGTILFMYMKPKS
 20 KETLNSDDL DATDKIISMFGVMTMPMNPLIYSLRNKDVKEAVKHLPNRRFFSK (SEQ ID NO:
 225)

ATGGAATGGGAAAACCAAACCTTCTGGTGGAATTTTTCTGAAGGGACATTCTGTTCCACC
 CAAGGCTTGAGTTACTCTTTTTGTGCTAATCTTCATAATGTATGTGGTCATCCTTCTGGGG
 AATGGTACTCTCATTTTAATCAGCATCTTGGACCCCTCACCTTCACACCCCTATGTACTTCTT
 25 TCTGGGGAACTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACACTAG
 TGAGCTTCTCTTTCAGAAAGAAAGACCATTTCCTTTTCTGGCTGTGCAGTGCAGATGTTCCCTT
 GGCTTGCCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCCTTTGACCGCTATG
 TGGCTATCTGCAACCCCTCTGAGATATCCCATCATCATGAGCAAGAATGCCTATGTACCCAT
 GGCTGTTGGGTCTGGTTTGCAGGGATTGTCAACTCTGCAGTACAACTACATTTGTAGTA
 30 CAATTGCCCTTCTGCAGGAAGAATGTCATCAATCATTTCTCATGTGAAATTCTAGCTGTCAT
 GAAGTTGGCCTGTGCTGACATCTCAGGCAATGAGTTCCTCATGCTTGTGGCCACAATATTG
 TTCACATTGATGCCACTGCTCTTGATAGTTATCTCTTACTCATTAAATCATTTCCAGCATCCT
 CAAGATTCACTCCTCTGAGGGGAGAAGCAAAGCTTCTCTACCTGCTCAGCCCATCTGACT
 GTGGTCATAATATTCTATGGGACCATCCTCTTCATGTATATGAAGCCCAAGTCTAAAGAGA
 35 CACTTAATTGAGATGACTTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTGAT
 GACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCAGT
 AAAACACCTACCGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 226)

AOLFR123 sequences:

40 MYRFTDFDVSNISITLNVHLYFTTQQAGDLEHMETRNYSAMTEFFLVGLSQYPELQLFLFLCL
 IMYMILLGNSLLIITILDSRLHTPMYFFLGNSFLDICYTSSSIPMLIIFMSERKSISFIGCALQM
 VVSLGLGSTECVLLAVMAYDHYVAICNPLRYSIIMNGVLYVQMAAWSWIIGCLTSLQTVLT
 MMLPFCGNVIDHITCEILALLKLVCSITINVLMTVTNIVSLVILLLLIFISYVFILSSILRINCAE
 GRKKAFTCSAHSIVVILFYGSALFMYMKPKSKNTNTSDEIIGLSYGVVSPMLNPIIYSLRNKEV
 45 KEAVKKVLSRHLHLLKM (SEQ ID NO: 227)

ATGTACAGATTTACAGATTTTGATGTATCAAACATTTCAATTTACCTGAATCATGTCCTTTT
 CTATACTACCCAGCAGGCAGGTGACCTAGAACACATGGAGACAAGAAATTACTCTGCCAT
 GACTGAATTTCTTCTGGTGGGGCTTTCCCAATATCCAGAGCTCCAGCTTTTCTGTTCCTGC
 50 TCTGCCTCATCATGTACATGATAATCCTCCTGGGAAATAGCCTCCTCATTATCAACCATC
 TTGGATTCTCGCCTCCATACTCCCATGTATTTCTTTCTTGGAAACCTCTCATTCTTGGACAT
 CTGTTACACATCCTCATCCATTCTCCAATGCTTATTATATTTATGTCTGAGAGAAAATCCA
 TCTCCTTCAATTGGCTGTGCTCTGCAGATGGTTGTGTCCCTTGGCTTGGGCTCCACTGAGTGT
 GTCCTCCTGGCTGTGATGGCCTATGACCACTATGTGGCCATCTGCAACCCACTGAGGTACT
 55 CCATCATCATGAACGGAGTGCTGTATGTGCAAAATGGCTGCATGGTCCTGGATCATAGGCTG
 TCTGACCTCCCTATTGCAAACAGTTCTGACAATGATGTTGCCTTTCTGTGGGAATAATGTC

- ATTGATCATATTACCTGTGAAATTTTGGCCCTTCTAAAACCTGTTTGTTTCAGATATCACCAT
CAATGTGCTTATCATGACAGTGACAAATATTGTTTCACTGGTGATTCTTCTACTGTAAATTT
TCATCTCCTATGTGTTTATTCTCTCTTCCATCCTGAGAATTAATTGTGCTGAGGGAAGAAAG
AAAGCCTTCTCTACCTGTTTCAGCGCACTCGATTGTGGTCATCTTATTCTACGGTTCAGCCCT
5 TTTTATGTACATGAAACCCCAAGTCAAAGAACTAATAACATCTGATGAGATTATTGGGCTG
TCTTATGGAGTGGTAAGCCCAATGTTAAATCCCATCATCTATAGCCTCAGGAATAAAGAGG
TCAAAGAGGCTGTAAAGAAAGTCTGAGCAGACATCTGCATTTATTGAAAATGTGA (SEQ
ID NO: 228)
- 10 **AOLFR124 sequences:**
MNHSVVTFFIILGLTKKPELQGHFLFLLIVYLVAFLGNMLIIIAKIYNNTLHTPMYVFLLLAVV
DICTTSIIPKMLGTMLTSENTISYAGCMSQLFLFTWSLGAEMVLFITMAYDRYVAICFPLHYST
VMNHHMVCVALLSMVMAIAVTNSWVHTALIMRLTFCGPNTIDHFFCEIPLALLSCSPVRINEV
MVYVADITLAIGDFILTCISYGFIIIVAILRIRTVGKRAKAFSTCSSHLTVVTLYYSPVIYTYIRPASS
15 YTFERDKVVAALYTLVPTLNPVMVYSFQNRMQAGIRKVFAFLKH (SEQ ID NO: 229)
- 20 ATGAATCACAGCGTTGTAAGTGAAGTTCATTATTCTGGGCCTCACCAAAAAGCCTGAAGTCC
AGGGAATTATCTTCCTCTTTTTTCTCATTGTCTATCTTGTGGCTTTTCTCGGCAACATGCTC
ATCATCATTGCCAAAATCTATAACAACACCTTGATACGCCCATGTATGTTTTCTTCTGAC
ACTGGCTGTTGTGGACATCATCTGCACAACAAGCATCATACCGAAGATGCTGGGGACCAT
GCTAACATCAGAAAATACCATTTTCATATGCAGGCTGCATGTCCCAGCTCTTCTTGTTCACA
TGGTCTCTGGGAGCTGAGATGGTTCTCTTACCACCATGGCCTATGACCGCTATGTGGCCA
TTTGTTCCTCTTTCATTACAGTACTGTTATGAACCACCATATGTGTGTAGCCTTGCTCAGC
25 ATGGTCATGGCTATTGCAGTCACCAATTCCTGGGTGCACACAGCTCTTATCATGAGGTTGA
CTTTCTGTGGGCCAAACACCATTGACCACTTCTTCTGTGAGATACCCCATGCTGGCTTTG
TCCTGTAGCCCTGTAAGAATCAATGAGGTGATGGTGTATGTTGCTGATATTACCCTGGCCA
TAGGGGACTTTATTCTTACCTGCATCTCCTATGGTGTATCATTGTTGCTATTCTCCGTATC
CGCACAGTAGAAGGCAAGAGGAAGGCCTTCTCAACATGCTCATCTCATCTCAGCTGAGTGTG
ACCCTTTACTATTCTCCTGTAATCTACACCTATATCCGCCCTGCTCCAGCTATACATTTGA
30 AAGAGACAAGGTGGTAGCTGCACTCTATACTCTTGTGACTCCACATTAAACCCGATGGTG
TACAGCTTCCAGAATAGGGAGATGCAGGCAGGAATTAGGAAGGTGTTTGCATTTCTGAAA
CACTAG (SEQ ID NO: 230)

- AOLFR125 sequences:**
35 MTNQTMMEFLVRFTEFNWVLLRLHALLFSLIYLTAVLMNLVILLMILDHRLHMAFYFFLRH
LSFLDLCLISATVPKLSILNSVASTDSISFLGCVLQLFLVLLAGSEIGILTAMSYDRYAAICCPHLC
EAVMSRGLCVQLMALSWLNRGALGLLYTAGTFSNLFYGSDELHQFFCDVPALLKLTCSEHAI
ISVSVAIGVCYAFSCLVCIVVSYYIFSAVLRISQRQRQSKAFSNCVPHLIVVTFLVTGAVAYL
KPGSDAPSILDLLVSFYSVAPPTLNPVYCLKNKDIKSALSKVLWNVRSSGVMKDD (SEQ ID
40 NO: 231)

- ATGACCAATCAGACACAGATGATGGAATTCCTTGCTGTGAGATTTACTGAGAATTGGGTGC
TCCTGAGGCTGCATGCTTTGCTCTTCTCACTGATCTACCTCACGGCTGTGCTGATGAATTTA
GTCATCATTCTCCTCATGATTCTGGACCATCGTCTCCACATGGCAATGTACTTTTTCTCCTCCG
45 ACATTTGTCTTCTTAGACCTGTGTCTCATTTCTGCCACAGTCCCCAAATCCATCCTCAACT
CTGTGCGCTCCACTGACTCCATCTCCTTCTGGGGTGTGTGTTGCAGCTCTTCTTGGTGGTA
CTGCTGGCTGGATCAGAGATTGGCATCCTTACTGCCATGTCCTATGACCGCTATGCTGCCA
TCTGCTGCCCCCTACACTGTGAGGCTGTGATGAGCAGAGGGCTCTGTGTCCAGTTGATGGC
TCTGTCTGGCTCAACAGAGGGGCTTGGGACTCTGTACACAGCTGGAACATTCTCTCTG
50 AATTTTTATGGCTCTGATGAGCTACATCAGTTCTTCTGCGATGTCCCTGCCCTACTAAAGCT
CACTTGTTCTAAAGAACATGCCATCATTAGTGTGAGTGTGGCCATTGGGGTCTGTTATGCA
TTTTCATGTTTAGTTTGCATTGTAGTTTCTATGTGTACATTTTCTGCTGTGTTAAGGAT
ATCACAGAGACAGAGACAATCCAAAGCCTTTTCCAACCTGTGTGCCTCACCTCATTGTTGTC
ACTGTGTTTCTTGTAAACAGGTGCTGTTGCTTATTTAAAGCCAGGGTCTGATGCACCTTCTAT
55 TCTAGACTTGCTGGTGTCTGTGTTCTATTCTGTCGACCTCCAACCTGAACCCTGTTATCT

ACTGTCTGAAGACAAGGACATTAAATCCGCTCTGAGTAAAGTCCTGTGGAATGTTAGAA
GCAGTGGGGTAATGAAAGATGACTAA (SEQ ID NO: 232)

AOLFR126 sequences:

5 MFLYLCFIFQRTCSEEMEEENATLLTEFVLTGFLHQPDCKIPLFLAFLVIYLITIMGNLGLIVLIW
KDPHLHIPMYLFLGSLAFVDASLSSTVTPKMLINFLAKSKMISLSECMVQFFSLVTTVTTECFLL
ATMAYDRYVAICKALLYPVIMTNELCIQLLVLSFIGGLLHALIHEAFSFRLTFCNSNIIQHFYCDII
PLLKISCTDSSINFLMVFIAGSVQVFTIGTILISYTHILFTILEKKSIIKIRKAVSTCGAHLISVSLY
YGPLTFKYLGASAPQADDQDMMESLFYTVIVPLLNPMIYSLRNKQVIASFTKMFKSNV (SEQ ID
10 NO: 233)

ATGTTCCCTTTACCTTTGCTTCATTTTTTCAGAGGACATGCAGTGAGGAGATGGAAGAGGAAA
ATGCAACATTGCTGACAGAGTTTGTCTCACAGGATTTTTACATCAACCTGACTGTAAAAT
ACCGCTCTTCCCTGGCATTCTTGGTAATATATCTCATCACCATCATGGGGAATCTTGGTCTAA
15 TTGTTCTCATCTGGAAAGACCTCACCTTCATATCCCAATGTACTTATTCCTTGGGAGTTTA
GCCTTTGTGGATGCTTCGTTATCATCCACAGTGACTCCGAAGATGCTGATCAACTTCTTAG
CTAAGAGTAAGATGATATCTCTCTGAATGCATGGTACAATTTTTTCCCTTGTAACCACT
GTAACCACAGAATGTTTTCTTGGCAACAATGGCATATGATCGCTATGTAGCCATTTGCA
AAGCTTTACTTTATCCAGTCATTATGACCAATGAACTATGCATTGAGCTATTAGTCTTGTA
20 TTTATAGGTGGCCTTCTTCATGCTTTAATCCATGAAGCTTTTTTTCATTGAGATTAACTTCTG
TAATTCCAACATAATACAACACTTTTACTGTGACATTATCCCATTTGTTAAAGATTTTCTGTGTA
CTGATTCCTCTATTAACCTTTCTAATGGTTTTATTTTCGCAGGTTCCTGTTCAAGTTTTTACCA
TTGGAACCTATTCTTATATCTTATACAATTATCCTCTTTACAATCTTAGAAAAGAAGTCTATC
AAAGGGATACGAAAAGCTGTCTCCACCTGTGGGGCTCATCTCTTATCTGTATCTTTATACT
25 ATGGCCCCCTCACCTTCAAATATCTGGGCTCTGCATCTCCGCAAGCAGATGACCAAGATAT
GATGGAGTCTCTATTTTACACTGTCTAGTTTCCTTTATTAATCCCATGATCTACAGCCTGA
GAAACAAGCAAGTAATAGCTTCATTACAAAAATGTTCAAAGCAATGTTTAG (SEQ ID
NO: 234)

30 **AOLFR127 sequences:**

MSNEDMEQDNTLLTEFVLTGLTYQPEWKMPFLVFLVIYLITIVWNLGLIALIWNDPQLHIPM
YFFLGSLAFVDAWISSTVTPKMLVNFLAKNRMISLSECMIQFFSFAGGTTTECFLLATMAYDRY
VAICKPLLYPVIMNNSLCIRLLAFSFLGGFLHALIHEVLIFRLTFCNSNIIHHFYCDIPLFMISCTD
PSINFLMVFILSGSIQVFTIVTVLNSYTFALFTILKKKSVRGVRKAFSTCGAHLISVSLYGGPLIF
35 MYLRPASQADDQDMDSVFYTHIPLNPIYSLRNKQVIDSFTKMVKRNV (SEQ ID NO: 235)

ATGTCGAATGAGGACATGGAACAGGATAATACAACATTGCTGACAGAGTTTGTCTCACA
GGACTTACATATCAGCCAGAGTGGAATAATGCCCTGTTCTTGGTGTTCTGATCTATC
TCATCACTATTGTGTGGAACCTTGGTCTGATTGCTTTATCTGGAATGACCCACAACCTCAC
40 ATCCCCATGTACTTTTTTCTTGGGAGTTTAGCCTTTGTTGATGCTTGGATATCTTCCACAGT
AACTCCCAAAATGTTGGTTAATTTCTTGGCCAAAAACAGGATGATATCTCTGTCTGAATGC
ATGATTCAATTTTTTCTTTGCATTTGGTGGAACCTACAGAATGTTTTCTCTTGGCAACAAT
GGCATATGATCGCTATGTAGCCATATGCAACCTTTACTATATCCAGTGATTATGAACAAT
TCACTATGCATACGGCTGTTAGCCTTCTCATTTTTAGGTGGCTTCCTCCATGCCTTAATTCA
45 TGAAGTCCTTATATTGAGATTAACCTTCTGCAATTCTAACATAATACATCATTTTTTACTGTG
ATATTATACCACTGTTTATGATTTCTGTACTGACCCTTCTATTAATTTTCTAATGGTTTTTA
TTTTGTCTGGCTCAATTCAGGTATTCACCATTTGTGACAGTTCTTAATTTCTTACACATTTGCT
CTTTTACAAATCCTAAAAAAGAAGTCTGTTAGAGGCGTAAGGAAAGCCTTTTCCACCTGTG
GAGCCCATCTCTTATCTGTCTCTTTATATTATGGCCCACTTATCTTCATGATTTTGCGCCCT
50 GCATCTCCACAAGCAGATGACCAAGATATGATAGACTCTGTCTTTTATACATCATCAATTC
CTTTGCTAAATCCCATTATCTACAGTCTGAGAAATAAACAAGTAATAGATTTCATTCACAAA
AATGGTAAAAAGAAATGTTTAG (SEQ ID NO: 236)

AOLFR128 sequences:

55 METQNLTVVTEFILLGLTQSQDAQLLVFLVLIFYLIILPGNFLIIFTIKSDPGLTAPLYFFLGNLA
LLDASYSFIVVPRMLVDFLSEKKVISYRSCITQLFFLHFLGAGEMFLLVVMFAFDRIACRPLHY

STIMNPRACYALSLVLWLGGFIHSIVQVALILHLPFCGPNQLDNFFCDVPQVIKLACTNTFVVEL
LMVSNGLLSLLCFLGLLASAYAVILCRIREHSSEKSKAISTCTTHIIIFLMFGPAIFIYTCPFQAFP
ADKVVSLFHTVIFPLMNPVIYTLRNQEVKASMRKLLSQHMF (SEQ ID NO: 237)

- 5 ATGGAAACACAGAACCTCACAGTGGTGACAGAAATTCATTCTTCTTGGTCTGACCCAGTCTC
AAGATGCTCAACTTCTGGTCTTTGTGCTAGTCTTAATTTTCTACCTTATCATCCTCCCTGGA
AATTTCTCATCATTTTACCATAAAGTCAGACCCTGGGCTCACAGCCCCCTCTATTTCTT
TCTGGGCAACTTGGCCTTACTGGATGCATCCTACTCCTTCATTGTGGTTCACAGGATGTTG
TGGACTTCTCTCTGAGAAGAAGGTAATCTCCTATAGAAGCTGCATCACTCAGCTCTTTT
10 TCTTGCATTTTCTTGGAGCGGGAGAGATGTTCTCCTCGTTGTGATGGCCTTTGACCGCTAC
ATCGCCATCTGCCGGCCTTTACACTATTCAACCATCATGAACCCTAGAGCCTGCTATGCAT
TATCGTTGGTTCTGTGGCTTGGGGCTTTATCCATTCCATTGTACAAGTAGCCCTTATCCTG
CACTTGCCTTTCTGTGGCCCAAACCAGCTCGATAACTTCTTCTGTGATGTTCCACAGGTCAT
CAAGCTGGCCTGCACCAATACCTTTGTGGTGGAGCTTCTGATGGTCTCCAACAGTGGCCTG
15 CTCAGCCTCCTGTGCTTCTGGGCCTTCTGGCCTCCTATGCAGTCATCCTCTGTCTGATAAG
GGAGCACTCCTCTGAAGGAAAGAGCAAGGCTATTTCCACATGCACCACCCATATTATCATT
ATATTTCTCATGTTTGGACCTGCTATTTTCTATCTACACTTGGCCCTTCCAGGCTTCCAGC
TGACAAGGTAGTTTCTTTTCCATACTGTCATCTTTCTTTGATGAACCCTGTTATTTATA
CGCTTCGCAACCAGGAGGTGAAAGCTTCCATGAGGAAGTTGTTAAGTCAACATATGTTTGT
20 CTGA (SEQ ID NO: 238)

AOLFR129 sequences:

- MALYFSLILHGMSDLFFLSTGHPRASCRMEAMKLLNQSQVSEFILLGLTSSQDVEFLFALFSVI
YVVTVLGNLLIIVTVFNTPNLNTPMYFLLGNLSFVDMTLASFATPKVILNLLKKQKVISFAGCFT
25 QIFLLHLLGGVEMVLLVSMADFDRYVAICKPLHYMTIMNKKVCVLLVVTSWLLGLLHSGFQIPF
AVNLPFCGPNVDSIFCDLPLVTKLACIDIYFVQVVIVANSGLSLSCFILLISYSLILITIKNHSPT
GQSKARSTLTAHITVILFFGPCIFIYIWPFGNHSVDKFLAVFYTHITPILNPIIYTLRNKEMKISMK
KLWRAFVNSREDT (SEQ ID NO: 239)

- 30 ATGGCTCTTTATTTTCACTCATACTCCATGGTATGAGTGATCTTTTCTTCTCTCTACAGG
TCATCCAAGAGCGAGCTGTAGGATGGAGGCCATGAACTATTAATCAATCTCAAGTGTC
AGAATTCATTTTGTGGGACTGACCAGCTCCCAGGATGTAGAGTTTCTTCTCTTGGCCCTCT
TCTCGTTATCTATGTGGTCACAGTTTGGGTAACTTCTTATTATAGTCAGTGTTTAAC
ACCCCTAACCTGAATACTCCCATGTATTTTCTCCTTGGTAATCTCTCTTTGTAGATATGAC
35 CCTTGCTTCTTTGCCACCCCTAAGGTGATTCTGAACCTGTTAAAAAGCAGAAGGTAATT
TCTTTTGTGGGTGCTTCACTCAGATATTTCTCCTTCACTTACTGGGTGGGGTTGAAATGGT
ACTGTTGGTCTCCATGGCTTTTACAGATATGTGGCCATTTGTAAGCCCTACACTACATG
ACCATCATGAACAAGAAGGTATGTGTTTTGCTTGTAGTGACCTCATGGCTCTTGGGTCTCC
TTCATCTAGGGTTTCAGATACCATTTGCTGTGAACCTTGCCCTTTTGTGGTCCCAATGTGGTA
40 GACAGCATTTTTTGTGACCTCCCTTTGGTTACTAAGCTTGCCTGTATAGACATATATTTGT
ACAGGTAGTCATTGTTGCCAACAGTGGCATAATCTCCCTGAGCTGTTTCAATATTTTGTCTA
TCTCTACAGTCTGATCCTCATAACCATTAAGAACCACTCTCCTACTGGGCAATCTAAAGC
CCGTCCACTTTGACTGCTCACATCACAGTGGTGATTCTTCTTTTGGCCACAGTGTTTTA
TCTACATTTGGCCCTTCGGCAACCACTCTGTAGATAAGTTCCCTGTGTGTTTTATACCATC
45 ATCACTCCTATCTTGAATCCAATTATCTATACTCTGAGAAACAAAGAAATGAAGATATCCA
TGAAAAAACTCTGGAGAGCTTTTGTGAATTCTAGAGAAGATACTTAG (SEQ ID NO: 240)

AOLFR131 sequences:

- MASTSNVTELIPTGLFQDPAVQSVCFVFLPVYLATVVGNGLIVLTVSISKSLDSPMYFFLSCLS
50 LVEISYSTIAPKFIDLLAKIKTISLEGCLTQIFFHFHFGVAEILLIVVMAYDCYVAICKPLHYMNI
ISRQLCHLLVAGSWLGGFCHSIQILVIIQLPFCGPNVIDHYFCDLQPLFKLACTDTFMEGVIVLA
NSGLFSVFSFLILVSSYIVILVNLNRHSAEGRHKALSTCASHITVILFFGPAIFLYMRPSSTFTED
KLAVAFYTVITPMLNPIIYTLRNAEVKIAIRRLWSKKENPGRE (SEQ ID NO: 241)

- 55 ATGGCCAGTACAAGTAATGTGACTGAGTTGATTTTCACTGGCCTTTTCCAGGATCCAGCTG
TGCAGAGTGTATGCTTTGTGGTGTCTCCCCGTGTACCTTGCCACGGTGGTGGGCAATGG

CCTCATCGTTCTGACGGTCAGTATCAGCAAGAGTCTGGATTCTCCCATGTACTTCTTCCTTA
GCTGCCTGTCCTTGGTGGAGATCAGTTATTCCTCCACTATCGCCCCATAAATTCATCATAGAC
TTACTTGCCAAAGATTA AAAACCATCTCTCTGGAAGGCTGTCTGACTCAGATATTCTTCTTCCA
CTTCTTTGGGGTTGCTGAGATCCCTTTTGATTGTGGTGATGGCCTATGATTGCTACGTGGCC
5 ATTTGCAAGCCTCTTCATTATATGAACATTATCAGTCGTCAACTGTGTACCTTCTGGTGGC
TGGTTCCTGGCTGGGGGGCTTTTGTCACTCCATAATTCAGATTCTCGTTATCATCCAATTGC
CCTTCTGTGGTCCCAATGTGATTGACCACTATTTCTGTGACCTCCAGCCTTTATTCAAGCTT
GCCTGCACTGACACCTTCATGGAGGGGGTTATTGTGTTGGCCAACAGTGGATTATTCTCTG
TCTTCTCCTTCCTCATCTTGGTGTCTCTTATATTGTCACTTCTGGTCAACTTGAGGAACCAT
10 TCTGCAGAGGGGAGGCACAAAAGCCCTCCACCTGTGCTTCTCACATCACAGTGGTCATCT
TGTTTTTGGACCTGCTATCTTCTCTACATGCGACCTTCTTCCACTTTCACTGAAGATAAA
CTTGTGGCTGTATTCTACACGGTCATCACCCCATGCTGAACCCCATCATTTACACACTCAG
GAATGCAGAGGTGAAAATCGCCATAAGAAGATTGTGGAGCAAAAAGGAGAATCCAGGGA
GGGAGTGA (SEQ ID NO: 242)

15

AOLFR132 sequences:

MVATNNVTEIIFVGF SQNWSEQRVISVMFLMYTAVVLGNGLIVVTILASKVLTSPMYFFLSYL
SFVEICYCSVMAPKLFDSFIKRVISLKGCLTQMFSLHFFGGTEAFLLMVMAYDRYVAICKPL
HYMAIMNQRMCGLLVRIAWGGGGLLSVGGTFLIFQLPFCGPNIMDHVFCDVHPVLELACADT
20 FFISLLITNGGSISVVSFFVLMASYLILHFLRSHNLEGQHKALSTCASHVTVDLFFIPCSLVYIR
PCVTLPADKIVAVFYTVVTPLLNPVIYSFRNAEVKNAMRRFIGGKVI (SEQ ID NO: 243)

ATGGTTGCTACAAACAATGTGACTGAAATAATTTTCGTGGGATTTTCCCAGAATTGGAGTG
AGCAGAGGGTCATTTCTGTGATGTTTCTCCTCATGTACACAGCTGTTGTGCTGGGCAATGG
25 CCTCATTGTGGTGACCATCCTGGCCAGCAAAGTGCTCACCTCCCCATGTATTTCTTTCTCA
GCTACTTATCCTTTGTGGAGATCTGCTACTGTTCTGTGATGGCCCCAAGCTTATCTTTGAC
TCCTTTTCAAGAGGAAAGTCATTTCTCTCAAGGGCTGCCTCACACAGATGTTTTCCCTCC
ATTTCTTTGGTGGCACTGAGGCCCTTTCTCCTGATGGTGATGGCCTATGACCGCTATGTGGC
CATCTGCAAGCCCTTGCACTACATGGCCATCATGAACCAGCGAATGTGTGGTCTCCTCGTG
30 AGGATAGCATGGGGCGGGGGCCTGCTGCATTCTGTTGGGCAAACCTTCCTGATTTTCCAGC
TCCCGTTCTGTGGCCCCAACATCATGGACCACTACTTCTGTGATGTCCACCCAGTGCTGGA
GCTGGCCTGCGCAGACACCTTCTTCATTAGCCTGCTGATCATACCAATGGCGGCTCCATC
TCCGTAGTCAGTTTCTTCGTGCTGATGGCTTCTACCTGATCATCCTGCACTTCTGAGAAG
CCACAACCTTGAGAGGGGAGCACAAGGCCCTCTCCACCTGTGCCTCTCATGTACAGTTGTC
35 GACCTGTTCTTCATACCTTGCTCCTTGGTCTATATTAGGCCCTGTGTACCCCTCCCTGCAGA
CAAGATAGTTGCTGTATTTTATACAGTGGTCACACCTCTCTTAAACCTGTGATTTACTCCT
TCAGGAATGCTGAAGTGAAAATGCCATGAGGAGATTTATTGGGGGAAAAGTAATTTGA
(SEQ ID NO: 244)

40

AOLFR133 sequences:

MTEFIFLVLSPNQEVQRVCFVIFLFLYTAIVLGNFLIVLTVMTSRSLGSPMYFFLSYLSFMEICYS
SATAPKLISDLLAERKVISWWGCMAQLFFLHFFGGTEIFLLTVMAYDHYVAICKPLSYTTIMN
WQVCTVLVGLAVVGGFMHSFAQILLIFHLLFCGPNVINHYFCDLVPLKLACSDTFILGLLIVAN
GGTLSVISFGVLLASYMVILLHLRTWSSEGWCKALSTCGSHFAVVILFFGPCVFNSLRPSTTLPI
45 DKMVAVFYTVITAILNPVIYSLRNAEMRKAMKRLWIRTLRLNEK (SEQ ID NO: 245)

ATGACTGAATTCATTTTTCTGGTACTTTCTCCCAACCAGGAGGTGCAGAGGGTTTGCTTTG
TGATATTTCTGTTCTTGACACAGCAATTGTGCTGGGGAATTTCTCATTGTGCTCACTGTC
ATGACCAGCAGAAGCCTTGGTTCCCCATGTACTTCTCCTCAGCTACCTCTCCTTCATGGA
50 GATCTGCTACTCCTCCGCTACAGCCCCCAAACCTCATCTCAGATCTGCTGGCTGAAAGGAAA
GTCATATCTTGGTGGGGCTGCATGGCACAGCTTTTCTTCTTGCACTTCTTTGGTGGCACTGA
GATTTTCTGCTCACTGTGATGGCCTATGACCACTATGTGGCCATCTGCAAGCCCCCTCAGC
TACACCACCATCATGAACTGGCAGGTGTGTA CTGCTTGTAGGAATAGCATGGGTGGGA
GGCTTCATGCATTCTTTGCACAAATCCTTCTCATCTTCCACCTGCTCTTCTGTGGCCCCAA
55 TGTGATCAATCACTATTTCTGTGACCTAGTTCCCTTCTCAAACCTGCCTGCTCTGACACCT
TCCTCATTGGTCTGCTGATTGTTGCCAATGGAGGCACCCTGTCTGTGATCAGTTTTGGGGT

CCTCTTAGCATCCTATATGGTCATCTTGCTCCATCTGAGAACCTGGAGCTCTGAAGGGTGG
 TGCAAAGCCCTCTCCACCTGTGGGTCCCATTTCGCTGTGGTTATCTTGTTCTTTGGGCCCTG
 CGTCTTCAACTCTCTGAGGCCTTCTACCACTCTGCCCATAGACAAGATGGTGGCTGTGTTCT
 ACACAGTGATAACCGCGATCCTGAACCCTGTCATCTACTCTCTGAGAAATGCTGAAATGAG
 5 GAAGGCCATGAAGAGGCTGTGGATTAGGACATTGAGACTAAATGAGAAATAG (SEQ ID
 NO: 246)

AOLFR134 sequences:

MTTILEVDNHTVTTRFILLGFPTPAFQLLFFSIFLATYLLTLENLLILAIHSDGQLHKPMYFFL
 10 SHLSFLEMWYVTVISPKMLVDFLSHDKSISFNGCMTQLYFFVTFVCTEYILLAIMAFDRYVAIC
 NPLRYPVIMTNQLCGTLAGGCWFCGLMTAMIKMVFIQLHYCGMPQINHYFCDISPLNVSCE
 DASQAEMVDFFLALMVIAIPLCVVVASYAAILATILRIPSAQGRQKAFSTCASHLTVVILFYSMT
 LFTYARPKLMYAYNSNKVSVLYTVIVPLLNPIIYCLRNHEVKAALRKTIHCRGSGPQNGAFS
 S (SEQ ID NO: 247)

15 ATGACCACCATAATTCTGGAAGTAGATAATCATACAGTGACAACACGTTTCATTCTTCTGG
 GGTTTCCAACACGACCAGCCTTCCAGCTTCTCTTTTCTCCATTTTCTGGCAACCTATCTG
 CTGACACTGCTGGAGAATCTTCTTATCATCTTAGCTATCCACAGTGATGGGCAGCTGCATA
 AGCCCATGTACTTCTTCTTGAGCCACCTCTCCTTCTGGAGATGTGGTATGTCACAGTCATC
 20 AGCCCCAAGATGCTTGTGACTTCCTCAGTCATGACAAGAGTATTTCTTCAATGGCTGCA
 TGACTIONACTTTACTTTTTTGTGACCTTTGTCTGCACTGAGTACATCCTTCTTGCTATCATG
 GCCTTTGACCGCTATGTAGCCATTGTAAATCCACTACGCTACCCAGTCATCATGACCAACC
 AGCTCTGTGGCACACTGGCTGGAGGATGCTGGTTCTGTGGACTCATGACTGCCATGATTAA
 GATGGTTTTTATAGCAAACTTCACTACTGTGGCATGCCTCAGATCAATCACTACTTTTGTG
 25 ATATCTCTCCACTCCTTAACGTCTCCTGTGAGGATGCCTCACAGGCTGAGATGGTGGACTT
 CTTCTTGGCCCTCATGGTCATTGCTATTCTCTTTGTGTTGTGGTGGCATCCTACGCTGCTA
 TCCTTGCCACCATCCTCAGGATCCCTTCTGCTCAGGGCCGCCAAAAGGCATTCTCCACCTG
 TGCCTCCACCTGACCGTCGTAATTCCTTCTATTCCATGACACTTTTCACCTATGCCCGTC
 CCAAACCTCATGTATGCCTACAATTCCAACAAAGTGGTATCTGTTCTCTACACTGTCATTGTT
 30 CCACTCCTCAACCCCATCATTTACTGTCTGAGGAACCATGAAGTAAAGGCAGCCCTCAGAA
 AGACCATAATTGCAGAGGAAGTGGGCCCCAGGGAATGGGGCTTTCAGTAGTTAA (SEQ
 ID NO: 248)

AOLFR135 sequences:

35 MIFPSHDSQAFTSVDMENVGNCTILTEFILLGFSADSQWQPILFGVFLMLYLITLSGNMTLVILRT
 DSHLHTPMYFFIGNLSFLDFWYTSVYTPKILASCVSEDKRISLAGCGAQLFFSCVVAYTECYLL
 AAMAYDRHAAICNPLLYSGTMTALCTGLVAGSYGGFLNAIAHTANTFRLHFCGKNIDHFFC
 DAPPLVKMSCTNTRVYEKVLGTVGFTVLSSILAILISYVNILLAILRIHSASGRHKAFSTCASHL
 40 ISVMLFYGSLLFMYSRPSTYSLERDKVAALFYTVINPLNPLIYSLRNKDIKEAFRKATQTIQPT
 T (SEQ ID NO: 249)

ATGATTTTCCCTTCTCATGATAGTCAGGCTTTACCTCCGTGGACATGGAAGTGGGAAATT
 GCACCATCCTGACTGAATTCATCTTGTGGGTTTCTCAGCAGATTCCCAGTGGCAGCCGAT
 TCTATTTGGAGTGTTTCTGATGCTCTATTTGATAACCTTGTGAGGAAACATGACCTTGGTTA
 45 TCTTAATCCGAACCTGATTCCCACTTGATACACCTATGTAATTTTTCATTGGCAATCTGTCT
 TTTTGGATTTCTGGTATACCTCTGTGTATACCCCAAAATCCTGGCCAGTTGTGTCTCAGA
 AGATAAGCGCATTTCTTGGCTGGATGTGGGGCTCAGCTGTTTTTCTGTGTTGTAGCCT
 AACTGAATGCTATCTCCTGGCAGCCATGGCATATGACCGCCATGCAGCAATTTGTAACCC
 ATTGCTTATTACAGGTACCATGTCCACCGCCCTCTGACTGGGCTTGTGCTGGCTCCTACA
 50 TAGGAGGATTTTGAATGCCATAGCCCATACTGCCAATACATTCCGCTGCATTTTGTGG
 TAAAAATATCATTGACCACTTTTCTGTGATGCACCACCATTTGGTAAAAATGTCCTGTACA
 AACACCAGGGTCTACGAAAAAGTCTGCTTGGTGTGGTGGGCTTCACAGTACTCTCCAGCA
 TTCTTGCTATCCTGATTTCTATGTCAACATCCTCCTGGCTATCCTGAGAATCCACTCAGCT
 TCAGGAAGACACAAGGCATTCTCCACCTGTGCTTCCACCTCATCTCAGTCATGCTCTTCTA
 55 TGGATCATTGTTGTTTATGTATTCAAGGCCTAGTTCCACCTACTCCCTAGAGAGGGACAAA
 GTAGCTGCTCTGTTCTACACCGTGATCAACCCACTGCTCAACCCTCTCATCTATAGCCTGAG

AAACAAAGATATCAAAGAGGCCTTCAGGAAAGCAACACAGACTATACAACCACAAACATG
A (SEQ ID NO: 250)

AOLFR136 sequences:

5 MTMENYSMAAQFVLDGLTQQAELQLPLFLLFLGIYVVTVVGNLGMILLIAVSPLLHTPMYYFL
SSLSFVDFCYSSVITPKMLVNFLGKKNTILYSECMVQLFFVVFVVAEGYLLTAMAYDRYVAIC
SPLLYNAIMSSWVCSLLVLAFFLGFSLALHTSMMKLSFCKSHIINHIFCDVPLLNLSCSNT
HLNELLFLIAGFNTLVPTLAVAVSYAFILYSILHIRSSEGRSKAFGTCSHLMVAVIFFGSITFMY
FKPPSSNSLDQEKVSSVFYTTVIPMLNPLIYSLRNKDVKKALRKVLVGK (SEQ ID NO: 251)

10 ATGACCATGGAAAATTATTCTATGGCAGCTCAGTTTGTCTTAGATGGTTTAACACAGCAAG
CAGAGCTCCAGCTGCCCCCTCTCCTCCTGTTCTGGAATCTATGTGGTCACAGTAGTGGG
CAACCTGGGCATGATTCTCCTGATTGCAGTCAGCCCTCTACTTCACACCCCCATGTACTATT
TCCTCAGCAGCTTGTCTTCGTGATTTCTGCTATTCTCTGTCTACTCCCAAAATGCTG
15 GTGAACTTCCTAGGAAAGAAGAATAACAATCCTTTACTCTGAGTGCATGGTCCAGCTCTTTT
TCTTTGTGGTCTTTGTGGTGGCTGAGGGTTACCTCCTGACTGCCATGGCATATGATCGCTA
TGTTGCCATCTGTAGCCCACTGCTTTATAATGCGATCATGTCCTCATGGGTCTGCTCACTGC
TAGTGCTGGCTGCCCTTCTTCTTGGGCTTTCTCTGCTTGAATCATAAGTGCCATGATG
AAACTGTCCTTTTGCAAATCCCACATTATCAACCATTACTTCTGTGATGTTCTTCCCCTCCT
20 CAATCTCTCCTGCTCCAACACACACCTCAATGAGCTTCTACTTTTTATCATTGCGGGGTTTA
ACACCTTGGTGCCCACTAGCTGTGCTGTCTCCTATGCCTTCATCCTCTACAGCATCCTT
CACATCCGCTCCTCAGAGGGCCGGTCCAAAGCTTTTGGAACATGCAGCTCTCATCTCATGG
CTGTGGTGATCTTCTTTGGGTCCATTACCTTCATGTATTTCAAGCCCCCTTCAAGTAACTCC
CTGGACCAGGAGAAGGTGTCCTCTGTGTTCTACACCAAGGTGATCCCCATGCTGAACCTT
25 TAATATACAGTCTGAGGAATAAGGATGTGAAGAAAGCATTAAAGGAAGGTCTTAGTAGGAA
AATGA (SEQ ID NO: 252)

AOLFR137 sequences:

30 MSPENQSSVSEFLLGLPIRPEQQAFFALFLGMYLTTVLGNLLIMLLIQLDSHLHTPMYFFLSH
LALTDISFSSVTVPKMLNMNMQTHLAVFYKGCISQTYFFFFADLDSFLITSMAYDRYVAICHPL
HYATIMTQSQCVMLVAGSWVIACACALLHTLLLAQLSFCADHIIPHYFCDLGALLKLSCSDTSL
NQLAIFTAALTAIMLPFLCILVSYGHIGVTILQPSTKGICKALSTCGSHLSVVTIYYRTIIGLYFLP
PSSNTNDKNILASVIYTAVTPMLNPFYSLRNKDIDKALRKLLSRGAVAHACNLSTLGG (SEQ
ID NO: 253)

35 ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCTCCTCCTGCGGCCTCCCCATCCGGC
CAGAGCAGCAGGCGGTGTTCTTCGCCCTGTTCTGCGGCATGTACCTGACCACGGTGCTGGG
GAACCTGCTCATCATGCTGCTCATCAGTCACTACTTACACCTTCACACCCCCATGTACTTCT
TCCTTAGCCACTTGCCCTCACTGACATCTCCTTTTCATCTGTCACTGTCCCTAAGATGCTG
40 ATGAACATGCAGACTCAGCACCTAGCCGTCTTTTACAAGGGATGCATTTTACAGACATATT
TTTTCATATTTTTTGTGACTTAGACAGTTTCTTATCACTTCAATGGCATATGACAGGTAT
GTGGCCATCTGTATCCTCTACATTATGCCACCATCATGACTCAGAGCCAGTGTGTCATGC
TGGTGGCTGGGTCTGGGTGTCGCTTGTGCGTGTGCTCTTTTGCATACCCTCCTCCTGGCC
CAGCTTTCCTTCTGTGCTGACCACATCATCCCTCACTACTTCTGTGACCTTGGTGCCCTGCT
45 CAAGTTGTCTGCTCAGACACCTCCCTCAATCAGTTAGCAATCTTTACAGCAGCATTGACA
GCCATTATGCTTCCATTCTGTGATCCTGGTTTCTTATGGTCACATTGGGGTCACCATCCT
CCAGATTCCCTCTACCAAGGGCATATGCAAAGCCTTGTCCACTTGTGGATCCCACCTCTCA
GTGGTGACTATCTATTATCGGACAATTATTGGTCTCTATTTTCTTCCCCCATCCAGCAACAC
CAATGACAAGAACATAATTGCTTCAGTGATATACACAGCAGTCACTCCCATGTTGAACCCA
50 TTCATTACAGTCTGAGAAATAAAGACATTAAGGGAGCCCTAAGAAAACCTCTTGAGTAGG
TCAGGCGCAGTGGCTCATGCCTGTAATCTCAGCACTTTGGGAGGCTGA (SEQ ID NO: 254)

AOLFR138 sequences:

55 MLNFTDVTEFILLGLTSRREWQVLFFIVFLVYIITVVGNIGMMLLIKVSPQLNSPMYFFLSHLS
FVDVWFSSNVTPKMLENLFSDDKKTISYADCLAQCFIFIALVHVEIFILAAIAFDRTVIGNPLLY
GSKMSRGVCIRLITFPYTYGFLTSLTATLWTYGLYFCGKIEINHIFCADPPLIKMACAGTFVKEY

TMLILAGINFTYSLTVIIISYLFILAILRMRSAEGRQKAFSTCGSHPTAVIIFYGTLIFMYLRRPTE
ESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 255)

5 ATGCTCAATTTACCGATGTGACAGAGTTCATTCTTTGGGGCTAACGAGCCGTCGGGAAT
GGCAAGTTCTCTTCTTCATCGTTTTCTTGTGGTCTACATTATCACCGTGGTGGGCAATATC
GGCATGATGTTGTTAATCAAGGTCAGTCCTCAGCTTAACAGCCCCATGTACTTTTCCCTCA
GTCATTGTGCATTTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAATGTTGGaAAAT
CTGTTATCAGATAAAAAACAATTTCTTATGCTGGCTGTTTAGCACAGTGTTCCTTCTTCAT
10 TGCTCTTGCCATGTGGAAATTTTATTCTTGCTGCGATTGCCTTTGATAGATACACAGTGA
TTGGAAATCCTTTGCTTTATGGCAGCAAAATGTCAAGGGATGTCTGTATTGACTGATTAC
TTTCCCTTACATTTATGGTTTTCTGACGAGTCTGACAGCAACATTATGGACTTATGGCTTGT
ACTTCTGTGGAAAAATTGAGATCAACCATTTCTACTGTGCAGATCCACCTCTCATCAAAAT
GGCCTGTGCCGGGACCTTTGTAAAAGAATATACAATGCTCATACTTGCCGGCATCAACTTC
ACATATTCCCTGACTGTAATTATCATCTCTTACTTATTCATCCTCATTGCCATTCTGCGAAT
15 GCGCTCAGCAGAAGGAAGGCAGAAAGGCCTTTTCCACATGTGGGTCCCATCTGACAGCTGT
CATCATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCACAGAGGAGTCTGTG
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCCATGTTGAATCCCATGA
TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT
GTTAA (SEQ ID NO: 256)

20

AOLFR139 sequences:

MGFPGIHSWQHWLSLPLALLYLLALSANILIIINKEAALHQPMMYYFLGILAMADIGLATTIMP
KILAILWFNAKTISLLECFQAQMYAIHCFVAMESSTFVCMADRYVAICRPLRYPSTITESFVKAN
GFMALRNSLCLISVPLLAQQRHYCSQNQIEHCLCSNLGVTSLSCDDRRINSINQVLLAWTLMGS
25 DLGLIILSYALILYSVLKLNSPAASKALSTCTSHLILFFYTVIIVISITRSTGMRVPLIPVLLNLV
HNVIPPALNPMVYALKNKELRQGLYKVLRLGVKGT (SEQ ID NO: 257)

ATGGGATTCCCTGGCATTACAGTTGGCAGCACTGGCTCTCCCTGCCCTGGCTCTGCTCT
ACCTCTTAGCTCTCAGTGCCAACATCCTTATCCTGATCATCATCAACAAAGAGGCAGCACT
30 GCACCAGCCTATGTACTATTTCTGGGCATCTTGGCTATGGCAGACATAGGCCTGGCTACC
ACCATCATGCCTAAGATTTTGCCATCTTATGGTTCAATGCTAAGACCATCAGTCTCCTGG
AGTGCTTTGCTCAGATGTATGCCATACATGTGCTTTGTGGCCATGGAATCAAGTACCTTTGT
CTGCATGGCTATTGATAGATATGTAGCCATTTGTGACCGCTACGATATCCATCAATCATC
ACTGAATCTTTTGTTTTCAAAGCAAATGGGTTTCATGGCACTGAGAAACAGCCTGTGTCTCA
35 TCTCAGTGCTCTGTTGGCTGCCAGAGGCATTACTGCTCCAGAATCAAATTGAGCACTG
TCTTTGTTCTAACCTTGGAGTCACTAGCCTATCTTGTGATGATCGAAGAATCAATAGCATT
AACCAGGTCTTTTGGCTTGGCACTCATGGGAAGTGACCTGGGTTTGATTATTTTATCAT
ATGCTCTAATACTTTACTCTGTCTGAAAGCTGAAGTCTCCAGAAGCTGCATCCAAGGCCTT
AAGTACCTGCACCTCCACCTCATCTTAATCCTTTTCTTCTACACAGTCATATTGTGATTT
40 CCATTACTCGTAGTACAGGAATGAGAGTTCCCTTATTCCAGTTCTACTTAATGTGCTACA
CAATGTCAATCCCCCTGCCCTGAACCCCATGGTATATGCACTCAAGAACAAGGAAGTCAAG
CAAGGCTTATACAAGGTACTTAGACTGGGAGTGAAGGGCACCTGA (SEQ ID NO: 258)

AOLFR140 sequences:

45 MLTLNKTDLIPASFILNGVPGLEDTQLWISFPFCSMYVAMVGNCGLLYLIHYEDALHKPMYY
FLAMLSFTDLVMCSSTIPKALCIFWFHLKDIGFDECLVQMFFIHTFTGMESGVLMLMALDRYV
AICYPLRYSTILTNPVIAKVGTATFLRGVLLIIPFTFLTKRLPYCRGNLPHTYCDHMSVAKLSCG
NVKVNAIYGLMVALLIGGFDILCITISYTMILRAVVSLSADARQKAFNTCTAHICAIVFSYTPAF
FSFFSHRFGEHIIPPSCHIIIVANIYLLLPPTMNPVYGVKTKQIRDCVIRILSGSKDTKSYSM (SEQ
50 ID NO: 259)

ATGCTAACTGAATAAAACAGACCTAATACCAGCTTCATTTATTCTGAATGGAGTCCAG
GACTGGAAGACACAACTCTGGATTTCTTCCCATCTGCTCTATGTATGTTGTGGCTAT
GGTAGGGAATTGTGGACTCCTCTACCTCACTACTATGAGGATGCCCTGCACAAACCCATG
55 TACTACTTCTGGCCATGCTTTCCTTTACTGACCTTGTTATGTGCTCTAGTACAATCCCTAA
AGCCCTCTGCATCTTCTGGTTTCATCTCAAGGACATTGGATTTGATGAATGCCTGTCCAG

ATGTTCTTCATCCACACCTTCACAGGGATGGAGTCTGGGGTGCTTATGCTTATGGCCCTGG
 ATCGCTATGTGGCCATCTGCTACCCCTTACGCTATTCAACTATCCTCACCAATCCTGTAATT
 GCAAAGGTTGGGACTGCCACCTTCCTGAGAGGGGTATTACTCATTATTCCCTTTACTTTTCT
 CACCAAGCGCCTGCCCTACTGCAGAGGCAATATACTTCCCCATACCTACTGTGACCACATG
 5 TCTGTAGCCAAATTGTCTGTGGTAATGTCAAGGTCAATGCCATCTATGGTCTGATGGTTG
 CCCTCCTGATTGGGGGCTTTGACATACTGTGTATCACCATCTCCTATACCATGATTCTCCGG
 GCAGTGGTCAGCCTCTCCTCAGCAGATGCTCGGCAGAAGGCCTTTAATACCTGCACTGCCC
 ACATTTGTGCCATTGTTTTCTCCTATACTCCAGCTTTCTTCTCCTTCTTTTCCCACCGCTTTG
 10 GGGAACACATAATCCCCCTTCTTGCCACATCATTGTAGCCAATATTTATCTGCTCCTACCA
 CCCACTATGAACCTATTGTCTATGGGGTGAAAACCAAACAGATACGAGACTGTGTCATAA
 GGATCCTTTTCAGGTTCTAAGGATACCAAATCCTACAGCATGTGA (SEQ ID NO: 260)

AOLFR141 sequences:

MSSTLGHNMESPNTDVPDPSVFLLGIPGLEQFHLWLSLPVCGLGTATTGNITLVVATEPVL
 15 HKPVYLFCLMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAQMFFIHAFMMESTVLLAM
 AFDRYVAICHPLRYATILDTIAHIGVAAVVRGSLMLPCPFLIGRLNFCQSHVILHTYCEHMA
 VVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALSAQAVLRLSSHEARSKALGTCGSHVC
 VILISYTPALFSFFTHRFHGHVPHIHILLANVYLLPPALNPVYGVKTKQIRKRVVRVFQSGQ
 GMGIKASE (SEQ ID NO: 261)

20
 ATGTCCAGCACTCTTGCCACAACATGGAATCTCCTAATCACACTGATGTTGACCCTTCTG
 TCTTCTTCCTCCTGGGCATCCCAGGTCTGGAACAATTTCAATTTGTGGCTCTCACTCCCTGTG
 TGTGGCTTAGGCACAGCCACAATTGTGGGCAATATAACTATTCTGGTTGTTGTTGCCACTG
 AACAGTCTTGCACAAGCCTGTGTACCTTTTTCTGTGCATGCTCTCAACCATCGACTTGGCT
 25 GCCTCTGTCTCCACAGTTCCTAAGCTACTGGCTATCTTCTGGTGTGGAGCCGGACATATAT
 CTGCCTCTGCCTGCCTGGCACAGATGTTCTTCATTTCATGCCTTCTGCATGATGGAGTCCACT
 GTGCTACTGGCCATGGCCTTTGATCGCTACGTGGCCATCTGCCACCCACTCCGCTATGCCA
 CAATCCTCACTGACACCATCATTGCCACATAGGGGTGGCAGCTGTAGTGCGAGGCTCCCT
 GCTCATGCTCCCATGTCCCTTCCTTATTGGGCGTTTGAACCTCTGCCAAAGCCATGTGATCC
 30 TACACACGTAAGTGTGAGCACATGGCTGTGGTGAAGCTGGCCTGTGGAGACACCAGGCCTA
 ACCGTGTGTATGGGCTGACAGCTGCACTGTTGGTCATTGGGGTTGACTTGTTTTGCATTGG
 TCTCTCCTATGCCCTAAGTGCACAAGCTGTCTTCCGCTCTCATCCCATGAAGCTCGGTCCA
 AGGCCCTAGGGACCTGTGGTTCCCATGTCTGTGTCATCCTCATCTTATACACCAGCCCTC
 TTCTCCTTTTTTACACACCGCTTTGGCCATCACGTTCCAGTCCATATTACATTCTTTTGGC
 35 CAATGTTTATCTGCTTTTGGCACCTGCTCTTAATCTGTGGTATATGGAGTTAAGACCAAAC
 AGATCCGTAAGAGAGTTGTCAAGGTGTTTCAAAGTGGGCAGGGAATGGGCATCAAGGCAT
 CTGAGTGA (SEQ ID NO: 262)

AOLFR143 sequences:

40 MLGLNGTPFPATLQLTGIPGIQTLTWVALIFCILYMISIVGNLSILTLVFWEPALHQPMMYYFL
 SMLALNDLGVFSFTLPTVISTFCFNYNHVAFNACLVMFFIHTFSFMESGILLAMSLDRFVAICY
 PLRYVTVLTHNRILAMGLILTKSFTTLFPFPFVVKRLPFCKGNVLHHSYCLHPDLMKVACGDI
 HVNNIYGLLVIFTYGMDSFTILLSYALILRAMLVIIISQEQRLKALNTCMSHICAVLAFYVPIAVS
 MIHRFWKSAPPVVHVMMSNVYLFVPPMLNPPIIYSVKTKBIRKILKFFHKSQA (SEQ ID NO:
 45 263)

ATGCTGGGTCTCAATGGCACCCCTTCCAGCCAGCAACACTCCAGCTGACAGGCATTCCTG
 GGATACAAACAGGCCTCACCTGGGTGCGCTGATTTTCTGCATCCTCTACATGATCTCCATT
 GTAGGTAACCTCAGCATTCTCACTCTGGTGTTTTGGGAGCCTGCTCTGCATGACGCCATGT
 50 ACTACTTCTCTCTATGCTCGCTCAATGATGCTGGGAGTGTCCTTTTCTACACTTCCACT
 GTGATTTCTACTTTCTGCTTCAACTCAACACCATGTTGCGTTTAAATGCTTGCTGGTCCAGAT
 GTTCTTCATCCACACTTTCTCCTTCATGGAGTCAGGCATACTGCTGGCCATGAGCTTGGATC
 GCTTTGTGGCTATTTGTTATCCATTACGCTATGTCACTGTGCTCACTCACAACCGTATATTG
 GCTATGGGTCTGGGCATCCTTACCAAGAGTTTCAACACTCTCTCCCTTTCCCTTTTGTGGT
 55 GAAACGACTGCCCTTCTGCAAAGGCAATGTTTTGCATCACTCCTACTGTCTCCATCCAGAT
 CTCATGAAAGTAGCATGTGGAGACATCCATGTTAACAACATTTATGGGCTCTTGGTGATCA

TTTTACCTATGGTATGGACTCAACTTTTCATCCTGCTTTCCTACGCATTGATCCTGAGAGCC
 ATGCTGGTCATCATATCCCAGGAACAGCGGCTCAAGGCACTCAACACCTGCATGTCACACA
 TCTGTGCAGTGTGGCCTTTTATGTGCCATAATTGCTGTCTCCATGATTCACCGCTTCTGG
 AAAAGTGTCTCCACCTGTTGTTTCATGTTCATGATGTCCAATGTCTACCTGTTTGTACCCCAT
 5 GCTCAACCCTATCATCTACAGTGTGAAAACCAAGGAGATCCGCAAAGGGATTCTCAAGTTC
 TTCCATAAATCCCAGGCCTGA (SEQ ID NO: 264)

AOLFR144 sequences:

MGLFNVTHPAFFLLTGIPGLESSHWSLGPCLVMYAVALGGNTVILQAVRVEPSLHEPMMYYFL
 10 SMLSFSDDVAISMATLPTVLRTFCLNARNITFDACLIQMFLIHFFSMMESGILLAMSFDRYVAICD
 PLRYATVLTTEVIAAMGLGAAARSFITLPLFLIKRLPICRSNVLSHSYCLHPDMMRLACADISI
 NSIYGLFVLVSTFGMDLFFIFLSYVILIRSVMATASREERLKALNTCVSHILAVLAFYVPMIGVS
 TVHRFGKHVPCYIHLMSNVYLFVPPVLNPLIYSAKTKAIRRAIFRMFHIIKI (SEQ ID NO: 265)

15 ATGGGGTTGTTCAATGTCACTCACCTGCATTCTTCCTCCTGACTGGTATCCCTGGTCTGGA
 GAGCTCTCACTCCTGGCTGTGAGGGCCCTCTGCGTGATGTATGCTGTGGCCCTTGGGGGA
 AATACAGTGATCCTGCAGGCTGTGCGAGTGAGGCCAGCCTCCATGAGCCCATGTACTACT
 TCCTGTCCATGTTGTCTTCAGTGATGTGGCCATATCCATGGCCACACTGCCCACTGTACTC
 CGAACCTTCTGCCTCAATGCCCCGAACATCACTTTTGATGCCTGTCTAATTCAGATGTTTCT
 20 TATTCACCTTCTTCTCCATGATGGAATCAGGTATTCTGCTGGCCATGAGTTTGACCGCTATG
 TGGCCATTTGTGACCCCTTGCCTATGCAACTGTGCTCACCCTGAAGTCATTGCTGCAAT
 GGGTTTAGGTGCAGCTGCTCGAAGCTTCATCACCTTTTCCCTCTTCCCTTTCTTATTAAGA
 GGCTGCCTATCTGCAGATCCAATGTTCTTCTCACTCCTACTGCCTGCACCCAGACATGATG
 AGGCTTGCCTGTGCTGATATCAGTATCAACAGCATCTATGGACTCTTTGTTCTTGATCCAC
 25 CTTTGGCATGGACCTGTTTTTATCTTCTCCTATGTGCTCATTCTGCGTTCTGTCATGG
 CCACTGCTTCCCGTGAGGAACGCCTCAAAGCTCTCAACACATGTGTGTCACATATCCTGGC
 TGTACTTGCATTTTATGTGCCAATGATTGGGGTCTCCACAGTGCACCGCTTGGGAAGCAT
 GTCCCATGCTACATACATGTCTCATGTCAAATGTGTACCTATTTGTGCTCCTGTGCTCAA
 CCCTCTCATTTATAGCGCCAAGACAAAGGAAATCCGCCGAGCCATTTTCCGCATGTTTCAC
 30 CACATCAAAATATGA (SEQ ID NO: 266)

AOLFR145 sequences:

MSVQYSLSPQFMLLSNITQFSPIFYLTSPGLEGIKHWIFIPFFFMYMYVAISGNCFILIIKTNPRHLH
 TPMYYLLSLALDGLCVSTLPTTMGIFWFNSQSIYFGACQIQMFCIHSFSFMESVLLMMSFD
 35 RFVAICHPLRYSVIITGQQVVRAGLVIFRGPVATIPVLLKAFPYCGSVVLSHSFCLHQEVIQLA
 CTDTTFNLYGLMVVFTVMLDLVLIALSYGLILHTVAGLASQEEQRRAFQTCTAHLCAVLVLF
 FVPMMLGLSLVHRFGKHAPPAIHLMLANVYLFVPPMLNPIIYSIKTKEIHRAIKLLGLKKASK
 (SEQ ID NO: 267)

40 ATGTCAGTCCAATATTCGCTCAGTCCTCAATTCATGCTGCTATCCAACATTACTCAGTTTAG
 CCCCATATTCTATCTCACCAGCTTTCCTGGATTGGAAGGCATCAAACACTGGATTTCATCC
 CCTTTTCTTTATGTACATGGTTGCCATCTCAGGCAATTGTTTCATTCTGATCATTATTAAG
 ACCAACCCCTCGTCTGCACACACCCATGTACTATCTACTATCCTTGCTGGCCCTCACTGACCT
 GGGGCTGTGTGTGTCCACGTTGCCACCACTATGGGGATCTTCTGGTTTAACTCCCAGAGT
 45 ATCTACTTTGGAGCGTGTCAAATCCAGATGTTCTGCATCCACTCTTTTCCCTTCATGGAGTC
 CTCAGTGCTCCTCATGATGTCTTTGACCGCTTTGTGGCCATCTGCCACCTCTGAGGTATT
 CGGTCAATTATCACTGGCCAGCAAGTGGTCAGAGCAGGCCTAATTGTCATCTTCCGGGGACC
 TGTGGCCACTATCCCTATTGTCCTCCTCCTGAAGGCTTTTCCCTACTGTGGATCTGTGGTCC
 TCTCCCACTCATTTTGCCTGCACCAAGGAAGTGATACAGCTGGCCTGCACAGATACCACCTT
 50 CAATAATCTGTATGGACTGATGGTGGTATGTTTCACTGTGATGCTGGACCTGGTGCTATC
 GCACTGTCTATGGACTCATCTGTCACACAGTAGCAGGCCTGGCCTCCCAAGAGGAGCAGC
 GCCGTGCCTTTCAGACATGCACCGCTCATCTCTGTGCTGTGCTAGTATTCTTTGTGCCCATG
 ATGGGGCTGTCCCTGGTGCACCGTTTTGGGAAGCATGCCCCACCTGCTATTCTCTTTAT
 GGCCAATGTCTACCTTTTGTGCTCCCATGCTTAACCCAATCATATACAGCATTAAGACC
 55 AAGGAGATCCACCGTGCCATTATCAAACCTCCTAGGTCTTAAAAAGGCCAGTAAATGA (SEQ
 ID NO: 268)

AOLFR146 sequences:

- MSQVTNTTQEGIFYLTDIPGFEASHIWISIPVCCLYTISIMGNTTILTVIRTEPSVHQRMVFLFLSM
 LALTDLGLTLTTLPTVMQLLWFNVRRISSEACFAQFFFLHGFSEFMESSVLLAMSVDCYVAICCP
 5 LHYASILTNEVIGRTGLAIICCCVLAVLPSLFLKRLPFCHSHLLSRSYCLHQDMIRLVCADIRLN
 SWYGFALALLIIVDPLLVISYTLILKNILGTATWAERLRALNNCLSHILAVLVLYPMVGVSM
 HRFKHAHSPLVHVIMANTYLLAPPVMNPITYSVKNKQIQWGMNLSLKNMHSR (SEQ ID NO:
 269)
- 10 ATGTCCCAGGTGACTAACACCACACAAGAAGGCATCTACTTCATCCTCACGGACATCCCTG
 GATTTGAGGCCTCCACATCTGGATCTCCATCCCCGTCTGCTGTCTCTACACCATCTCCATC
 ATGGGCAATAACCACCATCCTCACTGTCATTCGCACAGAGCCATCTGTCCACGAGCGCATGT
 ATCTGTTTCTCTCCATGTGGCCCTGACGGACCTGGGTCTCACCCCTACCACCTACCCACA
 GTCATGCAGCTTCTCTGGTTCAACGTTTCGTAAGAATCAGCTCTGAGGCCTGTTTTGCTCAGTT
 15 TTCTTCCTTCATGGATTCTCCTTTATGGAGTCTTCTGTCTCCTGGCTATGTCCGTTGACT
 GCTATGTGGCCATCTGCTGTCCCTCCATTATGCCTCCATCCTCACCATGAAGTCATTGGT
 AGAACTGGGTTAGCCATCATTTGCTGCTGTGTTCTGGCGGTTCTTCCCTCCCTTTTCTTACT
 CAAGCGACTGCCTTTCTGCCACTCCCACCTTCTCTCTCGCTCCTATTGCCTCCACCAGGATA
 TGATCCGCCTGGTCTGTGCTGACATCAGGCTCAACAGCTGGTATGGATTGCTCTTGCCCT
 20 GCTCATTATTATCGTGGATCCTCTGCTCATTGTGATCTCCTATACACTTATTCTGAAAAATA
 TCTTGGGCACAGCCACCTGGGCTGAGCGACTCCGTGCCCTCAATAACTGCCTGTCCCACAT
 TCTAGCTGTCTGGTCTCTACATTCCCATGGTTGGTGTATCTATGACTCATCGCTTTGCCA
 AGCATGCCTCTCCACTGGTCCATGTTATCATGGCCAATATCTACCTGCTGGCACCCCCGGT
 GATGAACCCCATCATTTACAGTGTAAGAACAAGCAGATCCAATGGGGAATGTTAAATTTC
 25 CTTTCCCTCAAAAATATGCATTCAAGATGA (SEQ ID NO: 270)

AOLFR147 sequences:

- MPSASAMIIFNLSSYNPGPFILVGIPGLEQFHVWIGIPFCIIYIVAVVGNICLLYLIVVEHSLHEPMP
 FFLSMLAMTDLILSTAGVPKALSIFWLGAIRETFPGCLTQMFFLHYNFVLDSAILMAMAFDHYV
 30 AICSPLRYTTILTPKTIKSAMGISFRSFCILPDVFLLTCLPFCRTRIIPHTYCEHIGVAQLACADISI
 NFWYGFVCPIMTVISDVILIAVSYAHILCAVFGLP SQDACQKALGTCGSHVCVILMFYTPAFFSI
 LAHRFGHNVSRTFHMIFANLYIVPPALNPMVYGVKTKQIRDKVILLFSKGTG (SEQ ID NO:
 271)
- 35 ATGCCATCTGCCTCTGCCATGATCATTTTTCAACCTGAGCAGTTACAATCCAGGACCCCTTCAT
 TCTGGTAGGGATCCCAGGCCTGGAGCAATTCATGTGTGGATTGGAATTCCCTTCTGTATC
 ATCTACATTGTAGCTGTTGTGGGAACTGCATCCTTCTCTACCTCATTGTGGTGGAGCATA
 GTCTTCATGAACCCATGTTCTTCTTCTCTCCATGCTGGCCATGACTGACCTCATCTTGTCC
 ACAGCTGGTGTGCCTAAAGCACTCAGTATCTTTTGGCTAGGGGCTCGCGAAATCACATTCC
 40 CAGGATGCCTTACACAAATGTTCTTCTTCACTATAACTTTGTCCTGGATTGAGCCATTCTG
 ATGGCCATGGCATTGATCACTATGTAGCTATCTGTTCTCCCTTGAGATATACCACCATCTT
 GACTCCCAAGACCATCATCAAGAGTGCTATGGGCATCTCCTTTCGAAGCTTCTGCATCATC
 CTGCCAGATGTATTCTTGCTGACATGCCTGCCTTTCTGCAGGACACGCATCATACCCCA
 CATACTGTGAGCATATAGGTGTTGCCAGCTCGCCTGTGCTGATATCTCCATCAACTTCTG
 45 GTATGGCTTTTGTGTTCCCATCATGACGGTCATCTCAGATGTGATTCTCATTGCTGTTTCT
 ACGCACACATCCTCTGTGCTGTCTTGGCCTTCCCTCCCAAGATGCCTGCCAGAAAGCCCT
 CGGCACTTGTGGTTCTCATGTCTGTGTCATCCTCATGTTTATACACCTGCCTTTTCTCCA
 TCTCGCCCATCGCTTTGGACACAATGTCTCTCGCACCTTCCACATCATGTTTGGCAATCTC
 TACATTGTTATCCCACCTGCACTCAACCCCATGGTTTACGGAGTGAA'GACCAAGCAGATCA
 50 GAGATAAGGTTATACCTTTGTTTCTAAGGGTACAGGATGA (SEQ ID NO: 272)

AOLFR148 sequences:

- MPTVNHSGTSHTVFHLGIPGLQDQHMWISIPFFISYVTALLGNSLLIFILTKRSLHEPMPYFLC
 MLAGADIVLSTCTIPQALAIWFVFRAGDISLDRCTQLFFIHSTFISEGILLVMAFDHYIAICYPLR
 55 YTILTNALIKKICVTVSLRSYGTIFPIIFLLKRLTFCQNNIIPHTFCEHIGLAKYACNDIRINIWYG

FSILMSTVVLDVVLIFISYMLILHAVFHMPSPDACHKALNTFGSHVCIILFYGSGIFTILTQRFRGR
HIPPCIHIPLANVCILAPPMNLNPIYGIKTKIQIEQVQVFLFIKQKITLV (SEQ ID NO: 273)

5 ATGCCTACTGTAAACCACAGTGGCACTAGCCACACAGTCTTCCACTTGCTGGGCATCCCTG
GCCTACAGGACCAGCACATGTGGATTTCTATCCCATTCCTCATTTCCTATGTCACCGCCCTT
CTTGGAACAGCCTGCTCATCTTCATTATCCTCACAAAGCGCAGCCTCCATGAACCCATGT
ACCTCTTCCTCTGCATGCTGGCTGGAGCAGACATTGTCCTCTCCACGTGCACCATTCCTCAG
GCCTTAGCTATCTTCTGGTTCCGTGCTGGGGACATCTCCCTGGATCGTTGCATCACTCAGCT
10 CTTCTTCATCCATTCCACCTTCATCTCTGAGTCAGGGATCTTGCTGGTGATGGCCTTTGACC
ACTATATTGCCATATGCTACCCACTGAGGTACACCACCATTCTTACAAATGCTCTGATCAA
GAAAATTTGTGTGACTGTCTCTCTGAGAAGTTATGGTACAATTTTCCCTATCATATTTCTTT
TAAAAAGATTGACTTTCTGCCAGAATAATATTATTCCACACACCTTTTGTGAACACATTGG
CCTAGCCAAATATGCATGTAATGACATTGCAATAAACATTTGGTATGGGTTTTCCATTCTA
15 ATGTCGACGGTGGTCTTAGATGTTGTACTAATTTTTATTTCCCTATATGCTGATTCTCCATGC
TGTCTTCCACATGCCTTCTCCAGATGCTTGCCACAAAGCTCTCAACACATTTGGCTCCCATG
TCTGCATCATCATCCTCTTTTATGGGTCTGGCATCTTCACAATCCTTACCCAGAGGTTTGA
CGCCACATTCCACCTTGTATCCACATCCCGTTGGCTAATGTCTGCATTCTGGCTCCACCTAT
GCTGAATCCCATTATTTATGGGATCAAAACCAAGCAAATCCAGGAACAGGTGGTTCAGTTT
20 TTGTTTATAAAACAGAAAATAACTTTGGTTTAA (SEQ ID NO: 274)

AOLFR149 sequences:

MSNASLLTAFILMGLPHAPALDAPLFGVFLVYVYLVTLGNLLILLVIRVDSHLHTTMYFLTNL
SFIDMWFSTVTVPKLLMTLVFPSGRAISFHSMAQLYFFHFLGGTECFLYRVMSCDRYLAISSP
25 LRYTSMMTGRSCTLLATSTWLSGSLHSAVQAILTFHLPYCGPNWQHLYLCDAPPILKLACADTS
AIETVIFVTVGIVASGCFVLIVLSYVSIVCSILRIRTSEGKHRAFQTCASHCIVVLCFFGPGFLFIYLR
PGRKAVDGVVAVFYTVLTPLLNPVYVTLRNEVKKALLKLKDKVAHSQSK (SEQ ID NO:
275)

30 ATGTCCAACGCCAGCCTACTGACAGCGTTCATCCTCATGGGCCTTCCCCATGCCCCAGCGC
TGGACGCCCCCTCTTTGGAGTCTTCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
CCTCATCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCACCATGTAATACTTCTCTCA
CCAACCTGTCGTTTATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAATTGCTGATGAC
TTTGGTGTTCCTCAAGTGGCAGGGCTATCTCCTTCCACAGCTGCATGGCTCAGCTCTATTCT
35 TTCATTCTAGGGGGCACCGAGTGTTCCTCTACAGGGTGCATGCTGCTGATCGCTACCT
GGCCATCAGTTACCCGCTCAGGTACACCAGCATGATGACTGGGCGCTCGTGTACTCTTCTG
GCCACCAGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGGCCATATTGACTTTCC
ATTTGCCCTACTGTGGACCCAACTGGATCCAGCACTATTTGTGTGATGCACCGCCCATCCT
GAAACTGGCCTGTGCAGACACCTCAGCCATAGAGACTGTCATTTTGTGACTGTTGGAATA
40 GTGGCCTCGGGCTGCTTTGTCCTGATAGTGCTGTCTATGTGTCCATCGTCTGTTCCATCCT
GCGGATCCGCACCTCAGAGGGGAAGCACAGAGCCTTTTACAGCCTGTGCCTCCCACTGTATC
GTGGTCTTTGCTTCTTTGGCCCTGGTCTTTTCACTTACCTGAGGCCAGGCTCCAGGAAAGC
TGTGGATGGAGTTGTGGCCGTTTCTACACTGTGCTGACGCCCCCTTCTCAACCTGTTGTGT
ACACCCTGAGGAACAAGGAGGTGAAGAAAGCTCTGTTGAAGCTGAAAGACAAAGTAGCAC
45 ATTCTCAGAGCAAATAG (SEQ ID NO: 276)

AOLFR150 sequences:

MELGNVTRVKEBIFLGLTQSQDQSLVFLFLCLVYMTLLGNLLIMVTVTCESRLHTPMYFLLR
NLAILDICFSSTTAPKVLLDLLSKKKTISYTSMTQIFLHLLGGADIFSLSVMAFDCYMAISKPL
HYVTMSRGQCTALISASWMGGFVHSIVQISLLPLPFCGPNVLDTFYCDVPQVLKLTCTDFTA
50 LEFLMISNNGLVTTLWFIFLLVSYTVILMTLRSQAGGGRRKAISTCTSPHHCGDPFACALHCLC
PALHCPPHRKGHLCHLHCHLPSAEPFDLHSEEPGNEVSHEKTEKTRAF (SEQ ID NO: 277)

55 ATGGAGTTGGGAAATGTCACCAGAGTAAAAGAATTTATATTTCTGGGACTTACTCAATCCC
AAGACCAGAGTTTGGTCTTGTCTTTTTTTATGTCTTGTGTACATGACGACTCTGTGGGA
AACCTCCTCATATGGTCACCGTGACCTGTGAGTCTCGCCTTACACCCCCATGTAATCTCT
GCTCCGCAATCTAGCCATCCTTGACATCTGCTTCTCCTCCACAAGTCTTAAAGTCTTGC

TGGACCTTCTGTCAAAGAAAAAGACCATATCCTATACAAGCTGCATGACACAGATATTTCT
 CTTCCACCTCCTTGGTGGGGCAGACATTTTTCTCTCTCTGTGATGGCGTTTGACTGCTACA
 TGGCCATCTCCAAGCCCCTGCACTATGTGACCATCATGAGTAGAGGGCAATGCACTGCCCT
 CATCTCTGCCTCTTGGATGGGGGGCTTTGTCCACTCCATCGTGCAGATCTCCCTGTTGCTGC
 5 CTCTCCCTTTCTGTGGACCCAATGTTCTTGACACTTTCTACTGCGATGTCCCCCAGGTCCTC
 AAACCTCACTTGCACTGACACTTTTGCTCTTGAGTTCTTGATGATTCCAACAATGGCCTGGT
 CACTACCCTGTGGTTTATCTTCCTGCTTGTGTCTACACAGTCATCCTAATGACGCTGAGGT
 CTCAGGCAGGAGGGGGCAGGAGGAAAGCCATCTCCACTTGACCTCCCCACATCACTGTG
 GTGACCCTGCATTTTGTGCCCTGCATCTATGTCTATGCCCCGCCCTTCACTGCCCTCCCCAC
 10 AGAAAAGGCCATCTCTGTCACTTCACTGTCTATCTCCCTCTGCTGAACCCTTTGATCTACA
 CTCTGAGGAACCAGGAAATGAAGTCAGCCATGAGAAGACTGAAGAGAAGACTCGTGCCTT
 CTGA (SEQ ID NO: 278)

AOLFR151 sequences:

15 MFSPNHTIVTEFILLGLTDDPVLEKILFGVFLAIYLITLAGNLCMILLIRTNSHLQTPMYFFLGHL
 FVDICYSSNVTNMLHNFLESEQKTSYAGCFTQCLLFIALVITEFYILASMLDRYVAICSPLHYS
 SRMSKNICVCLVTIPYMYGFLSGFSQSLLTFHLSFCGSLEINHFCADPPLMLACSDTRVKMA
 MFVVAGFNLSSSLFILLSYLFIFAIFRIRSAEGRHKAFSTCASHLTTVTLFYGTLCMYVRPPSE
 KSVEESKITA VFYTFLLSPMLNPLIYSLRNTDVLAMQQMIRGKSFHKIAV (SEQ ID NO: 279)

20 ATGTTCTCCCCAAACCACACCATAGTGACAGAATTCATTCTCTTGGGACTGACAGACGACC
 CAGTGCTAGAGAAGATCCTGTTTGGGGTATTCTTGCGATCTACCTAATCACTGGCAGG
 CAACCTGTGCATGATCCTGCTGATCAGGACCAATCCCACCTGAAACACCCATGTATTC
 TTCCTTGGCCACCTCTCCTTTGTAGACATTTGCTATTCTTCCAATGTTACTCCAAATATGCT
 25 GCACAATTTCTCTCAGAACAGAGACCATCTCCTACGCTGGATGCTTACACAGTGTCTT
 CTCTTCATCGCCCTGGTGATCACTGAGTTTACATCCTTGCTTCAATGGCATTGGATCGCTA
 TGTAGCCATTTGCAGCCCTTTGCATTACAGTTCCAGGATGTCCAAGAACATCTGTGTCTGT
 CTGGTCACTATCCCTTACATGTATGGGTTTCTTAGTGGGTTCTCTCAGTCACTGCTAACCTT
 TCACTTATCCTTCTGTGGCTCCCTTGAAATCAATCATTTCTACTGCGCTGATCCTCCTCTTA
 30 TCATGCTGGCCTGCTCTGACACCCGTGTCAAAAAGATGGCAATGTTTGTAGTTGCAGGCTT
 TAATCTCTCAAGCTCTCTCTTCATCATTCTTCTGTCTATCTTTTCATTTTGCAGCGATCTT
 CAGGATCCGTTCTGCTGAAGGCAGGCACAAAGCCTTTTCTACGTGTGCTTCCACCTGACA
 ATAGTCACTTTGTTTTATGGAACCCTCTTCTGCATGTACGTAAGGCCTCCATCAGAGAAAT
 CTGTAGAGGAGTCCAAAATAACTGCAGTCTTTTATACTTTTTTGAGCCCAATGCTGAACCC
 35 ATTGATCTATAGCCTACGGAACACAGATGTAATCCTTGCCATGCAACAAATGATTAGGGGA
 AAATCCTTTCATAAAATTGCAGTTTAG (SEQ ID NO: 280)

AOLFR152 sequences:

40 MDQINHTNVKEFFLELTRSRELEFFLVVFFAVYVATVLGNALIVVTITCESRLHTPMYFLLRN
 KSVLDIVFSSITVPKFLVDLLSDRKTISYNDCAQIFFHFAGGADIFFLSVMAYDRYLAIKPL
 HYVTMMRKEVWVALVVASWVSGGLHSIIQVILMLPPFFCGPNTLDAFYCYVLQVVKLACTDT
 FALELFMISNNGLVTLWFLLLLGSYTVILVMLRSHSGEGRNKALSTCTSHMLVVTLHFVPCV
 YIYCRPFMTLPMDTTISINNTVITPMLNPIIYSLRNQEMKSAMQRLQRRLGPSERKWWG (SEQ ID
 NO: 281)

45 ATGGACCAGATCAACCACACTAATGTGAAGGAGTTTTTCTTCTGGAACCTACACGTTCCC
 GAGAGCTGGAGTTTTTCTTGTGTTGTGGTCTTCTTGTGCTGTGATGTAGCAACAGTCCTGGG
 AAATGCACTCATTGTGGTCACTATTACCTGTGAGTCCCGCTACACACTCCTATGTACTTTC
 TCCTGCGGAACAAATCAGTCCCTGGACATCGTTTTTTCATCTATCACCCTCCCCAAGTTCCTG
 50 TTGGATCTTTTATCAGACAGGAAACCATCTCCTACAATGACTGCATGGCAGATGCTTTT
 TCTTCCACTTTGCTGGTGGGGCAGATATTTTTTCTCTCTGTGATGGCCTATGACAGATAC
 CTTGCAATCGCCAAGCCCCTGCACTATGTGACCATGATGAGGAAAGAGGTGTGGGTGGCC
 TTGGTGGTGGCTTCTTGGGTGAGTGGTGGTTTGCAATCAATCATCCAGGTAATTCTGATGC
 TTCCATTCCCCTTCTGTGGCCCCAACACACTGGATGCCTTCTACTGTTATGTGCTCCAGGTG
 55 GTAAAACCTGGCCTGCACTGACACCTTTGCTTTGGAGCTTTTCATGATCTCTAACAACGGAC
 TGGTGACCCTGCTCTGGTTCTCTGCTCCTGGGCTCCTACACTGTCATTCTGGTGATGCTG

AGATCCCACTCTGGGGAGGGGCGGAACAAGGCCCTCTCCACGTGCACGTCCCACATGCTG
 GTGGTGACTCTTCACTTCGTGCCTTGTGTTTACATCTACTGCCGGCCCTTCATGACGCTGCC
 CATGGACACAACCATATCCATTAATAACACGGTCATTACCCCATGCTGAACCCCATCATC
 TATTCCTGAGAAATCAAGAGATGAAGTCAGCCATGCAGAGGCTGCAGAGGAGACTTGGG
 5 CCTTCCGAGAGCAGAAAATGGGGTGA (SEQ ID NO: 282)

AOLFR153 sequences:

MSKTSLVTAFILTGPHAPGLDAPLFGIFLVVYVLTVLGNLLLVIRVDSHLHTPMYYFLTNLS
 FIDMWFSTVTVPKMLMTLVSPSGRAISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAISYPL
 10 RYTSMMSGSRCALLATSTWLSGLHSAVQTLTFHLPYCGPNQIQHYLCDAPPLKLACADTSA
 NEMVIFVDIGLVASGCFLLIVLSYVSIVCSILRIHTSEGRHRAFQTCASHCIVVLFFVXCVFIYLR
 PGSRDVVDGVVAIFYTVLTPLLNPVVYTLRNKEVKKAVLKLKRDKVAHSQGE (SEQ ID NO:
 283)

15 ATGTCCAAGACCAGCCTCGTGACAGCGTTCATCCTCACGGGCCTTCCCCATGCCCCAGGGC
 TGGACGCCCCACTCTTTGGAATCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
 CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCATGTACTACTTCTCA
 CCAACCTGTCCTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAAATGCTGATGAC
 CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTTT
 20 TCCACTTCTGGGGAGCACCGAGTGTTCCTCTACACAGTCATGTCCTATGATCGCTACTTG
 GCCATCAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGATGTGCCCTCCTGG
 CCACCAGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT
 TTGCCCTACTGTGGACCAACCAGATCCAGCACTATTTGTGTGATGCACCGCCCATCCTGA
 AACTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTGGACATTGGGCTAGT
 25 GGCCTCGGGCTGCTTTCTCTGATAGTGTCTTATGTGTCCATCGTCTGTTCCTCCTGC
 GGATCCACACCTCAGAGGGGAGGCAGAGCCTTTCAGACCTGTGCCTCCCATCCATCGT
 GGTCTTTGTCTTTTTGTNNCTGTGTTTTTCAATTAACCTGAGACCAGGCTCCAGGGACGTGC
 TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACACCCCTTCTCAACCCTGTTGTGTAC
 ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAAACTGAGAGACAAAGTAGCACAT
 30 TCTCAGGGAGAATAA (SEQ ID NO: 284)

AOLFR156 sequences:

MCWAMPSPFTGSSTRNMESRNQSTVTEFIFTGFPQLQDGSLLYFFPLLFIYTFIIDNLLIFSAVRL
 DTHLGNPMYNFISIFSLEIWTATIPKMLSNLISEKKAISMTGCILQMYFFHSLNSEGILLTT
 35 MAIDRYVAICNPLRYQMIMTPRLCAHLSAGSCLFGFLILLPEIVMISTLPFCGPNQIQHIFCDLVP
 VLSLACTDTSMLIEDVIHAVTIIITFLIALSYVRIVTVILRIPSSEGRQKAXSTCAGHLMVFLIFFG
 SVSLMYLRFSTNTYPPVLDTAIALMFTVLAPFFNPIIYSLRNKDMNNAIKKLFCLQKVLNKPGG
 (SEQ ID NO: 285)

40 ATGTGCTGGGCTATGCCCTCTCCATTTACAGGTAGCTCTACTAGAAATATGGAGAGCAGAA
 ACCAATCAACAGTGACTGAATTTATCTTCACTGGATTCCCTCAGCTTCAGGATGGTAGTCT
 CCTGTACTTCTTTCTTTACTTTTCATCTATACTTTTATTATCATTGATAACTTATTAATCTT
 CTCTGCTGTAAGGCTGGACACCCATCTGGGCAACCCCATGTATAATTTTATCAGTATATTTT
 CCTTTCTGGAGATCTGGTACACCACAGCCACCATCCCAAGATGCTCTCCAACCTCATCAG
 45 TGAAGAAAGAGGCCATCTCAATGACTGGCTGCATCTTGACAGATGTATTTCTTCCACTCACTT
 GAAAACTCAGAGGGGATCTTGCTGACCACCATGGCCATTGACAGATACGTTGCCATCTGCA
 ACCCTCTTCGCTATCAAAATGATCATGACCCCCCGGCTCTGTGCTCACCTCTCTGCAGGTTC
 TGCCTCTTCGGTTTCCTTATCCTGCTTCCCAGATTGTGATGATTTCCACACTGCCTTTCTG
 TGGGCCCCAACCAATCCATCAGATCTTCTGTGACTTGGTCCCTGTGCTAAGCCTGGCCTGT
 50 ACAGACACGTCATGATTCTGATTGAGGATGTGATTGATGCTGTGACCATCATCATTACCT
 TCCTAATCATTGCCCTGTCTATGTAAGAATTGTCACTGTGATATTGAGGATTCCCTCTTCT
 GAAGGGAGGCAAAAGGCTNTTCTACCTGTGCAGGCCACCTCATGGTCTTCTGATATTCT
 TTGGCAGTGTATCACTCATGTACTTGCCTTTCAGCAACACTTATCCACCAGTTTGGACAC
 AGCCATTGCACTGATGTTTACTGTACTTGTCTCCATTCTTCAATCCCATCATTTATAGCCTGA
 55 GAAACAAGGACATGAACAATGCAATTAATAAACTGTTCTGTCTTCAAAAAGTGTGAAACA
 AGCCTGGAGGTTAA (SEQ ID NO: 286)

AOLFR157 sequences:

MAMDNVTA V FQ FLLIGISNYPQWRDTFFTLVLIYLSLTLGNGFMIFLIHFDPNLHTPIYFFLSNL
 SFLDL CYGTASMPQALVHCFSTHPYLSYPRCLAQTSVSLALATAECLLLAAMAYDRVVAISNP
 5 LRYSVVMNGPVCVCLVATSWGTSVL TAMLILSLRLHFCGANVINHFACEILSLIKLTCSDTSL
 NEFMILITSIFTL L L PFGFVLLSYIRIAMAIRSLQGR L K A F T T C G S H L T V V T I F Y G S A I S M Y M K T
 QKSSPDQDKFISVFY GALTPMLNPLIYSLRKKDVKRAIRKVMLKRT (SEQ ID NO: 287)

ATGGCCATGGACAATGTCACAGCAGTGTTCAGTTTCTCCTTATTGGCATTCTAACTATCC
 10 TCAATGGAGAGACACGTTTTTACATTAGTGCTGATAATTTACCTCAGCACATTGTTGGGG
 AATGGATTTATGATCTTTCTTATTCACTTTGACCCCAACCTCCACACTCCAATCTACTTCTT
 CCTTAGTAACCTGTCTTTCTTAGACCTTTGTTATGGAACAGCTTCCATGCCCCAGGCTTTGG
 TGCATTGTTTCTCTACCCATCCCTACCTCTCTTATCCCCGATGTTTGGCTCAAACGAGTGTC
 TCCTTGGCTTTGGCCACAGCAGAGTGCTCCTACTGGCTGCCATGGCCTATGACCGTGTGG
 15 TTGCTATCAGCAATCCCCTGCGTTATTCACTGGTTATGAATGGCCAGTGTGTGTCTGCTT
 GGTGCTACCTCATGGGGGACATCACTTGTGCTCACTGCCATGCTCATCCTATCCCTGAGG
 CTTCACTTCTGTGGGGCTAATGTCATCAACCATTTTGCCTGTGAGATTCTCTCCCTCATTA
 GCTGACCTGTTCTGATACCAGCCTCAATGAATTTATGATCCTCATCACCAGTATCTTCAACC
 TGCTGCTACCATTTGGGTTTGTCTCCTCTCCTACATACGAATTGCTATGGCTATCATAAGG
 20 ATTCGCTCACTCCAGGGCAGGCTCAAGGCCTTTACCACATGTGGCTCTCACCTGACCGTGG
 TGACAATCTTCTATGGGTCAGCCATCTCCATGTATATGAAACTCAGTCCAAGTCCCTCCCC
 TGACCAGGACAAGTTTATCTCAGTGTTTATGGAGCTTTGACACCCATGTTGAACCCCTG
 ATATATAGCCTGAGAAAAAAGATGTTAAACGGGCAATAAGGAAAGTTATGTTGAAAAGG
 ACATGA (SEQ ID NO: 288)

25

AOLFR158 sequences:

MKAGNFSDTPEFFLLGLSGDPELQPIFLFMSMYLATMLGNLLILAVNSDSLHPTMYFLLSI
 LSLVDICFTSTTMPKMLVNIQAQAQSINYTGCLTQICFVLVFGLENGILVMMAYDRFVAICHP
 LRYNVIMNPKLCGLLLLSFIVSVLDALLHTLMVLQLTFCIDLEIPHFCELAHILKLACSDVLIN
 30 NILVYLVTSL LGVVPLSGIIFSYTRIVSSVMKIPSAAGKYKAFSICGSHLIVVSLFYGTGFGVYLLS
 GATHSSRKGAIASVMYTVVTPMLNPLIYSLRNKMDL KALRKLISRIPSFH (SEQ ID NO: 289)

ATGAAAGCAGGAACTTCTCAGACACTCCAGAATTCTTTCTCTTGGGATTGTCAGGGGATC
 CGGAGCTGCAGCCCATCCTCTTCATGCTGTTCTGTCCATGTACCTGGCCACAATGCTGGG
 35 GAACCTGCTCATCATCCTGGCCGTCACCTGACTCCACCTCCACACCCCCATGTACTTCC
 TCCTCTCTCCTGTCTTGGTCGACATCTGTTTACCTCCACCACGATGCCCAAGATGCTG
 GTGAACATCCAGGCACAGGCTCAATCCATCAATTACACAGGCTGCCTCACCCAAATCTGCT
 TTGTCCTGGTTTTTGTGGATTGGAATGGAATTCTGGTCAATGATGGCCTATGATCGATT
 TGTGGCCATCTGTACCCACTGAGGTACAATGTCATCATGAACCCCAAACTCTGTGGGCTG
 40 CTGCTTCTGCTGTCTTCATCGTTAGTGTCTGGATGCTCTGCTGCACACGTTGATGGTGT
 ACAGCTGACCTTCTGCATAGACCTGGAAATCCCCACTTTTTCTGTGAAGTATGCTCATATTC
 TCAAGCTCGCCTGTTCTGATGTCCTCATCAATAACATCCTGGTGTATTTGGTGACCAGCCT
 GTTAGGTGTTGTTCTCTCTCTGGGATCATTTTCTCTTACACACGAATTGCTCTCCTCTGTCA
 TGAATAATCCATCAGCTGGTGGAAGTATAAAGCTTTTCCATCTGCGGGTCACATTTAAT
 45 CGTTGTTTCTTGTGTTTATGGAACAGGGTTTGGGGTGTACCTTAGTTCTGGGGCTACCCACT
 CCTCCAGGAAGGGTGCAATAGCATCAGTGATGTATACCGTGGTCACCCCATGCTGAACCC
 ACTCATTTACAGCCTGAGAAACAAGGACATGTTGAAGGCTTTGAGGAACTAATATCTAG
 GATACCATCTTTCCATTGA (SEQ ID NO: 290)

AOLFR159 sequences:

MGPRNQTA VSEFLLMKVTEDEPELKLIPFSLFMSMYLVITLGNLLILLA VISDSLHPTMYFLLFN
 LSFTDICLTTTTVPKILVNIQAQNSITYTGCLTQICLVLFAGLESCFLAVMAYDRYVAICHP
 RYTVLMNVHFWGLLLSMFMSTMDALVQSLMVLQLSFCKNVEIPLFFCEVVQVIKLACSDVTL
 INNILYFASSVFGAIPLSGIIFSYSQIVTSVLRMP SARGKYKAFSTCGCHLSVFSFYGTAFGTYIS
 55 SAVAESSRITAVASVMYTVVTPQMMNPFTYSLRNKEMKKALRKLIGRLF (SEQ ID NO: 291)

ATGGGACCCAGAAACCAAACAGCTGTTTCAGAAATTTCTTCTCATGAAAGTGACAGAGGAC
 CCAGAACTGAAGTTAATCCCTTTTCAGCCTGTTCCCTGTCCATGTACCTGGTCACCATCCTGG
 GGAACCTGCTCATTCTCCTGGCTGTCATCTCTGACTCCACCTCCACACCCCCATGTACTTC
 CTTCTCTTAATCTCTCCTTTACTGACATCTGTTTAACCACAACCACAGTCCCAAAGATCCT
 5 AGTGAACATCCAAGCTCAGAATCAGAGTATCACTTACACAGGCTGCCTCACCAGATCTGT
 CTTGTCTTGGTTTTTGCTGGCTTGAAAGTTGCTTTCTTGCAGTCATGGCCTACGACCGCTA
 TGTGGCCATTTGCCACCCACTGAGGTACACAGTCTCATGAATGTCCATTTCTGGGGCTTG
 CTGATTCTTCTCTCCATGTTTCATGAGCACTATGGATGCCCTGGTTCAGAGTCTGATGGTATT
 GCAGCTGTCTTCTGCAAAAACGTTGAAATCCCTTTGTTCTTCTGTGAAGTCGTTCAAGTC
 10 ATCAAGCTCGCCTGTTCTGACACCCCTCATCAACAACATCCTCATATATTTTGCAAGTAGTGT
 ATTTGGTGCAATTCCTCTCTCTGGAATAATTTTCTCTTATTCTCAAATAGTCACCTCTGTTC
 TGAGAATGCCATCAGCAAGAGGAAAGTATAAAGCGTTTTCCACCTGTGGCTGTCACCTCTC
 TGTTTTTTCCTTGTCTATGGGACAGCTTTTGGGGTGACATTAGTTCTGCTGTTGCTGAGT
 CTTCCCGAATTACTGCTGTGGCTTCAGTGATGTACACTGTGGTCCCTCAAATGATGAACCC
 15 CTTCTATCTACAGCCTGAGAAATAAGGAGATGAAGAAAGCTTTGAGGAACTTATTGGTAG
 GCTGTTTCCTTTTAG (SEQ ID NO: 292)

AOLFR160 sequences:

MPMQLLLTDFIIFSRFIINSMEARNQTAISKFLLGLIEDPELQPVLFSLFLSMYLVITLGNLLILL
 20 AVISDSHLHTPMYFFLSNLSFLDICTSTTTPKMLVNIQAQNRSTYSGLTQICFVLFAGLENC
 LLAAMAYDRYVAICHPLRYTVIMNPRLCGLLLSLLTSVNVNALLSLMVLRLSFCTDLEIPLFF
 CELAQVIQLTCSDTLINNLIYFAACIFGGVPLSGHLSYQITSCVLRMPASGKHKA VSTCGSHL
 SIVLLFYGAGLGVYISSVVTDSRKTAVASVMYSVFPQMVNPFYSLRNKDMKGLRKFGRIP
 SLLWCAICFGFRFLE (SEQ ID NO: 293)

25 ATGCCGATGCAGCTGCTGCTTACAGATTTTATTATCTTTTCCATCAGATTCATCATCAACAG
 CATGGAAGCGAGAAACCAAACAGCTATTTCAAATTCCTTCTCCTGGGACTGATAGAGGAT
 CCGGAACCTGCAGCCCGTCTTTTCAGCCTGTTCCCTGTCCATGTACTTGGTCACCATCCTGGG
 GAACCTGCTCATCTCTTGGCTGTCATCTCTGACTCTCACCTCCACACCCCCATGTACTTCT
 30 TCCTCTCCAATCTCTCCTTTTTGGACATTTGTTTAAGCACAACCACGATCCCAAAGATGCTG
 GTGAACATCCAAGCTCAGAATCGGAGCATCACGTA CTAGGCTGCCTCACCAGATCTGCT
 TTGTCTTGTTTTTTGTGCTGGCTTGAAAAATTGTCTCCTTGCAGCAATGGCCTATGACCGCTAT
 GTGGCCATTTGTACCCCCCTTAGATACACAGTCATCATGAACCCCCGCCTCTGTGGCCTGC
 TGATTCTTCTCTCTCTGTTGACTAGTGTGTGAATGCCCTTCTTCTCAGCCTGATGGTGTG
 35 AGGCTGTCTTCTGCAACAGACCTGGAAATCCCGCTCTTCTTCTGTGAACTGGCTCAGGTCA
 TCCAACCTACCTGTTTCAGACACCCCTCATCAATAACATCCTGATATATTTTGACGTTGCATA
 TTTGGTGGTGTCTCTGTCTGGAATCATTTTGTCTTACACTCAGATCACCTCTGTGTTTT
 GAGAATGCCATCAGCAAGTGGAAAGCACAAGACAGTTTCCACCTGTGGGTCTCACCTCTCC
 ATTGTTCTCTTGTCTATGGGGCAGGTTTGGGGGTGTACATTAGTTCTGTGGTTACTGACTC
 40 ACCTAGGAAGACTGCAGTGGCTTCAGTGATGTATTCTGTGTTCCCTCAAATGGTGAACCCC
 TTTATCTATAGTCTGAGGAATAAGGACATGAAAGGAACCTTGAGGAAGTTCATAGGGAGG
 ATACCTTCTCTTCTGTGGTGTGCCATTTGCTTTGGATTGAGTTTCTAGAGTAA (SEQ ID
 NO: 294)

AOLFR161 sequences:

45 MEPRNQTSA SQFILLGLSEKPEQETLLFSLFFCMYLVMMVGNLLIILAISIDSHLHTPMYFFLANL
 SLVDFCLATNTIPKMLVSLQTGSKAISYPCCLIQMYFFHFFGIVDSVIIAMMAYDRFVAICHPLH
 YAKIMSLRLCRLLVGALWAFSCFISLTHILLMARLVFCGSHEVPHYFCDLTPILRLSCTDTSVNR
 IFILIVAGMVIATPFVCILASYARILVAIMKVPSAGGRKKAFTSCSSHLSVVALFYGTTIGVYLCF
 50 SSVLTVKEKASAVMYTAVTPMLNPFYSLRNRLDKGALRKL VNRKITSSS (SEQ ID NO: 295)

55 ATGGAACCAAGAAACCAAACAGTGCATCTCAATTCATCCTCCTGGGACTCTCAGAAAAGC
 CAGAGCAGGAGACGCTTCTCTTTTCCCTGTTCTTCTGCATGTACCTGGTCATGGTCGTGGG
 GAACCTGCTCATCATCCTGGCCATCAGCATAGACTCCACCTCCACACCCCCATGTACTTCT
 TCCTGGCCAACTGTCCCTGGTTGATTTCTGTCTGGCCACCAACACCATCCCTAAGATGCT
 GGTGAGCCTTCAAACCGGGAGCAAGGCCATCTCTTATCCCTGCTGCCTGATCCAGATGTAC

TTCTTCCATTTCTTTGGCATCGTGGACAGCGTCATAATCGCCATGATGGCTTATGACCGGTT
 CGTGGCCATCTGCCACCCATTGCACTACGCCAAGATCATGAGCCTACGCCTCTGTGCGCTG
 CTGGTCCGGCGCCCTCTGGGCGTTTCTCTGCTTCATCTCACTCACTCACATCCTCCTGATGGC
 CCGTCTCGTTTTCTGCGGCAGCCATGAGGTGCCTCACTACTTCTGCGACCTCACTCCCATCC
 5 TCCGACTTTCGTGCACGGACACCTCTGTGAATAGGATCTTCATCCTCATTGTGGCAGGGAT
 GGTGATAGCCACGCCCTTTGTCTGCATCCTGGCCTCCTATGCTCGCATCCTGTGGCCATCA
 TGAAGGTCCCCTCTGCAGGCGGCAGGAAGAAAGCCTTCTCCACCTGCAGCTCCCACCTGTC
 TGTGGTTGCTCTCTTCTATGGGACCACCATTGGCGTCTATCTGTGTCCCTCCTCGGTCTCA
 CCACTGTGAAGGAGAAAGCTTCTGCGGTGATGTACACAGCAGTCACCCCCATGCTGAATCC
 10 CTTTCATCTACAGCTTGAGGAACAGAGACCTGAAAGGGGCTCTCAGGAAGCTGGTCAACAG
 AAAGATCACCTCATCTTCTGA (SEQ ID NO: 296)

AOLFR162 sequences:

MMRLMKEVRGRNQTEVTEFLLGLSDNPDQGVLFALFLIYMANMVGNLGMIVLIKIDLCLH
 15 TPMYFFLSSLSFVDASYSSSVTPKMLVNLMAENKAISFHGCAAQFYFFGSFLGTECFLLAMMA
 YDRYAAIWNPLLYPVLVSGRICFLLIATSLAGCGNAAIHTGMTFRLSFCGSNRINH FYCDTPPL
 LKLSGSDTHFNQVIMAFSSFIVISCMIVLISYLCIFIAVLKMPSLGRHKAFTSCASYLMAVTF
 FGILFMYLRPTSSYSMEQDKVVSFVYTVIIPVLNPLIYSLKNKDVKKALKKILWKHIL (SEQ ID
 NO: 297)
 20
 ATGATGAGACTTATGAAAGAGGTTTCGAGGCAGAAATCAAACAGAAGTAACAGAATTTCTC
 CTCTTAGGACTTTCCGACAATCCAGATCTACAAGGAGTCCTCTTTGCATTGTTTCTGTTGAT
 CTATATGGCAAACATGGTGGGCAATTTGGGGATGATTGTATTGATTAAAGATTGATCTCTGT
 CTCCACACCCCCATGTATTTCTTCTCAGTAGCCTCTCTTTTGTAGATGCCTCTTACTCTTCT
 25 TCCGTCACTCCCAAGATGCTGGTGAACCTCATGGCTGAGAATAAGGCCATTTCTTTTCATG
 GATGTGCTGCCAGTTCTACTTCTTTGGCTCCTTCTGCGGACTGAGTGCTTCTGTTGGCC
 ATGATGGCATATGACCGCTATGCAGCCATTTGGAACCCCTGCTCTACCCAGTTCTCGTGT
 CTGGGAGAATTTGCTTTTGTCTAATAGCTACCTCCTTCTTAGCAGGTTGTGGAAATGCAGC
 CATACTACAGGGATGACTTTTAGGTTGTCTTTTGTGGTTCTAATAGGATCAACCATTTCT
 30 ACTGTGACACCCCGCCACTGCTCAAACCTCTCTTGCTCTGATACCCACTTCAATGGCATTGTG
 ATCATGGCATTCTCAAGTTTATTGTCTCAGCTGTGTTATGATTGCTCCTCATTTCTTACCT
 GTGTATCTTCATTGCCGTCTTGAAGATGCCTTCGTTAGAGGGCAGGCACAAAGCCTTCTCC
 ACCTGTGCCTCTTACCTCATGGCTGTCAACATATTCTTTGGAACAATCCTCTTCATGTACTT
 GCGCCCTACATCTAGCTACTCAATGGAGCAAGACAAGGTTGTCTGTCTTTTATACAGTA
 35 ATAATCCCTGTGCTAAATCCCTCATCTATAGTTAAAAAATAAGGATGTAAAAAAGGCC
 TAAAGAAGATCTTATGGAAACACATCTTGTAG (SEQ ID NO: 298)

AOLFR163 sequences:

MQRSNHTVTEFILLGFTTDPGMQLGLFVFLGVYSLTVVGNSTLIVLICNDLSCLHTPMYFFTG
 40 LSFLDLWYSSVYTPKILVTCISEDKISFAGCLCQFFFSAGLAYSECYLLAAVAYDRYVAISKPL
 LYAQAMSIKLCALLVAVSYCGGFINSSIITKKTFSFNFCRENIIDFFCDLLPLVELACGEKGGYK
 IMMYFLLASNVICPAVLILASYLFIITSVLRISSSKGYLKAFSTCSSHLTSVTLYYGSILYIYALPRS
 SYSFDMDKIVSTFYTVFPMLNLMYSLRNKDVKEALKKLLP (SEQ ID NO: 299)
 45
 ATGCAGAGGAGCAATCATACAGTGAAGTGTATTTACTGCTGGGCTTACCACAGACCCA
 GGAATGCAGCTGGGCCTCTTCGTGGTGTCTCTGGGCGTGAATCTCTCACTGTGGTAGGAA
 ATAGCACCTCATCGTGTGATCTGTAATGACTCCTGCCTCCACACACCCATGTATTTTTTC
 ACTGGAAATCTGTCGTTTCTGGATCTCTGGTATTCTTCTGTCTACACCCCAAAGATCCTAGT
 GACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTGAGTCTCTCTCT
 50 CTGCGAGGCTGGCCTATAGTGAGTGCTACCTGCTGGCTGCCGTGGCTTATGACCGCTACGT
 GGCCATCTCCAAGCCCCTGCTTTATGCCAGGCCATGTCCATAAAGCTGTGTGCATTGCTG
 GTAGCAGTCTCATATTGTGGTGGCTTTATTAACCTCTTCAATCATCACCAGAAAACGTTTTCT
 CTTTAACTTCTGCCGTGAAAACATCATTGATGACTTTTTCTGTGATTGTCTTCCCTTGGTGG
 AGCTGGCCTGTGGCGAGAAGGGCGGCTATAAAATTATGATGTACTTCTGCTGGCCTCCAA
 55 TGTCATCTGCCCCGAGTGCTCATCTGGCCTCCTACCTCTTATCATCACCAGTGTCTTGA
 GGATCTCCTCCTCCAAGGGCTACCTCAAAGCCTTCTCCACATGCTCCTCCACCTGACCTCT

GTCACTTTATACTATGGCTCCATTCTCTACATCTACGCTCTCCCCAGATCTAGCTATTCTTT
TGATATGGACAAAATAGTTTCTACATTTTACACTGTGGTATTCCCCATGTTGAATCTCATG
ATCTACAGCCTAAGGAATAAGGATGTGAAAGAGGCTCTGAAAAACTTCTCCATAA (SEQ
ID NO: 300)

5

AOLFR164 sequences:

MFLTERNTTSEATFTLLGFSDYLELQIPLFFVFLAVYGFSVVGNLGMIVIIKINPKLHTPMYFFLN
HLSFVDFCYSSIIAPMMLVNLVVEDRTISFSGLVQFFFFCTFVVTELILFAVMAYDHFVAICNP
LLYTVAISQKLCAMLVVVLYAWGVACSLTLACSALKLSFHGFNTINHHFCELSLISLSPDSYL
10 SQLLLFTVATFNEISTLLIILTSYAFIIVTTLKMPSASGHRKVFSTCASHLTAITIFHGTLFLYCVP
NSKNRHTVKVASVFYTVVPLLNPLIYSLRNKDVKDAIRKIINTKYFHIKHRHWYPFNFVIEQ
(SEQ ID NO: 301)

ATGTTTCTGACAGAGAGAAATACGACATCTGAGGCCACATTCCTCTCTTGGGCTTCTCAG
15 ATTACCTGGAAGTCAAATTTCCCTCTTCTTTGTATTTCTGGCAGTCTACGGCTTCAGTGTG
GTAGGGAATCTTGGGATGATAGTCATCAAAAATTAACCCAAAATTGCATACCCCCATGT
ATTTTTTCCCTCAACCACCTCTCCTTTGTGGATTTCTGCTATTCTCCATCATTGCTCCCATGA
TGCTGGTGAACCTGGTTGTAGAAGATAGAACCATTTCATTCTCAGGATGTTTGGTGCAATT
CTTTTTCTTTGCACCTTTGTAGTGAATTAATTCTATTTGCGGTGATGGCCTATGACC
20 ACTTTGTGGCCATTTGCAATCCTCTGCTCTACACAGTTGCCATCTCCAGAACTCTGTGCC
ATGCTGGTGGTTGTATTGTATGCATGGGGAGTCGCATGTTCCCTGACACTCGCGTGCTCTG
CTTTAAAGTTATCTTTTCATGGTTTCAACACAATCAATCATTTCTTCTGTGAGTTATCCTCC
CTGATATCACTCTCTTACCCTGACTCTTATCTCAGCCAGTTGCTTCTTTTCACTGTTGCCAC
TTTAAATGAGATAAGCACACTACTCATCTTCTGACATCTTATGCATTATCATTTGTCACCA
25 CCTGAAGATGCCTTCAGCCAGTGGGCACCGCAAAGTCTTCTCCACCTGTGCCTCCACCT
GACTGCCATCACCATCTTCCATGGCACCATCCTCTTCTCTACTGTGTACCCAACTCCAAAA
ACTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGATCCCTGTTGAA
TCCCCTGACTACAGTCTGAGAAATAAAGATGTTAAGGATGCAATCCGAAAAATAATCAAT
ACAAAATATTTTCATATTAAACATAGGCATTGGTATCCATTTAATTTTGTATTGAACAATA
30 A (SEQ ID NO: 302)

AOLFR165 sequences:

MAVGRNNTIVTKFILLGLSDHPQMKIFLFLGLYLLTLAWNLSLIALIKMDSHLHMPMYFFL
SNLSFLDICYVSSSTAPKMLSDIITEQKTSIFVGCATQYFVFCGMGLTECFLLAAMAYDHYAICN
35 PLLYTVLISHTLCLKMVVGAYVGGFLSSFETYSVYQHDFCGPYMINHFFCDLPPVLALSCSDTF
TSEVVTFIVSVVGVSVLVVLISYGYIVA AVVKISSATGRTKAFSTCASHLTA VTLFYGSGFFM
YMRPSSSYSLNRDKVVSIFYALVIPVNPITYSFRNKEIKNAMRKAMERDPGISHGGPFIFMTLG
(SEQ ID NO: 303)

ATGGCTGTAGGAAGGAACAACACAATTGTGACAAAATTCATTCTCCTGGGACTTTCAGACC
40 ATCCTCAAATGAAGATTTTCCCTTTTCATGTTATTTCTGGGGCTCTACCTCCTGACGTTGGCC
TGGAAGCTTAAGCCTCATTGCCCTCATTAAAGATGGACTCTCACCTGCACATGCCCATGTACT
TCTTCTCAGTAACCTGTCTTCTGACATCTGCTATGTGTCTCCACCGCCCTAAGATG
CTGTCTGACATCATCACAGAGCAGAAAACCAATTCCTTTGTTGGCTGTGCCACTCAGTACT
45 TTGTCTTCTGTGGGATGGGGCTGACTGAATGCTTTCTCCTGGCAGCTATGGCCTATGACCG
GTATGCTGCAATCTGCAACCCCTTGCTTTACACAGTCCTCATATCCCATACTTTGTTAA
AGATGGTGGTTGGCGCCTATGTGGGTGGATTCCCTAGTTCTTTCAATTGAAACATACTCTGT
CTATCAGCATGATTTCTGTGGGCCCTATATGATCAACCACTTTTCTGTGACCTCCCTCCAG
TCCTGGCTCTGTCTGCTCTGATACCTTACCAGCGAGGTGGTGACCTTCATAGTCAGTGT
50 GTCGTTGGAATAGTGTCTGTGCTAGTGGTCTCTCTTATGTTACATTGTGCTGTGT
TGTGAAGATCAGCTCAGCTACAGGTAGGACAAAGGCCTTCAGCACTTGTGCTCTCACCTG
ACTGCTGTGACCCTCTTCTATGGTTCTGGATTCTTCATGTACATGCGACCCAGTCCAGCTA
CTCCCTAAACAGGGACAAGGTGGTGTCCATATTCTATGCCTTGGTGATCCCGTGGTGAAT
CCCATCATCTACAGTTTTAGGAATAAGGAGATTA AAAATGCCATGAGGAAAGCCATGGAA
55 AGGGACCCCGGGATTTCTACGGTGGACCATTCTTTTATGACCTTGGGCTAA (SEQ ID
NO: 304)

AOLFR166 sequences:

MEMENCTRVKEFFLGLTQNREVSIVLFLFLLLVYVTTLLGNLLIMVTVTCESRLHTPMYFLLH
 NLSIADICFSSITVPKVLVDLLSERKTISFNHCFTQMFLFHLIGGVDVFSLSVMALDRYVAISKPL
 5 HYATIMSRDHCIGLTVAAWLGGFVHSIVQISLLPLPFCGPNVLDTFYCDVHRVLKLAHTDIFIL
 ELLMISNNGLLTTLWFFLLLVSYIVLSLPKSQAGEGRRKAISTCTSHITVVTLHFVPCIVYVYARP
 FTALPMDKAISVTFVISPLLNPLIYTLRNHEMKSAMRRLKRRLVPSDRK (SEQ ID NO: 305)

ATGGAGATGGAAAACCTGCACCAGGGTAAAAGAATTTATTTTCCTTGGCCTGACCCAGAATC
 10 GGGAAGTGAGCTTAGTCTTATTTCTTTCTACTCTTGGTGTATGTGACAACTTTGCTGGGA
 AACCTCCTCATCATGGTCACTGTTACCTGTGAATCTCGCCTTCACACGCCCATGTATTTTT
 GCTCCATAAATTTATCTATTGCCGATATCTGCTTCTCTTCCATCACAGTGCCCAAGGTTCTGG
 TGGACCTTCTGTCTGAAAGAAAAGACCATCTCCTTCAATCATTGCTTCACTCAGATGTTTCTA
 TTCCACCTTATTGGAGGGGTGGATGTATTTTCTCTTTCGGTGATGGCATTGGATCGATATG
 15 TGGCCATCTCCAAGCCCTGCACTATGCGACTATCATGAGTAGAGACCATTGCATTGGGCT
 CACAGTGGCTGCCTGGTTGGGGGGCTTTGTCCACTCCATCGTGCAGATTTCCCTGTTGCTC
 CCACTCCCTTTCTGCGGACCCAATGTTCTTGACACTTTCTACTGTGATGTCCACGGGGTCT
 CAACTGGCCCATACAGACATTTTCATACTTGAAGTACTAATGATTTCCAACAATGGACTG
 CTCACCACACTGTGGTTTTTCTGCTCCTGGTGTCTACATAGTCATATTATCATTACCCAA
 20 GTCTCAGGCAGGAGAGGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCCACATCACTGT
 GGTGACCCTGCATTTCTGTCCCTGCATCTATGTCTATGCCCGGGCCCTTCACTGCCCTCCCCA
 TGGATAAGGCCATCTCTGTACCTTCACTGTCTATCTCCCTCTGCTCAACCCCTTGATCTAC
 ACTCTGAGGAACCATGAGATGAAGTCAGCCATGAGGAGACTGAAGAGAAGACTTGTGCCT
 TCTGATAGAAAATAG *SEQ ID NO: 306)

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AOLFR167 sequences:

MSITKAWNSSSVTMFILLGFTDHPQLALLFVTFGLGYLTTLAWNLAIFLIRGDTHLHTPMYFF
 LSNLSFIDICYSSAVAPNMLTDFWEQKTISFVGCQAQFFFFVGMGLSECLLLTAMAYDRYAAI
 SSPLLYPTIMTQGLCTRMVVGAYVGGFLSSLIQASSIFRLHFHFCGPNINHHFFCDLPPVLALSCSDT
 30 FLSQVVNFLVVTVGGSFLQLLISYGYIVSAVLKIPSAEGRWKACNTCASHLMVVTLLFGTAL
 FVYLRPSSSYLLGRDKVVSFVSLVPMNLNPLIYSLRNKEIKDALWKVLERKKVFS (SEQ ID
 NO: 307)

ATGTCCATAACCAAAGCCTGGAACAGCTCATCAGTGACCATGTTTCATCCTCCTGGGATTCA
 35 CAGACCATCCAGAACTCCAGGCCCTCCTCTTTGTGACCTTCTGGGCATCTATCTTACCACC
 CTGGCCTGGAACCTGGCCCTCATTTTCTGATCAGAGGTGACACCCATCTGCACACACCCA
 TGTACTTCTTCTTAAGCAACTTATCTTTCTATTGACATCTGCTACTCTTCTGTGGTGTCCC
 AATATGCTCACTGACTTCTTCTGGGAGCAGAAGACCATATCATTGTGGGCTGTGCTGCTC
 AGTTTTTTTTTCTTTGTGCGCATGGGTCTGTCTGAGTGCCTCCTCCTGACTGCTATGGCATA
 40 GACCGATATGCAGCCATCTCCAGCCCCCTTCTTACCCCACTATCATGACCCAGGGCCTCT
 GTACACGCATGGTGGTGGGGCATATGTTGGTGGCTTCTGAGCTCCCTGATCCAGGCCAG
 CTCCATATTTAGGCTTCACTTTTGTGCGGACCCAACATCATCAACCACTTCTTCTGCGACCTCC
 CACCACTCCTGGCTCTGTCTTGTCTGACACCTTCTCAGTCAAGTGGTGAATTTCTCGTG
 GTGGTCACTGTGCGAGGAACATCGTTTCTCCAACCTCCTTATCTCCTATGGTTACATAGTGT
 45 CTGCGGTCTGAAGATCCCTTACGACAGAGGGCCGATGGAAAGCCTGCAACACGTGTGCCT
 CGCATCTGATGGTGGTGAATCTGCTGTTTGGGACAGCCCTTTTCGTGTACTTGGCAGCCAG
 CTCCAGCTACTTGCTAGGCAGGACAAAGTGGTGTCTGTTTCTATTCAATTGGTGTATCCCC
 ATGCTGAACCTCTCATTTACAGTTTGAAGAACAAAGAGATCAAGGATGCCCTGTGGAAG
 GTGTTGGAAAGGAAGAAAGTGTCTTCTTAG (SEQ ID NO: 308)

50

AOLFR168 sequences:

MEKINNVTETIFWGLSQSPEIEKVCFVVSFFYIILLGNLLIMLTVCLSNLFKSPMYFFLSFLSFV
 DICYSSTVAPKMIVDLLAKDKTISYVGCMLQLLGTVHFFGCTEIFILTVMAYDRYVAICKPLHYM
 TIMNRETCKNMLLGTWVGFLHSIIQVALVQLPFCGPNEDHYFCDVHPVLKLACTETIYVG
 55 VVVTANSGLIALGSFVILLISYSIILVSLRKQSAEGRRKALSTCGSHIAMVVIFFGPCTFMYMRPD

TTFSEDKMVAVFYTTITPMLNPLIYTLRNAEVKNAMKKLWGRNVFLEAKGK (SEQ ID NO: 309)

5 ATGGAATAAACAACGTAACCTGAATTCATTTTCTGGGGTCTTTCTCAGAGCCCAGAGA
TTGAGAAAGTTTGTGTTTGTGGTGTCTTTCTTCTACATAATCATTCTTCTGGGAAATCTC
CTCATCATGCTGACAGTTTGCCTGAGCAACCTGTTAAGTCACCCATGTATTTCTTTCTCAG
CTTCTTGTCTTTTGTGGACATTTGTTACTCTTCAGTCACAGCTCCCAAGATGATTGTTGACC
TGTTAGCAAAGGACAAAACCATCTCCTIATGTGGGGTGCATGTTGCAACTGCTGGAGTAC
ATTTCTTTGGTTGCACTGAGATCTTCATCCTTACTGTAATGGCCTATGATCGTTATGTGGCT
10 ATCTGTAAACCCCTACATTATATGACCATCATGAACCGGGAGACATGCAATAAAATGTTAT
TAGGGACGTGGGTAGGTGGGTCTTACACTCCATTATCCAAGTGGCTCTGGTAGTCCAACCT
ACCCTTTTGTGGACCAATGAGATAGATCACTACTTTTGTGATGTTCAACCTGTGTTGAAA
CTTGCTGCACAGAAACATACATTGTTGGTGTGTTGTGACAGCCAACAGTGGTACCATTG
CTCTGGGGAGTTTGTATCTTGCTAATCTCCTACAGCATCATCCTAGTTTCCCTGAGAAAG
15 CAGTCAGCAGAAGGCAGGCGCAAAGCCCTCTCCACCTGTGGCTCCCACATTGCCATGGTCCG
TTATCTTTTTCGGCCCCTGTACTTTTATGTACATGCGCCCTGATACGACCTTTTCAGAGGAT
AAGATGGTGGCTGTATTTTACACCATTATCACTCCCATGTTAAATCCTCTGATTTATACACT
GAGAAATGCAGAAGTAAAGAATGCAATGAAGAAACTGTGGGGCAGAAATGTTTTCTTGGA
GGCTAAAGGGAAATAG (SEQ ID NO: 310)

20

AOLFR169 sequences:

MMDNHSSATEFHLLGFFPSQGLHHILFAIFFFFYLVTLMGNTVIIIVVCVDKRLQSPMYFFLSHL
STLEILVTIIVPMMLWGLLFLGCRQYLSLHVS LNFCGTM EFALLGVMAVD RYVAVCNPLRY
NIIMNSSTCIWVVIVSWVFGFLSEIWPIYATFQFTFRKSNSLDHFYCDRGQLLKS DNTLLTEFI
25 LFLMAVFILIGSLIPTVSYTYIISTILKIPSASGRRKAFSTFASHFTCVVIGYGSCLFLYVKPKQTQ
GVEYNKIVSLLVSVLTPFLNPFIFTLRNDKVKEALRDGMKRCCQLLD (SEQ ID NO: 311)

ATGATGGACAACCACTCTAGTGCCACTGAATTCACCTTCTAGGCTTCCCTGGGTCCCAAG
GACTACACCACATTCTTTTGTCTATATTCTTTTCTTCTATTTAGTGACATTAATGGGAAAC
30 ACGGTCATCATTTGTGATTGTCTGTGTGGATAAACGTCTGCAGTCCCCATGTATTTCTTCTCT
CAGCCACCTCTCTACCCCTGGAGATCCTGGTCACAACCATAATTGTCCCCATGATGCTTTGG
GGATTGCTCTTCTGGGATGCAGACAGTATCTTTCTCTACATGTATCGCTCAACTTTTCTCTG
TGGGACCATGGAGTTTGCACTTCTGGAGTGATGGCTGTGGACCGTTATGTGGCTGTGTGT
AACCCTTTGAGGTACAACATCATTATGAACAGCAGTACCTGTATTTGGGTGGTAATAGTGT
35 CATGGGTGTTTGGATTCTTTCTGAAATCTGGCCCATCTATGCCACATTTACGTTTACCTTC
CGAAATCAAATTCATTAGACCATTTTTACTGTGACCGAGGGCAATTGCTCAAACCTGTCCT
GCGATAACACTCTTCTCACAGAGTTTATCCTTTTCTTAATGGCTGTTTTTATTCTCATTGGT
TCTTTGATCCCTACGATTGTCTCTCTACACCTACATTATCTCCACCATCCTCAAGATCCCGTC
AGCCTCTGGCCGGAGGAAAGCCTTCTCCACTTTTGCTCCCACTTCACCTGTGTTGTGATTG
40 GCTATGGCAGCTGCTTGTCTCTACGTGAAACCAAGCAAAACACAGGGAGTTGAGTACAA
TAAGATAGTTTCCCTGTTGGTTTCTGTGTTAACCCCTTCCTGAATCCTTTCATCTTTACTCT
TCGGAATGACAAAGTCAAAGAGGCCCTCCGAGATGGGATGAAACGCTGCTGTCAACTCCT
GAAAGATTAG (SEQ ID NO: 312)

AOLFR170 sequences:

MSFTSLPSLCFSLTLPFLFCYLSLLPFLSAFLFITRWLLAFLSLFSVSVPVSSVSSSMVLCLYLSVS
ASPSVFCFSCMQGPILWIMANLSQPSEFVLLGFSSFGELQALLYGPFLMLYLLAFMGNTIIIVMVI
ADTHLHTPMYFFLGNFSLLEILVTMTAVPRMLSLLVPHKVITFTGCMVQFYFHFSLGSTSFLIL
TDMALDRFVAICHPLRYGTLMSRAMCVQLAGAAWAAPFLAMVPTVLSRAHLDYCHGDVINH
50 FFCNDNEPLLQLSCSDTRLLEFWDLFMALTFVLSFLVTLISYGYVTTVLRIPSASSCQKAFSTCG
SHLTLVFIGYSSTIFLYVRPGKAHSVQVRKVVALVTSVLTPFLNPFILTCNQTVKTVLQGMQ
RLKGLCKAQ (SEQ ID NO: 313)

55 ATGTCCTTTCACCTTCTCTCATACCCCTCACTCTGTTTCTCCTTGACTCTCCCATTCCTGTTTTGT
TATCTTTCTTTATTGCCGTTTCTTTCTGCTTTTCTGTTTATCACTCGCTGGCTACTTGCCCTT
CTCTCTCTATTCTCTGTCTCTGTCCCTGTTTCTTCTGTTTCAAGTTCAATGGTTCTCTGTCTC

TATCTCTCTGTTTCTGCCTCTCCGTCTGTCTTTTGTCTTCTTGCATGCAGGGCCCCATACTG
 TGGATCATGGCAAATCTGAGCCAGCCCTCCGAATTTGTCTCTTGGGCTTCTCCTCCTTTGG
 TGAGCTGCAGGCCCTTCTGTATGGCCCCCTTCCTCATGCTTTATCTTCTCGCCTTCATGGGAA
 ACACCATCATCATAGTTATGGTCATAGCTGACACCCACCTACATACACCCATGTACTTCTTC
 5 CTGGGCAATTTTCCCTGCTGGAGATCTTGGTAACCATGACTGCAGTGCCAGGATGCTCT
 CAGACCTGTTGGTCCCCACAAAGTCATTACCTTCACTGGCTGCATGGTCCAGTTCTACTTC
 CACTTTTCCCTGGGGTCCACCTCCTTCTCATCTGACAGACATGGCCCTTGATCGCTTTGT
 GGCCATCTGCCACCCACTGCGCTATGGCACTCTGATGAGCCGGGCTATGTGTGTCCAGCTG
 GCTGGGGCTGCCTGGGCAGCTCCTTTCCCTAGCCATGGTACCCACTGTCTCTCCCGAGCTC
 10 ATCTTGATTACTGCCATGGCGACGTCATCAACCACTTCTTCTGTGACAATGAACCTCTCCTG
 CAGTTGTCATGCTCTGACACTCGCCTGTTGGAATTCCTGGGACTTTCTGATGGCCTTGACCTT
 TGTCTCAGCTCCTTCTGCTGACCTCATCTCCTATGGCTACATAGTGACCACTGTGCTGC
 GGATCCCCCTCTGCCAGCAGCTGCCAGAAGGCTTTCTCCACTTGCGGGTCTCACCTCACACT
 GGTCTTCATCGGCTACAGTAGTACCATCTTCTGTATGTCAGGCCTGGCAAAGCTCACTCT
 15 GTGCAAGTCAGGAAGGTCGTGGCCTTGGTGACTTCAGTTCTCACCCTTTCTCAATCCCT
 TTATCCTTACCTTCTGCAATCAGACAGTTAAAACAGTGCTACAGGGGGCAGATGCAGAGGCT
 GAAAGGCCTTTGCAAGGCACAATGA (SEQ ID NO: 314)

AOLFR171 sequences:

20 MVGNLLIWVTTIGSPSLGSLMYFFLAYLSLMDAISTAMSPKLMIDLLCDKIAISLSACMGQLFI
 EHLLGGAEVFLVVMAYDRYVAISKPLHYLNIMNRLVCILLVAMIGGFVHSVQIVFLYSLP
 ICGPNVIDHSVCDMYPLELLCLDTYFIGLTVVANGGIICMVIFTLLISCGVILNFLKTYSQEER
 HKALPTCISHIIVVALVFVPCIFMYVRPVSNFPDKLMTVFYSITLMLNPLIYSLRQSEMKNAM
 KNLWCEKLSIVRKRVSPTLNFIPSSKATNRR (SEQ ID NO: 315)

25 ATGGTGGGAAACCTCCTCATTTGGGTGACTACTATTGGCAGCCCCCTCCTTGGGCTCCCTAA
 TGTACTTCTTCCCTTGCCACTTGTCACTTATGGATGCCATATATTCCACTGCCATGTCACCC
 AAATTGATGATAGACTTACTCTGTGATAAAATCGCTATTTTCTTGTGAGCTTGCATGGGTC
 AGCTCTTCATAGAACACTTACTTGGTGGTGCAGAGGTCTTCTTTTGGTGGTGATGGCCTA
 30 TGATCGCTATGTGGCTATCTTAAGCCGCTGCACTATTTGAACATCATGAATCGACTGGTT
 TGCATCCTTCTGTTGGTGGTGGCCATGATTGGAGGTTTTGTGCACTCTGTGGTTCAAATTGT
 CTTTCTGTACAGTCTACCAATCTGTGGCCCCAATGTTATTGACCACTCTGTCTGTGACATGT
 ACCCATTGTTGGAACCTGTTGTGCCCTTGACACCTACTTTATAGGACTCACTGTGGTTGCCAA
 TGGTGGAAATAATTTGTATGGTCATCTTTACCTTTCTGCTAATCTCCTGTGGAGTCATCCTAA
 35 ACTTCCTTAAACCTTACAGTCAGGAAGAGAGGCATAAAGCCCTGCCTACCTGCATCTCCCA
 CATCATTGTGGTTGCCCTCGTTTTTGTTCCTGTATTTTATGTATGTTAGACCCGTTTCCA
 ACTTTCCCTTTGATAAATTAATGACTGTGTTTTATTCAATTATCACACTCATGTTGAATCCT
 TTAATATACTCGTTGAGACAATCAGAGATGAAAAATGCTATGAAAAATCTCTGGTGTGAA
 AAGTTAAGTATAGTTAGAAAAAGAGTATCTCCCACTGAACATATTTATTCCTAGTTCTA
 40 AGGCAACAAATAGGCGGTAA (SEQ ID NO: 316)

AOLFR172 sequences:

MAETLQLNSTFLHPNFILTGFPGLGSAQTWLTLVFGPIYLLALLGNGALPAVVWIDSTLHQPM
 FLLAILAATDLGLATSIAPGLLAVLWLGPRSVPYAVCLVQMFFVHALTAMESGVLLAMACDR
 45 AAAIGRPLHYVPLVTKACVGYAALALALKAVAIIVFPPLLVAKFHFQAKTIGHTYCAHMAV
 VELVVGNTQATNLYGLALSIAISGMDILGITGSYGLIAHAVLQLPTREAHAKAFGTCSSHICVIL
 AFYIPGLFSYLAHFRFGHHTVPKPVHILLSNIYLLPPALNPLIYGARTKQIRDRLLTFTFRKSPL
 (SEQ ID NO: 317)

50 ATGGCAGAAACTCTACAACCTCAATTCCACCTTCTACACCCAAACTTCTTCATACTGACTG
 GCTTTCCAGGGCTAGGAAGTGCCAGACTTGGCTGACACTGGTCTTTGGGCCCCATTTATCT
 GCTGGCCCTGCTGGGCAATGGAGCACTGCCGGCAGTGGTGTGGATAGACTCCACACTGCA
 CCAGCCCATGTTTCTACTGTTGGCCATCCTGGCAGCCACAGACCTGGGCTTAGCCACATCT
 ATAGCCCCAGGGTTGCTGGCTGTGCTGTGGCTTGGGCCCCGATCTGTGCCATATGCTGTGT
 55 GCCTGGTCCAGATGTTCTTTGTACATGCACTGACTGCCATGGAATCAGGTGTGCTTTTGGC
 CATGGCCTGTGATCGTGCTGCGGCAATAGGGCGTCCACTGCACTACCCTGTCTGGTCACC

AAAGCCTGTGTGGGTTATGCAGCCTTGCCCTGGCACTGAAAGCTGTGGCTATTGTTGTAC
 CTTTCCCACTGCTGGTGGCAAAGTTTGAGCACTTCCAAGCCAAGACCATAGGCCATACCTA
 TTGTGCACACATGGCAGTGGTAGAACTGGTGGTGGGTAACACACAGGCCACCAACTTATA
 TGGTCTGGCACTTCACTGGCCATCTCAGGTATGGATATTCTGGGTATCACTGGCTCCTAT
 5 GGACTCATTGCCCATGCTGTGCTGCAGCTACCTACCGGGAGGCCCATGCCAAGGCCTTTG
 GTACATGTAGTTCTCACATCTGTGTCATTCTGGCCTTCTACATACCTGGTCTCTTCTCCTAC
 CTCGCACACCGCTTTGGTCATCACACTGTCCCAAAGCCTGTGCACATCCTTCTCTCCAACAT
 CTACTTGCTGCTGCCACCTGCCCTCAACCCCTCATCTATGGGGCCCCGACCAAGCAGATC
 AGAGACCGACTCCTGGAAACCTTCACATTTCAGAAAAAGCCCGTTGTAA (SEQ ID NO: 318)

10

AOLFR173 sequences:

MSHTNVITFHPAVFVLPGPGLAAYHIWLSIPLCLIYTTAVLGNLSILVIVMERNLHVPMPYFFLS
 MLAVMDILLSTTTVPKALAI FWLQAHNIAFDACVTQGGFVHMMFVGESAILLAMAFDRFVAIC
 APLRYTTVLTWPVVGRIALAVITRSCIFPVIFLLKRLPFCLTNIVPHSYCEHIGVARLACADITV
 15 NTWYGFSPVIVMVILDVILIAVSYSLLRAVFLPSQDARHKALSTCGSHLCVILMFYVPSFFTL
 THHFRNIPQHVHILLANLYVAVPPMLNPVYGVKTKQIREGVAHRFFDIKTWCCTSP LGS
 (SEQ ID NO: 319)

ATGAGTCACACCAATGTTACCATCTTCCATCCTGCAGTTTTTGTCTTCTGGCATCCCTGG
 20 GTTGGAGGCTTATCACATTTGGCTGTCAATACCTCTTTCCTCATTTACATCACTGCAGTCC
 TGGGAAACAGCATCCTGATAGTGGTTATTGTCATGGAACGTAACCTTCATGTGCCCATGTA
 TTTCTTCTCTCAATGCTGGCCGTCATGGACATCCTGCTGTCTACCACCACTGTGCCCAAGG
 CCCTAGCCATCTTTTGGCTTCAAGCACATAACATTGCTTTTGATGCCTGTGTACCCAAAGG
 TTCTTTGTCCATATGATGTTTGTGGGGGAGTCAGCTATCCTGTTAGCCATGGCCTTTGATCG
 25 CTTTGTGGCCATTTGTGCCCCACTGAGATATACAACAGTGCTAACATGGCCTGTTGTGGGG
 AGGATTGCTCTGGCCGTCATCACCCGAAGCTTCTGCATCATCTTCCCAGTCATATTCTTGCT
 GAAGCGGCTGCCCTTCTGCCTAACCAACATTGTTCTCACTCCTACTGTGAGCATATTGGA
 GTGGCTCGTTTAGCCTGTGCTGACATCACTGTAAACATTTGGTATGGCTTCTCAGTGCCCAT
 TGTATGGTCATCTTGGATGTTATCCTCATCGCTGTGTCTTACTCACTGATCCTCCGAGCAG
 30 TGTTTCGTTTGCCTCCCAGGATGCTCGGCACAAGGCCCTCAGCACTTGTGGCTCCACCT
 CTGTGTCATCCTTATGTTTTATGTTCCATCCTTCTTTACCTTATTGACCCATCATTTTGGGCG
 TAATATTCTCAACATGTCCATATCTTGCTGGCCAATCTTTATGTGGCAGTGCCACCAATGC
 TGAACCCCATTTGCTATGGTGTGAAGACTAAGCAGATACGTGAGGGTGTAGCCACCGGTT
 CTTTGACATCAAGACTTGGTGCTGTACCTCCCCTCTGGGCTCATGA (SEQ ID NO: 320)

35

AOLFR175 sequences:

MHFLSQNDLNLINLPHLCLHRHSVIAGAFTIHRHMKIFNSPNSSTFTGFILLGFPCPREGQILLFV
 LFTVVYLLTLMGNGSIICAVHWDQRLHAPMYILLANFSFLEICYVTSTVPSMLANFLSDTKIISF
 SGCFLQFYFFSLGSTECFFLA VMAFDRLAJCRPLRYPTIMTRRLCTNLVVCNWVLGFIWFLPI
 40 VNISQMSFCGSRIDHFLCDPAPLLTLTCKKGPVIELVFSVLSPLPVFMLFLFIVGSYALVVRVIL
 RVPSAAGRRKAFSTCGSHLAVVSLFYGSVLVVMYGSPPSKNEAGKQKTVTLFYSVVTPLLNPVI
 YSLRNKDMRKALKKFWGT (SEQ ID NO: 321)

ATGCATTTTCTTTCCCAAATGATTTAAATATAAATCTGATTCCCCATCTATGTTTGCACCG
 45 TCATTAGTAATTGCTGGTGCTTTTACAATTCACAGGCACATGAAAATCTTCAACAGCCCC
 AGCAACTCCAGCACCTTCACTGGCTTCATCCTCCTGGGCTTCCCTTGCCCCAGGGAGGGGC
 AGATCCTCCTCTTTGTGCTCTTCACTGTTGTTTACCTCCTGACCCTCATGGGCAATGGTTCC
 ATCATCTGTGCTGTGCACTGGGATCAGAGACTCCACGCCCCCATGTACATCCTGCTCGCCA
 ACTTCTCCTTCTGGAGATATGTTATGTCACTCCACAGTCCCAGCATGCTGGCCAACTTC
 50 CTCTCTGACACCAAGATCATCTCGTCTCTGGCTGCTTCCCTCCAGTTCTACTTTTCTTCTCC
 TTGGGCTCTACAGAATGCTTTTCTGCGCAGTTATGGCATTGATCGATACCTTGCCATCTG
 TCGGCCTCTACGCTATCCAACCATTATGACCAGACGTCTCTGTACCAATCTTGTGGTCAATT
 GCTGGGTACTTGGTTTCATCTGGTTCTTGATTCTATCGTCAACATCTCCCAAATGTCCTTC
 TGTGGATCTAGGATTATTGACCACTTCCTATGTGACCCAGCTCCTCTTCTAACTCTCACTTG
 55 CAAAAAAGGCCCTGTGATAGAGCTTGTCTTTTCTGTCTTAAGTCCTCTGCCTGTCTTTATGC
 TCTTCTCTTCATTGTGGGGTCTATGCTCTGGTCTGTGAGAGCTGTGTTGAGGGTCCCTTCA

GCAGCTGGGAGAAGAAAGGCTTTCTCCACCTGTGGGTCTCACCTGGCTGTGGTTTCACTGT
TCTACGGCTCAGTACTGGTCATGTATGGGAGCCCAACATCTAAGAATGAAGCTGGAAAGC
AGAAGACTGTGACTCTGTTTTATTCTGTTGTTACCCCACTGCTTAACCCTGTGATATATAGT
CTTAGGAACAAAGATATGAGAAAAGCTCTGAAGAAATTTGGGGAACATAA (SEQ ID NO:
5 322)

AOLFR176 sequences:

MFFIIHSLVTSVFLTALGPQNRTHFVTEFVLLGFHGQREMQSCFFSFILVLYLLTLLGNGAIVC
AVKLDRLHTPMYILLGNFAFLEIWYISSTVPNMLVNILSEIKTISFSGCFLQFYFFFSLGTTCEFF
10 LSV MAYDRYLAICRPLHYPSIMTGKFCILVCVCWVGGLFCYPVPIVLISQLPFCGPNIDHLVCD
PGPLFALACISAPSTELICYTFNSMIIFGPFLSILGSYTLVIRAVLCIPSGAGRTKAFSTCGSHLMV
VSLFYGTLMVMYVSPTSNGNPMQKIITLVYTAMTFFLNPLIYSLRNKDMKDALKRVLGLTVS
QN (SEQ ID NO: 323)

15 ATGTTCTTTATTATTTCATTCTTTGGTTACTTCTGTTTTTCTAACAGCTTTGGGACCCAGAA
CAGAACAATGCATTTTGTGACTGAGTTTGTCTCTGCTGGGTTTCCATGGTCAAAGGGAGATG
CAGAGCTGCTTCTTCTCATTTCATCCTGGTTCTCTATCTCTGACACTGCTAGGGAATGGAGC
TATTGTCTGTGCAGTGAAATTGGACAGGCGGCTCCACACACCCATGTACATCCTTCTGGGA
AACTTTGCCTTTCTAGAGATCTGGTACATTTCTCTCACTGTCCCAAACATGCTAGTCAATAT
20 CCTCTCTGAGATTAAAACCATCTCCTTCTCTGGTTGCTTCTGCAATTCTATTTCTTTTTTC
ACTGGGTACAACAGAGTGTCTTTTATCAGTTATGGCTTATGATCGGTACCTGGCCATC
TGTCGTCCATTACACTACCCCTCCATCATGACTGGGAAGTTCTGTATAATTCTGGTCTGTGT
ATGCTGGGTAGGCGGATTTCTCTGCTATCCAGTCCCTATTGTTCTTATCTCCCAACTTCCCT
TCTGTGGGCCCAACATCATTGACCACTTGGTGTGTGACCCAGGCCCATGTTTGCACCTGGC
25 CTGCATCTCTGCTCCTTCCACTGAGCTTATCTGTTACACCTTCAACTCGATGATTATCTTTG
GGCCCTTCTCTCCATCTTGGGATCTTACACTCTGGTCATCAGAGCTGTGCTTTGTATATCCC
TCTGGTCTGGTGAACCTTATGGTGATGTATGTGAGCCCAACATCAGGGAACCCAGCAGGAAT
TATTCTATGGAACCTTATGGTGATGTATGTGAGCCCAACATCAGGGAACCCAGCAGGAAT
GCAGAAGATCATCACTCTGGTATACACAGCAATGACTCCATTCTTAAATCCCTTATCTAT
30 AGTCTTCGAAACAAAGACATGAAAGATGCTCTAAAGAGAGTCCTGGGGTTAACAGTTAGC
CAAACTGA (SEQ ID NO: 324)

AOLFR177 sequences:

MSFFFVDLRPMNRSATHIVTEFILLGFPGCWKIQIFLSLFLVIYVLTLLGNGAIIYAVRCNPLLH
35 TPMYFLLGNFAFLEIWYVSSSTIPNMLVNILSKTKAISFSGCFLQFYFFFSLGTTCECLFLAVMAYD
RYLAICHPLQYPAIMTVRFCGKLVSF CWLIGFLGYPIPIFYISQLPFCGPNIDHFLCDMDPLMAL
SCAPAPITECIFYTQSSLVLFSTSMYILRSYILLTAVFQVPSAAGRRKAFSTCGSHLVVVSIFYG
TVMVMYVSPTYGIPTLLQKILTLVSVTTPLEFNPLIYTLRNKDMKLALRNVLFGMRIRQNS
(SEQ ID NO: 325)

40 ATGTCTTTCTTCTTTGTAGACTTAAGACCCATGAACAGGTCAGCAACACACATCGTGACAG
AGTTTATTCTCTGCGGATTCCCTGGTTGCTGGAAGATTGAGATTTTCTCTTCTCATTGTTT
TTGGTGATTTATGTCTTGACCTTGCTGGGAAATGGAGCCATCATCTATGCAGTGAGATGCA
ACCCACTACTACACACCCCATGTACTTTCTGCTGGGAAATTTGCCTTCTTGTAGATCTGG
45 TATGTGCTCTCACTATTCTAACATGCTAGTCAACATTCTCTCCAAGACCAAGGCCATCTC
ATTTTCTGGGTGCTTCTCTCAGTTCTATTTCTTCTTTTCACTGGGAACAACCTGAATGTCTCT
TTCTGGCAGTAATGGCTTATGATCGATACCTGGCCATCTGCCACCCACTGCAGTACCCTGC
CATCATGACTGTAAGGTTCTGTGGTAAGCTGGTGTCTTTCTGTTGGCTTATTGGATTCTTGT
GATACCCAATTCCCATTTTCTACATCTCCCAACTCCCTTCTGTGGTCCTAATATCATTGAT
50 CACTTCTGTGTGACATGGACCCATTGATGGCTCTATCCTGTGCCCCAGCTCCCACTCACTG
AATGTATTTTCTATACTCAGAGCTCCCTTGTCTCTTTTCACTAGTATGTACATTCTTCGA
TCCTATATCCTGTTACTAACAGCTGTTTTTCAGGTCCCTTCTGCAGCTGGTCGGAGAAAAG
CCTTCTCTACCTGTGGTTCTCATTTGGTTGTGGTATCTCTTTCTATGGGACAGTCATGGTA
ATGTATGTAAGTCTACATATGGGATCCCAACTTTATTGCAGAAGATCCTCACACTGGTAT
55 ATTCAGTAACGACTCTCTTTTAACTCTGATCTATACTCTCGTAATAAGGACATGAAA

CTCGCTCTGAGAAATGTCCTGTTTGAATGAGAATTCGTCAAAATTCGTGA (SEQ ID NO: 326)

AOLFR178 sequences:

5 MVGANHSVVSEFVFLGLTNSWEIRLLLLVFSSMFYMASMMGNSLILLTVTSDPHLHSPMYFLL
ANLSFIDLGVSSVTSPKMIYDLFRKHEVISFGGCIQIFFIHVIGGVEMVLLIAMAFDRYVAICKP
LQYLITMSPRMCMFFLVAAWVTGLIHSVVLVFNLPFCGPNVSDSFYCDLPRFIKLACTDSY
RLEFMVTANSFISLGSFFILIISYVVILTVLKHSSAGLSKALSTLSAHVSVVVLFFGPLIFVYTW
PSPSTHLDKFLAIFDAVLTPVLNPIYTFRN (SEQ ID NO: 327)

10 ATGGTTGGGGCAAATCACTCCGTGGTGTGAGAGTTTGTGTTCTCTGGGACTCACCAATTCCT
GGGAGATCCGACTTCTCCTCCTTGTGTTCTCCTCCATGTTTACATGGCCAGTATGATGGGA
AACTCTCTCATTTTGTCACTGTGACTTCTGACCCTCACTGCACTCCCCCATGTATTTTCT
GTTAGCCAACCTCTCCTTCATTGACCTGGGTGTTTCTCTGTCACTTCTCCCAAATGATTT
15 ATGACCTGTTTCAAGAACGACGAAGTCATCTCCTTTGGAGGCTGCATCGCTCAAATCTTCTT
CATCCACGTCATTGGCGGTGTGGAGATGGTGCTGCTCATAGCCATGGCCTTTGACAGATAT
GTGGCCATATGTAAGCCCTCCAGTACCTGACCATTATGAGCCCAAGAATGTGCATGTTCT
TCTTAGTGGCTGCCTGGGTGACCGGCCTTATCCACTCTGTAGTTCAATTGGTTTTTGTAGTA
AACTTGCCCTTCTGTGGTCTAATGTATCGGACAGCTTTTACTGTGACCTTCTCGGTTTCAT
20 CAAACTTGCTGCACAGACAGCTACCGACTGGAGTTCATGGTTACAGCCAACAGTGGATTCT
ATCTCTCTGGGCTCCTTCTTCATACTGATCATTTCTATGTGGTTCATCATTCTCACTGTTCT
GAAACACTCTTCAGCTGGTTTATCCAAGGCTCTGTCCACCCTTTCACTCAGCTCAGTGTG
GTAGTTTTGTTCTTTGGTCTTTGATTTTTGTCTATACGTGGCCATCTCCCTCCACACACCT
GGATAAGTTTCTGGCCATCTTTGATGCAGTCTCTCACTCCTGTTTTAAATCCTATCATCTACA
25 CATTGAGGAATTGA (SEQ ID NO: 328)

AOLFR179 sequences:

MNGMNHSVVSEFVFMGLTNSREIQLLLFVFSLLFYFASMMGNLVIVFTVTMDAHLHSPMYFLL
ANLSIIDMAFCSITAPKMICDIFKKHKAISFRGCITQIFFSHALGGTEMVLLIAMAFDRYMAICKP
30 LHYLTITMSPRMCLYFLATSSIIGLIHSVLVFNVDLPFCGPNIFDSFYCDLPRLLRLACTNTQEL
EFMVTVNSGLISVGSFVLLVISYIFLFTVWKHSSGGLAKALSTLSAHVTVVILFFGPLMFFYTW
PSPSTHLDKYLAIFDAFITPFLNPVIYTFRNKDMKVAMRRLCSRLAHFTKIL (SEQ ID NO: 329)

35 ATGAATGGAATGAATCACTCTGTGGTATCAGAATTTGTATTTCATGGGACTCACCAACTCAC
GGGAGATTCAGCTTCTACTTTTGTCTTCTTGTGTTCTACTTTGCGAGCATGATGGGA
AACCTTGTCAATTGATTCATGTAACCATGGATGCTCATCTGCACTCCCCCATGTATTTCT
CCTGGCTAACCTCTCAATCATTGATATGGCATTITGCTCAATTACAGCCCCTAAGATGATTT
GTGATATTTCAAGAAGCACAAGGCCATCTCCTTTGCGGGATGTATTACTCAGATCTTCTT
TAGCCATGCTCTTGGGGCACTGAGATGGTGCTGCTCATAGCCATGGCCTTTGACAGATAC
40 ATGGCCATATGTAAACCTCTCCACTACCTGACCATCATGAGCCCAAGAATGTGTCTATACT
TTTAGCCACTTCTCTATCATTGGCCTTATCCACTCATTGGTCCAATTAGTTTTTGTGGTA
GATTTACCTTTTTGTGGTCTAATATCTTTGACAGTTTTTACTGTGATCTCCCTCGGCTCCT
CAGACTTGCTGTACCAACACCCAAGAAGTGGAGTTCATGGTCACTGTCAATAGTGGACTC
ATTTCTGTGGGCTCCTTTGTCTTGCTGGTAATTTCTACATCTTCATTCTGTTCAGTGTG
45 GAAACATCTTCTGGTGGTCTAGCCAAGGCCCTCTCTACCTGTGAGCTCATGTCACTGTG
GTCATCTTGTCTTTGGGCCACTGATGTTTTCTACACATGGCCTTCTCCACATCACACCT
GGATAAATATCTTGCTATTTTTGATGCATTTATTACTCCTTTTCTGAATCCAGTTATCTACA
CATTGAGGAACAAAGACATGAAAGTGGCAATGAGGAGACTGTGCAGTCGTCTTGCGCATT
TTACAAAGATTTGTAA (SEQ ID NO: 330)

50

AOLFR180 sequences:

MTNKMAYIYIKNLNYFSFLIVQCLQPTMAIFNNTTSSSSNFLLTAFPGLECAHVWISIPVCCLYTI
ALLGNSMIFLVIITKRRRLHKPMYYFLSMLAAVDLCLTITLPTVLGVLWFHAREISFKACFIQMF
FVHAFSLLESSVLVAMAFDRFVAICNPLNYATILTDRMVLVIGLVICIRPAVFLPLLVAINTVSF
55 HGGHELSHPFYHPEVIKYTYSKPWISSFWGLFLQLYLNGLTDVLFILFSYVLILRTVLGIVARKK

QQKALSTCVCHICAVTIFYVPLISLSLAHRLFHSTPRVLCSTLANIYLLPVLNPIIYSLKTKTIR
QAMFQLQSKGSWGFNVRGLRGRWD (SEQ ID NO: 331)

5 ATGACTAATAAAATGTATGCTATATATATAAAGAATCTTAATTATTTTCTTTCCTCATAGT
TCAGTGTCTTCAACCAACCATGGCAATATTCAATAACACCACTTCGTCTTCTCAAACCTCC
TCCTCACTGCATTCCCTGGGCTGGAATGTGCTCATGTCTGGATCTCCATTCCAGTCTGCTGT
CTCTACACCAATTGCCCTCTTGGGAAACAGTATGATCTTTCTTGTCACTACTAAGCGGA
GACTCCACAAACCCATGTATTATTTCTCTCCATGCTGGCAGCTGTTGATCTATGTCTGACC
10 ATTACGACCCTTCCCACTGTGCTTGGTGTTCTCTGGTTTCATGCCCCGGGAGATCAGCTTTAA
AGCTTGCTTCATTCAAATGTTCTTTGTGCATGCTTTCTCCTTGCTGGAGTCCCTCGGTGCTGG
TAGCCATGGCCTTTGACCGCTTCGTGGCTATCTGTAACCCACTGAACTATGCTACTATCCTC
ACAGACAGGATGGTCTGGTGATAGGGCTGGTCATCTGCATTAGACCAGCAGTTTCTTAC
TTCCCTTCTTGTAGCCATAAACACTGTGTCTTTTCATGGGGGTCACGAGCTTTCCCATCCA
TTTGTCTACCACCCAGAAGTGATCAAATACACATATTCCAAACCTTGGATCAGCAGTTTTT
15 GGGGACTGTTTCTTCAGCTCTACCTGAATGGCACTGACGTATTGTTTATTCTTTCTCCTAT
GTCCTGATCCTCCGTACTGTTCTGGGCATTGTGGCCCCGAAAGAAGCAACAAAAAGCTCTCA
GCACTTGTGTCTGTACATCTGTGCAGTCACTATTTTCTATGTGCCACTGATCAGCCTCTCT
TTGGCACACCGCCTCTTCCACTCCACCCCAAGGGTGCTCTGTAGCACTTTGGCCAATATTTA
TCTGCTCTTACCACCTGTGCTGAACCTATCATTACAGCTTGAAGACCAAGACAATCCGC
20 CAGGCTATGTTCCAGCTGCTCCAATCCAAGGGTTCATGGGGTTTAAATGTGAGGGGTCTTA
GGGGAAGATGGGATTGA (SEQ ID NO: 332)

AOLFR181 sequences:

25 MSVLNNSEVKLFLGIPGLEHAHIWFSIPICLMYLLAIMGNCTILFIKTEPSLHEPMYYFLAML
AVSDMGLSLSSLPTMLRVFLFNAMGISPNACFAQEFFIHGFTVMESSVLLIMSLDRFLAIHNPLR
YSSILTSNRVAKMGLILAIRSILLVIPFFTLRLKLYCQKNLLSHSYCLHQDTMKLACSDNKTNV
IYGFIALCTMLDLALIVLSYVLILKTLISLASLAERLKALNTCVSHICAVLTFYVPIITLAAMHHF
AKHKSPLVVILIADMFLVPLMNPVIVYCVKTRQIWEKILGKLLNVCGR (SEQ ID NO: 333)

30 ATGTCTGTTCTCAATAACTCCGAAGTCAAGCTTTTCTTCTGATTGGGATCCCAGGACTGG
AACATGCCACATTGGTTCTCCATCCCCATTGGCTCATGTACCTGCTTGCCATCATGGGC
AAGTGCACCATTTCTTTATTATAAAGACAGAGCCCTCGCTTCATGAGCCCATGTATTATTT
CCTTGCCATGTTGGCTGTCTCTGACATGGGCCTGTCCCTCTCCTCCCTTCTACCATGTTGA
GGGTCTTCTTGTCAATGCCATGGGAATTTACCTAATGCCTGCTTTGCTCAAGAATCTTCTC
35 ATTCATGGATTCACTGTGCATGGAATCCTCAGTACTTCTAATTATGTCTTTGGACCGCTTTCT
TGCCATTACAATCCCTTAAGATACAGTTCTATCCTCACTAGCAACAGGGTTGCTAAAATG
GGACTTATTTTAGCCATTAGGAGCATTCTCTTAGTGATTCCATTTCCCTTACCTTAAGGAG
ATTAAAATATTGTCAAAAGAATCTTCTTTCTCACTCATACTGTCTTCATCAGGATACCATGA
AGCTGGCCTGCTCTGACAACAAGACCAATGTCATCTATGGCTTCTTCATTGCTCTCTGTACT
40 ATGCTGGACTTGGCACTGATTGTTTTGTCTTATGTGCTGATCTTGAAGACTATACTCAGCAT
TGCATCTTTGGCAGAGAGGCTTAAGGCCCTAAATACCTGTGTCTCCACATCTGTGCTGTG
CTCACCTTCTATGTGCCATCATCACCTGGCTGCCATGCATCACTTTGCCAAGCACAAAA
GCCCTCTTGTGTGATCCTTATTGCAGATATGTTCTTGTGTTGGTGCCGCCCTTATGAACCCC
ATTGTGTACTGTGTAAAGACTCGACAAATCTGGGAGAAGATCTTGGGGAAGTTGCTTAAT
45 GTATGTGGGAGATAA (SEQ ID NO: 334)

AOLFR182 sequences:

50 MTLGSLGNSSSVSATFLLSGIPGLERMHIWISIPLCFMYLVSIPGNCTILFIKTERSLHEPMYFL
SMLALIDLGLSLCTLPTVLGIFWVGAREISHDACFAQLFFIHCFSFLESSVLLSMAFDRFVAICHP
LHYVSILNTVIGRIGLVSLGRSVALIFPLPMLKRFPCGSPVLSHSYCLHQEVMKLACADMK
ANSIYGMFVIVSTVGIDSLILFSYALILRTVLSIASRAERFKALNTCVSHICAVLLFYTPMIGLSV
IHRFGKQAPHLVQVVMGFMYLLFPPVMNPVIVSVKTKQIRDRVTHAFY (SEQ ID NO: 335)

55 ATGACCCTGGGATCCCTGGGAAACAGCAGCAGCAGCGTTTCTGCTACCTTCTGCTGAGTG
GCATCCCTGGGCTGGAGCGCATGCACATCTGGATCTCCATCCCACTGTGCTTCATGTATCT
GGTTTCCATCCCGGGCAACTGCACAATTCTTTTTATCATTAAACAGAGCGCTCACTTCAT

GAACCTATGTATCTCTTCCTGTCCATGCTGGCTCTGATTGACCTGGGTCTCTCCCTTTGCAC
 TCTCCCTACAGTCCTGGGCATCTTTTGGGTGGAGCACGAGAAATTAGCCATGATGCCTGC
 TTTGCTCAGCTCTTTTTCATTCACTGCTTCTCCTTCGAGTCCTCTGTGCTACTGTCTATG
 GCCTTTGACCGCTTTGTGGCTATCTGCCACCCCTTGCACTATGTTTCCATTCTACCAACAC
 5 AGTCATTGGCAGGATTGGCCTGGTCTCTCTGGGTGCTAGTGTAGCACTCATTTTTCCATTA
 CCTTTTATGCTCAAAAGATTCCCCTATTGTGGCTCCCCAGTTCTCTCACATTCTTATTGTCT
 CCACCAAGAAGTGATGAAATTGGCCTGTGCCGACATGAAGGCCAACAGCATCTACGGCAT
 GTTTGTCACTGCTCTACAGTGGGTATAGACTCACTGCTCATCCTCTTCTCTTATGCTCTGA
 TCCTGCGCACCGTGCTGTCCATCGCCTCCAGGGCTGAGAGATTCAAGGCCCTTAACACCTG
 10 TGTTCACCATCTGTGCTGTGCTGCTCTTCTACACTCCCATGATTGGCCTCTCTGTCTATCC
 ATCGCTTTGAAAAGCAGGCACCCACCTGGTCCAGGTGGTCATGGGTTTCATGTATCTTCT
 CTTTCTCCTGTGATGAATCCCATTGTCTACAGTGTGAAGACCAACAGATCCGGGATCGA
 GTGACGCATGCCTTTTGTACTAA (SEQ ID NO: 336)

15 **AOLFR183 sequences:**

MTNLNASQANHRNFILTGIPGTPDKNPWLAFPLGFLYTLTLLGNGTILAVIKVEPSLHEPTYFYL
 SILALTDVLSMSTLPSMLSIYWFNAPQIVFDACIMQMFFIHVFGIVESGLVSMADFDFVAIRN
 PLHYVSILTHDVIRKTGISVLTRA VCVVPFVFLIKCLPFCHSNVLSHSYCLHQNMMLACASTR
 INSLYGLIVVIFTLGLDVLLTLLSYVLTLKTVLGIVSRGERLKTLSCLSHMSTVLLFYVPMGA
 20 ASMIHRFWEHLSPVVMVMADIYLLPVLNPIVYSVKTKQI (SEQ ID NO: 337)

ATGACGAACTTGAATGCATCACAGGCCAACCCCGTAACTTCATTCTGACAGGTATCCAG
 GAACGCCAGACAAGAACCCATGGTTGGCTTTCCCTGGGATTTCTCTACACACTCACACT
 CCTGGGAAATGGTACCATCCTAGCTGTCTCAAGGTGGAGCCAAGTCTCCATGAGCCCACG
 25 TATTACTTCCTTTCTATCTTGGCTCTCACTGACGTTAGTCTCTCCATGTCCACCTTGCCCTCC
 ATGCTCAGCATCTACTGGTTTAATGCCCTCAGATTGTTTTGATGCATGCATCAGAT
 GTTCTTCATCCATGTATTTGGAATAGTAGAATCAGGAGTCCTAGTGTCCATGGCCTTGAC
 AGATTTGTGGCCATCCGAAACCCATTACACTATGTTTCCATCCTCACTCACGATGTTATTGCG
 AAAGACTGGAATATCTGTCTCACCCGGGCGAGTCTGTGTGGTATTCCCTGTGCCCTTCCTT
 30 ATAAAGTGCTACCTTCTGCCATTCCAATGTCTTGTCTCATTCTACTGTCTTACCAAAA
 CATGATGCGGCTAGCTTGTGCCAGCACCCGCATCAACAGCCTCTACGGCCTCATCGTCGTC
 ATCTTCACTGGGGCTCGATGTTCTCCTCACTCTACTGTCTTATGTACTACCCCTGAAGAC
 TGTGCTGGGCATTGTCTCCAGAGGTGAAAAGGCTGAAAACCCCTCAGCACATGCCTCTCTCAC
 ATGTCTACCGTGCTCCTCTTCTATGTTCTTTTATGGGTGCTGCCTCCATGATCCACAGATT
 35 TTGGGAGCATTTATCACCAGTAGTGACATGGTCATGGCTGATATATACCTACTGCTCCCG
 CCTGTGCTAAACCCCATGTCTACAGTGTGAAGACCAAGCAAATTTGA (SEQ ID NO: 338)

AOLFR184 sequences:

MSTLPTQIAPNSSTSMAPTFLLVGMPGLSGAPSWWTLPLIAVYLLSALGNGTILWIALQPALHR
 40 PMHFFLFLSVSDIGLVTALMPTLLGIALAGAHTVPASACLLQMVFIHVFSVMESSVLLAMSID
 RALAICRPLHYPALLTNGVISKISLAISFRCLGLHPLPFLLAYMPYCLPQVLTHSYCLHPDVARL
 ACPEAWGAAYSLFVVL SAMGLDPLLIFFSYGLIGKVLQGVESREDRWKAGQTCAAHLSAVLLF
 YIPMILLALINHPelpITQHTHTLLSYVHFLPPLNPILYSVKMKRILNRLQPRKVGGAAQ
 (SEQ ID NO: 339)

ATGTCAACATTACCAACTCAGATAGCCCCAATAGCAGCACTTCAATGGCCCCACCTTCT
 TGCTGGTGGGCATGCCAGGCCTATCAGGTGCACCTCCTGGTGGACATTGCCCTCATTGC
 TGTCTACCTTCTCTCTGCACTGGGAAATGGCACCATCCTCTGGATCATTGCCCTGCAGCCC
 GCCCTGCACCGCCCAATGCACCTTCTTCTCTTCTGCTTAGTGTGTCTGATATTGGATTGGT
 50 CACTGCCCTGATGCCACACTGCTGGGCATCGCCCTTGTGGTGCTCACACTGTCCCTGCC
 TCAGCCTGCCTTCTACAGATGGTTTTTATCCATGTCTTTTCTGTCTGAGTCTCTGTCTT
 GCTCGCCATGTCCATTGATCGGGCACTGGCCATCTGCCGACCTCTCCACTACCCAGCGCTC
 CTCACCAATGGTGTAAATTAGCAAAATCAGCCTGGCCATTCTTTTCGATGCCTGGGTCTCC
 ATCTGCCCTGCCATTCTGCTGGCCTACATGCCCTACTGCCTCCACAGGTCTTAACCCAT
 55 TCTTATTGCTTGCATCCAGATGTGGCTCGTTTGGCCTGCCAGAAAGCTTGGGGTGCAGCCT
 ACAGCCTATTTGTGGTCTTTCAGCCATGGGTTTGGACCCCTGCTTATTTTCTTCTCTAT

GGCCTGATTGGCAAGGTGTTGCAAGGTGTGGAGTCCAGAGAGGATCGCTGGAAGGCTGGT
 CAAACCTGTGCTGCCCACCTCTCTGCAGTGCTCCTCTTCTATATCCCTATGATCCTCCTGGC
 ACTGATTAAACCATCTGAGCTGCCAATCACTCAGCATACCCATACTCTTCTATCCTATGTCC
 ATTTCTTCTTCTCCTCCATTGATAAACCTATTCTCTATAGTGTCAAGATGAAGGAGATTAGA
 5 AAGAGAATACTCAACAGGTTGCAGCCCAGGAAGGTGGGTGGTGTCTCAGTGA (SEQ ID NO:
 340)

AOLFR185 sequences:

MFYPILNDISTKNNSNIMSCCNILFIKTVEILVYNQQTSPWYPIVPSKSLVYNNNTCFDCYHLQR
 10 VDCVPSRDHINQSMVLASGNSSSHPVSFILLGIPGLESFQLWIAFPFCATYAVAVVGNITLLHVIR
 IDHTLHEPMYLFLAMLAITDLVLSSTQPKMLAIFWFHAHEIQYHACLIQVFFIHAFSSVESGVL
 MAMALDCYVATCFPLRHSSILTPSVVIKLGTTVMRLRGLLWVSPFCFMVSRMPFCQHQAIPQSYC
 EHMAVLKLVCADTSISRGYGLFVAFSVAGFDMIVIGMSYVMILRAVLQLPSGEARLKAFSTRA
 SHICVILALYLPALFSFLTYRFGHDVPRVVHILFANLYLLPPMLNPIYGVRTKQIGDRVIQGCCG
 15 NIP (SEQ ID NO: 341)

ATGTTCTACCCCATTTTGAATGACATAAGTACGAAAAACAACAGTAACATCATGTCTGTT
 GTAACATATTATTTATTAACAGTTGAAATTATTCTAGTTTATAATCAAACCCAATCACC
 CTGGTATCCAATAGTCCCATCCAAAAGCCTTGTATATAATAACACTTGTTTTGATTGTT
 20 ATCATCTGCAGAGAGTAGATTGCGTTCCCAGCAGAGACCATATTAACAGTCCATGGTGCT
 GGCTTCAGGGAACAGCTCTTCTCATCCTGTGTCTTTCATCCTGCTTGGAAATCCAGGCCCTG
 GAGAGTTTCCAGTTGTGGATTGCCTTTCGGTTCGTGCCACGTATGCTGTGGCTGTTGTGG
 AAATATCACTCTCCTCCATGTAATCAGAATTGACCACACCCTGCATGAGCCCATGTACCTC
 TTTCTGGCCATGCTGGCCATCACTGACCTGGTCTCTCCTCCTCCACTCAACCTAAGATGTT
 25 GGCCATATTCTGGTTTCATGCTCATGAGATTACGTACCATGCCTGCCTCATCCAGGTGTTCT
 TCATCCATGCCTTTTCTTCTGTGGAGTCTGGGGTGCTCATGGCTATGGCCCTGGACTGCTAC
 GTGGCTACCTGCTTCCCACTCCGACACTCTAGCATCCTGACCCCATCGGTCGTGATCAAAC
 TGGGGACCATCGTGATGCTGAGAGGGCTGCTGTGGGTGAGCCCTTCTGCTTCATGGTGTC
 TAGGATGCCCTTCTGCCAACACCAAGCCATTCCCCAGTCATACTGTGAGCACATGGCTGTG
 30 CTGAAGTTGGTGTGTGCTGATACAAGCATAAGTCGTGGGTATGGGCTCTTTGTGGCCTTCT
 CTGTGGCTGGCTTTGATATGATTGTCATTGGTATGTCATACGTGATGATTTTGAGAGCTGT
 GCTTCAGTTGCCCTCAGGTGAAGCCCGCTCAAAGCTTTTAGCACACGTGCCTCCCATATC
 TGTGTCATCTTGGCTCTTTATATCCCAGCCCTTTTTTCTTTCCTCACCTACCGCTTTGGCCAT
 GATGTGCCCCGAGTTGTACACATCCTGTTTGCTAATCTCTATCTACTGATACCTCCCATGCT
 35 CAACCCCATCATTTATGGAGTTAGAACCAAACAGATCGGGGACAGGGTTATCCAAGGATG
 TTGTGGAAACATCCCCTGA (SEQ ID NO: 342)

AOLFR186 sequences:

MSNASLVTAFILTGLPHAPGLDALLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
 40 FIDMWFSTVTVPKMLMTLVSPSGRAISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAISYPL
 RYTSMMSGSRCALLATGTWLSGSLHSAVQILTFLHPYCGPNQIQHYFCDAPPILKLACADTSA
 NVMVIFVDIGIVASGCFVLIVLSYVSIVCSILRITSDGRRRAFQTCASHCIVVLCTFFVPCVVITYLR
 PGSMDAMDGVVAIFYTVLTPLLNPVVYTLRNLKEVKKAVLKLRDKVAHPQRK (SEQ ID NO:
 343)

ATGTCCAACGCCAGCCTCGTGACAGCATTCATCCTCACAGGCCTTCCCCATGCCCCAGGGC
 TGGACGCCCTCCTCTTTGGAATCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
 CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTCTCTCA
 CCAACCTGTCTTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAAATGCTGATGAC
 50 CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTTT
 TCCACTTCTGCGGGAGCACCGAGTGTTCCTCTACACAGTCATGTCTATGATCGCTACTTG
 GCCATCAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGGTGTGCCCTCCTGG
 CCACCGGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT
 TTGCCCTACTGTGGACCCAACCAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCTGA
 55 AACTGGCCTGTGCAGACACCTCAGCCAACGTGATGGTCATCTTGTGGACATTGGGATAGT
 GGCCTCAGGCTGCTTTGTCTGATAGTGCTGTCTATGTGTCCATCGTCTGTTCCATCCTGC

GGATCCGCACCTCAGATGGGAGGCGCAGAGCCTTTCAGACCTGTGCCTCCCACTGTATTGT
GGTCCTTTGCTTCTTTGTTCCCTGTGTTGTCATTTATCTGAGGCCAGGCTCCATGGATGCCA
TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACGCCCTTCTCAACCTGTTGTGTAC
ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAACTTAGAGACAAAGTAGCACAT
5 CCTCAGAGGAAATAA (SEQ ID NO: 344)

AOLFR187 sequences:

MAQVRALHKIMALFSANSIGAMNSDTRIAGCFLTGIPGLEQLHIWLSIPFCIMYIAALEGNGLI
CVILSQAILHEPMYIFLSMLASADVLLSTTTMPKALANLWLGYSHSIFDGLTQKFFIHFLFIHSA
10 VLLAMAFDRYVAICSPRLRYVTILTSKVIGKIVATLSRSFIIMFPSIFLLEHLHYCQINIAHTFCEH
MGIAHLSCSDISINVWYGLAAALLSTGLDIMLITVSYIHILQAVFRLLSQDARSKALSTCGSHICV
ILLFYVPALFSVFAYRFGGRSIPCYVHILLASLYVIPPMLNPVIYGVRTKPILEGAKQMFSNLAK
GSK (SEQ ID NO: 345)

15 ATGGCACAGGTGAGGGCGCTGCATAAAATCATGGCCCTTTTTTCTGCTAACAGCATAGGTG
CTATGAACAACTCTGACACTCGCATAGCAGGCTGCTTCCTCACTGGCATCCCTGGGCTGGA
GCAACTACATATCTGGCTGTCCATCCCCCTTCTGCATCATGTACATCGCTGCCCTGGAAGGC
AATGGCATCCTAATTTGTGTCATCCTCTCCCAGGCAATCCTGCATGAGCCCATGTACATAT
TCTTATCTATGCTGGCCAGTGCTGATGTCTTGCTCTCTACCACCACCATGCCTAAGGCCCTG
20 GCCAATTTGTGGCTAGGTTATAGCCACATTTCCCTTTGATGGCTGCCTCACTCAAAAGTTCTT
CATTCACTTCCCTCTTCACTTCACTCTGCTGTCTGCTGGCCATGGCCTTTGACCGCTATGTGG
CCATCTGCTCCCCCTGCGATATGTCACAATCCTCACAAGCAAGGTCATTGGGAAGATCGT
CACTGCCACCCTGAGCCGCGAGCTTCATCATTATGTTTCCATCCATCTTTCTCCTTGAGCACC
TGCACTATTGCCAGATCAACATCATTGCACACACATTTTGTGAGCACATGGGCATTGCCCA
25 TCTGTCTGTTCTGATATCTCCATCAATGTCTGGTATGGGTTGGCAGCTGCTCTTCTCTCCA
CAGGCCTGGACATCATGCTTATTACTGTTTCTACATCCACATCCTCCAAGCAGTCTTCCGC
CTCCTTTCTCAAGATGCCCGCTCCAAGGCCCTGAGTACCTGTGGATCCCACATCTGTGTCAT
CCTACTCTTCTATGTCCCTGCCCTTTTTTCTGTCTTTGCCTACAGGTTTGGTGGGAGAAGCA
TCCCATGCTATGTCCATATTCTCCTGGCCAGCCTCTACGTTGTCATTCCCTCCTATGCTCAAT
30 CCCGTTATTTATGGAGTGAGGACTAAGCCAATACTGGAAGGGGCTAAGCAGATGTTTTCA
AATCTTGCCAAAGGATCTAAATAA (SEQ ID NO: 346)

AOLFR188 sequences:

MFPSLCPCVLLVQLPLMNENMQCFVFCSDSLLRMMVSRFIHVFPVKMKRIIVGGYSKHFFSN
35 ELLCVRPWSGKTWSIRHHIFDMELLTNLKFITDPFVCLRLHLSPTPSEEHMKNNKNNVTEFILL
GLTQNPEGQKVLVFTFLIYMTIMGNLLIIVTIMASQSLGSPMYFFLASLSFIDTVYSTAFAPK
MIVDLLSEKKTISFQGCMAQLFMDHLFAGAEVILLVVMAYDRYMAICKPLHELITMNRRCVIL
MLLAAWIGGFLHSLVQFLFYQLPFCGPNVIDNFLCDLYPLLKLACTNTYVTGLSMIANGGAIC
AVTFFTILLSYGVLHSLKTQSLEGRKAFYTCASHVTVVILFFVPCIFLYARPNSTFPIDKSMTV
40 VLTFTPMLNPLIYTLKNAEMKSAMRKLWSKKVSLAGKWLYHS (SEQ ID NO: 347)

ATGTTCCCCTCCCTGTGTCCATGTGTTCTCCTTGTTCAACTCCCCTTATGAATGAGAACAT
GCAGTGTTTTGTTTTCTGTTCTTGTGATAGTTGCTGAGAATGATGGTTTTCCCGCTTCATCC
ATGTCCCATTGTGAAAAATGAAAAGGATAATTGTGGGAGGATATTCTAAACACTTCTTTTC
45 TAATGAGCTGCTCTGTGTGAGGCCCTGGTCAGGGAAAACGTGGTCGATAAGGCATCACAT
TTTTGACATGGAGCTTCTGACAAATAATCTCAAATTTATCACTGACCCTTTTGTGTTAGGC
TCCGACACCTGAGTCCAACACCTTCAGAAGAACACATGAAAAATAAGAACATGTGACTG
AATTTATCCTCTTAGGGCTCACACAGAACCTGAGGGGCAAAAGGTTTTATTTGTCACATT
CTTACTAATCTACATGGTGACGATAATGGGCAACCTGCTTATCATAGTGACCATCATGGCC
50 AGCCAGTCCCTGGGTCCCCCATGTACTTTTTCTGGCTTCTTATCATTATCATAGATACCGT
CTATTCTACTGCATTTGCTCCCAAAATGATTGTTGACTTGCTCTCTGAGAAAAAGACCATT
CCTTTCAGGGTTGTATGGCTCAACTTTTTATGGATCATTTATTTGCTGGTGCTGAAGTCATT
CTTCTGGTGGTAATGGCCTATGATCGATACATGGCCATCTGTAAGCCTCTTCATGAATTGA
TCACCATGAATCGTCGAGTCTGTGTTCTTATGCTGTTGGCGGCCTGGATTGGAGGCTTTCT
55 TCACTCATTGGTTCAATTTCTCTTTATTTATCAGCTCCCTTTCTGTGGACCCAATGTCATTG
ACAACTTCTGTGTGATTTGTATCCCTTATTGAAACTTGCTTGACCAATACCTATGTCACT

GGGCTTTCTATGATAGCTAATGGAGGAGCGATTGTGCTGTACCTTCTTCACTATCCTGC
TTTCTATGGGGTCATATTACACTCTCTTAAGACTCAGAGTTTGGAAAGGGAAACGAAAAGC
TTTCTACACCTGTGCATCCACGTCAGTGTGGTCATTTTATTCTTTGTCCCCTGTATCTTCTT
GTATGCAAGGCCCAATTCTACTTTTCCCATTGATAAATCCATGACTGTAGTTCCTAACTTTTA
TAACCTCCCATGCTGAACCCACTAATCTATACCCTGAAGAATGCAGAAATGAAAAGTGCCAT
GAGGAAACTTTGGAGTAAAAAAGTAAGCTTAGCTGGGAAATGGCTGTATCACTCATGA
(SEQ ID NO: 348)

AOLFR189 sequences:

10 MQQNSVPEFILLGLTQDPLRQKIVFVIFLFYMGTVVGNMLIVTKSSRTLGSPPMYFFLFYLSF
ADSCFSTSTAPRLIVDALSEKKIITYNECMTQVFALHLFGCMEIFVLILMAVDRYVAICKPLRYP
TMSQVQCILIVLAWIGSLIHSTAQILALRLPFCGPYLIDHYCCDLQPLLLKACMDTYMINLLL
VSNSGAICSSSFMLIISYVILHSLRNHSAKGKKKALSACTSHIIVVILFFGPCIFYTRPPTTFPMD
KMVAVEYTGTPFLNPLYITSEECRSEKCHEK (SEQ ID NO: 349)

15 ATGCAGCAAAAATAACAGTGTGCCTGAATTCATACTGTTAGGATTAACACAGGATCCCTTGA
GGCAGAAAAATAGTGTGTTTGTAACTCTTCTTAATTTTCTATATGGGAAGTGTGGTGGGGAATA
GCTCATTATTGTGACCATCAAGTCCAGCCGGACACTAGGAAGCCCCATGTACTTCTTTCTA
TTTTATTTGTCTTTGCAGATTCTTGCTTTTCAACTTCCACAGCCCCTAGATTAATTGTGGA
20 TGCTCTCTCTGAAAAGAAAATTATAACCTACAATGAGTGCATGACACAAGTCTTTGCACTA
CATTTATTTGGCTGCATGGAGATCTTTGTCTCATTCTCATGGCTGTTGATCGCTATGTGGC
CATCTGTAAGCCCTTGCGTTACCCAACCATCATGAGCCAGCAGGTCTGCATCATCCTGATT
GTTCTTGCCCTGGATAGGGTCTTTAATACACTCTACAGCTCAGATTATCCTGGCCTTAAGATT
GCCTTTCTGTGGACCCTATTTGATTGATCATTATTGCTGTGATTTGCAGCCCTTGTTGAAAC
25 TTGCCTGCATGGACACTTACATGATCAACCTGCTGTTGGTGTCTAACAGTGGGGCAATTTG
CTCAAGTAGTTTCATGATTTTGATAATTTCATATATTGTCATCTTGCATTCACTGAGAAACC
ACAGTGCCAAAGGGAAGAAAAGGCTCTCCGCTTGCACGCTCTCACATAATTGTAGTCAT
CTTATTCTTTGGCCCATGTATATTATATATACACGCCCCCGACCACITTTCCCCATGGACA
AGATGGTGGCAGTATTTTATACATAATTGGAACACCCTTTCTCAATCCACTCATCTACACATCT
30 GAGGAATGCAGAAGTGAAAAATGCCATGAGAAAG (SEQ ID NO: 350)

AOLFR190 sequences:

35 MQRSNHTVTEFILLGFTTDPGMQLGLFVVFVLGVYCLTVVGSSTLIVLICNDSRLHTPMYFVIGN
LSFLDLWYSSVHTPKILVTCISEDKKSISFAGCLCQFFSARLAYSECYLLAAMAYDHYVAISKPLL
YAQTMPPRRLCISCLVLVLSYTGGFVNAILTSNTFTLDFCGDNVIDDFDCVPPLVKLACSVRESYQ
AVLHFLLASNVISPTVLILASVLSIITHRIHSTQGRKVFSTCSSHLISVTLVYGSILYNYSRPSS
YSLKRDKMVSTFYTMLFPLNPNMYSRLRSKDMKDALKKFFKSA (SEQ ID NO: 351)

ATGCAGAGGAGCAATCACACAGTGACTGAGTTCATCCTGCTGGGCTTCACCACAGATCCAG
40 GGATGCAACTGGGCCTCTTTGTGGTGTTCCTGGGTGTGTA CTGTCTGACTGTGGTAGGAAG
TAGCACCCCTCATCGTGTGTGATCTGTAATGACTCCCGCCTACACACACCCATGTATTTTGTCA
TTGGAAATCTGTCAATTCTGGATCTCTGGTATTCTTCTGTCCACACCCCAAAGATCCTAGTG
ACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTGTCAGTTCTTCTCTGC
CAGGCTGCCCTATAGTGAGTGTCTACCTACTGGCTGCCATGGCTTAGACCACTACGTGGCC
45 ATCTCCAAGCCCTGCTTTATGCTCAGACCATGCCAAGGAGATTGTGCATCTGTTTGGTTTT
ATATTCCTATACTGGGGGTTTTGTCAATGCAATAATATTAACCAGCAACACATTCACATTG
GATTTTTGTGGTGACAATGTCATTGATGACTTTTTCTGTGATGTTCCACCCCTCGTGAAGCT
GGCATGCAGTGTGAGAGAGAGCTACCAGGCTGTGCTGCACTTCCTTCTGGCCTCCAATGTC
ATCTCCCCTACTGTGCTCATCCTTGCTCTTACCTCTCCATCATCACCACCATCCTGAGGAT
50 CCACTCTACCCAGGGCCGCATCAAAGTCTTCTCCACATGCTCCTCCCACCTGATCTCCGTTA
CCTTATACTATGGCTCCATTCTCTACAACTACTCCCGGCCAAGTTCAGCTACTCCCTCAAG
AGGGACAAAATGGTTTCTACCTTTTATACTATGCTGTTCCCCATGTTGAATCCCATGATCTA
CAGTCTGAGGAGTAAAGACATGAAAGACGCTCTGAAAAAATTCTTCAAGTCAGCATAA
(SEQ ID NO: 352)

AOLFR191 sequences:

MTGGGNITEITYFILLGFSDFPRIKVLFTIFLVITYTSLAWNLSLIVLIRMDSHLHTPMYFFLSNLS
 FIDVCYISSTVPKMLSNLLQEQQTITFVGCIQYFIFSTMGLESCLMTAMAYDRYAAICNPLLYS
 SIMSPTLCVWMVLGAYMTGLTASLFQIGALLQLHFCGSNVIRHFFCDMPQLLLSCTDTFFVQV
 5 MTAILTMFFGIASALVMISYGYIGISIMKITSAGSPKAFNTCASHLTAVSLFYTSYGIFVYLRSSS
 GGSSSDFRFASVFYTVVIPMLNPLIYSLRNKEIKDALKRLQKRKCC (SEQ ID NO: 353)

ATGACTGGGGGAGGAAATATTACAGAAATCACCTATTTTCATCCTGCTGGGATTCTCAGATT
 TCCCCAGGATCATAAAAGTGCTCTTCACTATATTCTGGTGATCTACATTACATCTCTGGCC
 10 TGGAAACCTCTCCCTCATTGTTTTAATAAGGATGGATTCCCACCTCCATACACCCATGTATTT
 CTTCTCAGTAACCTGTCCCTCATAGATGTCTGCTATATCAGCTCCACAGTCCCCAAGATGC
 TCTCCAACCTCTTACAGGAACAGCAAATATCACTTTTGTGGTGTATTATTTCAGTACTTT
 ATCTTTTCAACGATGGGACTGAGTGAGTCTTGTCTCATGACAGCCATGGCTTATGATCGTT
 ATGCTGCCATTTGTAACCCCTGCTCTATTTCATCCATCATGTACCCACCCCTCTGTGTTTGG
 15 ATGGTACTGGGAGCCTACATGACTGGCCTCACTGCTTCTTATTCCAAATTGGTGCTTTGCT
 TCAACTCCACTTCTGTGGGTCTAATGTCATCAGACATTTCTTCTGTGACATGCCCCAACTGT
 TAATCTTGTCTGTACTGACACTTTCTTTGTACAGGTCATGACTGCTATATTAACCATGTTT
 TTTGGGATAGCAAGTGCCCTAGTTATCATGATATCCTATGGCTATATTGGCATCTCCATCA
 TGAAGATCACTTCAGCTAAAGGCAGTCCAAAGGCATTCAACACCTGTGCTTCTCATCTAAC
 20 AGCTGTTTCCCTCTTCTATACATCAGGAATCTTTGTCTATTTGAGGTCCAGCTCTGGAGGTT
 CTTCAAGCTTTGACAGATTTGCATCTGTTTTCTACACTGTGGTCATTCCCATGTTAAATCCC
 TTGATTTACAGTTTGAGGAACAAAGAAATTAAGATGCCTTAAAGAGGTTGCAAAAGAGA
 AAGTGCTGCTGA (SEQ ID NO: 354)

AOLFR192 sequences:

MENNTEVTEFILVGLTDDPELQIPLFIVFLFIYLTITLVGNLGMIELILLDSCLHTPMYFFLSNLSLV
 DFGYSSAVTPKVMVGFLTGDKFILYNACATQFFFFVAFITAESFLLASMA YDRYAALCKPLHY
 TTTMTTNVCACLAIGSYICGFLNASIHTGNTFRLSFCRSNVVEHFFCDAPPLTLSCSDNYISEM
 VIFFVVGFNDFSLVILISYLFIFITIMKMRSPGROKAFSTCASHLTAVSIFYGTGIFMYLRPNSS
 30 HFMGTDKMASVFYAIVIPMLNPLVYSLRNKEVKSAFKKTVGKAKASIGFIF (SEQ ID NO: 355)

ATGGAGAACAACACAGAGGTGACTGAATTCATCCTTGTGGGGTTAACTGATGACCCAGAA
 CTGCAGATCCCACCTTTCATAGTCTTCTCTTTCATCTACCTCATCACTCTGGTTGGGAACCT
 GGGGATGATTGAATTGATTCTACTGGACTCCTGTCTCCACACCCCCATGTACTTCTTCCCTCA
 35 GTAACCTCTCCCTGGTGGACTTTGGTTATTCCTCAGCTGTCACTCCCAAGGTGATGGTGGG
 GTTTCTCAGAGGAGACAAATTCATATTATATAATGCTTGTGCCACACAATTCTTCTCTTTG
 TAGCCTTTATCACTGCAGAAAGTTTCTCTGGCATCAATGGCCTATGACCGCTATGCAGC
 ATTGTGTAACCCCTGCATTACACCACCACCATGACAACAAATGTATGTGCTTGCCCTGGCC
 ATAGGCTCCTACATCTGTGGTTTCTCTGAATGCATCCATTCTACTGGGAACACTTTCAGGC
 40 TCTCCTTCTGTAGATCCAATGTAGTTGAACACTTTTTCTGTGATGCTCCTCCTCTCTTGACT
 CTCTCATGTTTCAGACAACTACATCAGTGAGATGGTTATTTTTTTTGTGGTGGGATTCAATG
 ACCTCTTTTCTATCCTGGTAATCTTGATCTCCTACTTATTTATATTTATCACCATCATGAAG
 ATGCGCTCACCTGAAGGACGCCAGAAGGCCTTTTCTACTTGTGCTTCCACCTTACTGCAG
 TTTCCATCTTTTATGGGACAGGAATCTTTATGTACTTACGACCTAACTCCAGCCATTTTCATG
 45 GGCACAGACAAAATGGCATCTGTGTTCTATGCCATAGTCATTCCCATGTTGAATCCACTGG
 TCTACAGCCTGAGGAACAAAGAGGTTAAGAGTGCCTTTAAAAAGACTGTAGGGAAGGCAA
 AGGCCTCTATAGGATTCATATTTTAA (SEQ ID NO: 356)

AOLFR193 sequences:

MENKTEVTQFILLGLTNDSELQVPLFITFPFIYIITLVGNLGIIVLIFWDSCLHNP MYFFLSNLSLV
 DFCYSSAVTPIVMAGFLIEDKVISYNACAAQMYFVAFATVENYLLASMA YDRYAAVCKPLHY
 TTTMTTTVCARLAIGSYLCGFLNASIHTGDTFSLSFCKSNEVHHFFCDIPAVMVLSCSDRHISEL
 VLIYVVSFNIFIALLVILISYTFIFITILKMHSASVYQKPLSTCASHFLAVGIFYGTIIFMYLQPSSSH
 SMDTDMKMAPVFYTMVIPMLNPLVYSLRNKEVKSAFKKVVEKAKLSVGWSV (SEQ ID NO:
 55 357)

ATGGAAAATAAGACAGAAAGTAACACAATTCATTCTTCTAGGACTAACCAATGACTCAGAA
 CTGCAGGTCCCCCTCTTTATAACGTTCCCCCTCATCTATATTATCACTCTGGTTGGAAACCT
 GGAATTATTGATTGATATTCTGGGATTCTGTCTCCACAATCCCATGTACTTTTTCTCA
 GTAACTTGCTCTAGTGGACTTTTGCTACTCTTCAGCTGTCACTCCCATCGTCATGGCTGGA
 5 TTCCTTATAGAAGACAAGGTCATCTCTTACAATGCATGTGCTGCTCAAATGTATATCTTTGT
 AGCTTTTGCCACTGTGGAAAATTACCTCTTGGCCTCAATGGCCTATGACCGCTATGCAGCA
 GTGTGCAAACCCCTACATTACACCACAACCATGACAACAACCTGTGTGTGCTCGTCTGGCCA
 TAGGCTCCTACCTCTGTGGTTTCCTGAATGCCTCCATCCACACTGGGGACACATTTAGTCTC
 TCTTTCTGTAAGTCCAATGAAGTCCATCACTTTTTCTGTGATATTCCAGCAGTCATGGTTCT
 10 CTCTTGCTCTGATAGACATATTAGCGAGCTTGTTCTTATTTATGTTGTGAGCTTCAATATCT
 TTATAGCTCTCCTGGTTATCTTGATATCCTACACATTCATTTTTATCACCATCCTAAAGATG
 CACTCAGCTTCAGTATACCAGAAGCCTTTGTCCACCTGTGCCTCTCATTTTCATTGCAGTCGG
 CATCTTCTATGGGACTATTATCTTCATGTACTTACAACCCAGCTCCAGTCACTCCATGGACA
 CAGACAAAATGGCACCTGTGTTCTATACAATGGTCATCCCCATGCTGAACCCTCTGGTCTA
 15 TAGTCTGAGGAACAAGGAAGTGAAGAGTGCATTCAAGAAAGTTGTTGAGAAGGCAAAATT
 GTCTGTAGGATGGTCAGTTTAA (SEQ ID NO: 358)

AOLFR194 sequences:

MERQNOQSCVVEFILLGFSNYPELQGQLFVAFVLVYLVTLIGNAIIIVVSLDQSLHVP MYLFLNL
 20 SVVDLSFSAVIMPEMLVVLSTEKTTISFGGCF AQMYFILLFGGAECFLLGAMAYDRFAAICHPL
 NYQMIMNKGVFMKLIIFSWALGFMLGT VQTSWVSSFPFCGLNEINHISCETPAVLELACADTF
 FEIYAFGTFLIILVPFLILLSYIRVLFAILKMPSTTGRQKAFSTCAAHLTSVTLFYGTASMTYLQ
 PKSGYSPETKKVMSLSYSLLTPLNLLIYSLRNSEMKRALMKLWRRRVVLHTI (SEQ ID NO:
 359)

25 ATGGAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCTTGGGCTTTTCTAACTATC
 CTGAGCTCCAGGGGAGCTCTTTGTGGCTTTCCTGGTTATTTATCTGGTGACCTGATAGG
 AAATGCCATTATTATAGTCATCGTCTCCCTAGACCAGAGCCTCCACGTTCCCATGTACCTGT
 TTCTCCTGAACCTTATCTGTGGTGGACCTGAGTTTCAGTGCAGTTATTATGCCTGAAATGCT
 30 GGTGGTCTCTCTACTGAAAAAACTACAATTTCTTTTGGGGGCTGTTTTGCACAGATGTAT
 TTCATCCTTCTTTTTGGTGGGGCTGAATGTTTTCTTCTGGGAGCAATGGCTTATGACCGATT
 TGCTGCAATTTGCCATCCTCTCAACTACCAAATGATTATGAATAAAGGAGTTTTTATGAAA
 TTAATTATATTTTCATGGGCCTTAGGTTTTATGTTAGGTACTGTTCAAACATCATGGGTATC
 TAGTTTTCCCTTTTGTGGCCTTAATGAAATTAACCATATATCTTGTGAAACCCAGCAGTGT
 35 TAGAACTTG CATGTGCAGACACGTTTTTGTGTTGAAATCTATGCATTACAGGCACCTTTTTG
 ATTATTTTGGTTCCTTTCTTGTGATACTCTTGTCTTACATTGAGTTCGTGTTGCCATCCTG
 AAGATGCCATCAACCACTGGGAGACAAAAGGCCTTTTCCACCTGTGCCGCTCACCTCACAT
 CTGTGACCCTATTCTATGGCAGCCAGTAGTACTTATTACAACCCAAATCTGCTCACTC
 ACCGAAACCAAGAAAGTGATGTCATTGTCTTACTCACTTCTGACACCACTGCTGAATCTG
 40 CTTATCTACAGTTTGCGAAATAGTGAGATGAAGAGGGCTTTGATGAAATTATGGCGAAGG
 CGAGTGGTTTTACACACAATCTGA (SEQ ID NO: 360)

AOLFR195 sequences:

45 MIVQLICTVCFLAVNTFHVRSFDFLKADDMGEINQTLVSEFLLLGLSGYPKIEIVYFALILVMY
 LVILIGNVLIASIFDSHFHTPMYFFLGNLSFLDICYTSSSVPS TLVSLISKRNISFSGCAVQMFF
 GFAMGSTECLLLGMMAFDRYVAICNPLRYPIILSKVAYVLMASVSWLSGGINS AVQTLLAMRL
 PFCGNNIINHFACEILAVLKLACADISLNIITMVISNMAFLVPLMVIFFSYMFILY TILQMNSATG
 RRKAFSTCSAHLTVVIIFYGTIFFMYAKPKSQDLIGEEKLQALDKLISLFYGVVTPMLNPIL YSLR
 NKDVKAAVKYLLNKKPIH (SEQ ID NO: 361)

50 ATGATTGTT CAGTTAATTTGTACTGTTTGTCTTCTGGCAGTAAATACATTTTCATGTTAGATC
 TTCTTTTGATTTCTGAAAGCAGATGACATGGGTGAGATTAACCAGACACTTGTGTGAGAA
 TTTCTTCTTCTGGGTCTTTCTGGATACCCAAAGATTGAGATTGTTTACTTTGCTCTCATTCT
 AGTTATGTACCTAGTGATTCTAATTGGCAATGGTGTCTAATCATAGCCAGCATCTTTGATT
 55 CTCATTTTCACACACCAATGTACTTCTCTGGGCAACCTCTCTTTCTGGATATCTGCTAT
 ACATCCTCCTCTGTTCCCTCAACATTGGTGAGCTAATCTCAAAGAAAAGAAACATTTCT

TCTCTGGATGTGCAGTGCAGATGTTCTTTGGGTTTGCAATGGGGTCAACAGAATGTCTGCT
 TCTTGGCATGATGGCATTGATCGTTATGTGGCCATCTGCAACCCACTGAGATACCCCATC
 ATCCTGAGCAAGGTGGCGTATGTATTGATGGCTTCTGTGTCCTGGCTGTCCGGTGGGAATAA
 ATTCAGCTGTGCAACATTACTTGCCATGAGACTGCCTTTCTGTGGGAATAATATTATCAA
 5 TCATTTCGCATGTGAAATATTAGCTGTCTCAAGCTGGCCTGTGCTGATATATCCCTCAATA
 TTATCACCATGGTGATATCAAATATGGCCTTCTGGTTCTTCCACTGATGGTCATTTTTTTC
 TCCTATATGTTTCATCTCTACACCATCTTGCAAATGAATTCAGCCACAGGAAGACGCAAGG
 CATTTTCCACGTGCTCAGCTCACCTGACTGTGGTGATCATATTTTACGGTACCATCTTCTTT
 ATGTATGCGAAACCGAAGTCTCAAGACCTGATTGGGGAAGAAAAATTGCAAGCATTAGAC
 10 AAGCTCATTTCTCTGTTTTATGGGGTAGTGACCCCATGCTGAATCCTATACTCTATAGCTT
 GAGAAATAAGGATGTAAAGCTGCTGTAAATATTTGCTGAACAAAAACCAATTCACTA
 A (SEQ ID NO: 362)

AOLFR196 sequences:

15 MLESNYTMPTEFLVVGFTDYLPLRVTLFLVFLLVYTLTMVGNILLILVNINSSLQIPMYFSLNL
 SFLDISCSTAITPKMLANFLASRKSISPYGCALQMFFFAFADAECCLLAAMAYDRYAAICNPPL
 YTTLMSRRVCVCFIVLAYFSGSTTSLVHVCLTFRLSFCGSNIVNHFFCDIPPLALSCDTQINQL
 LLFALCSFIQTSTFVVFISYFCILITVLSIKSSGGRSKTFSTCASHLIAVTLFYGALLFMYLQPTTS
 20 YSLDTDKVVAVFYTVVFPMPFNPIIYSFRNKDVKNALKKLLERIGYSNEWYLNRLRIVNI (SEQ
 ID NO: 363)

ATGTTGGAGAGTAATTACACCATGCCAACTGAGTTCCTATTTGTTGGATTACAGATTATC
 TACCTCTCAGAGTCACACTGTTCTTGGTATTCTTCTGGTATATACATTAECTATGGTCGGA
 AATATACTCTTAATAATTCTAGTTAATATTAATTCAAGCCTTCAAATTCCTCATGTATTATTT
 25 TCTTAGCAACTTATCTTTCTTAGACATCAGCTGTTCTACAGCAATCACTCCTAAATGCTGG
 CAAACTTCTTGGCATCCAGGAAAAGCATCTCTCCTTATGGGTGTGCACTACAAATGTTTTT
 CTTGCTTCTTTTGGTGTGCTGAGTGCCTTATCCTGGCAGCAATGGCTTATGACCGTATG
 CAGCCATCTGCAACCCACTGCTCTATACTACACTGATGTCTAGGAGAGTCTGTGTCTGCTT
 CATTGTGTTGGCATATTTAGTGGAAGTACAACATCACTGGTCCATGTGTGCTCACATTC
 30 AGGCTGTCATTTTGTGGCTCCAATATCGTCAATCATTTTTTCTGTGATATCCCACCTCTTCT
 GGCTTTATCATGTACAGACACTCAGATCAACCAGCTTCTGCTCTTTGCTTTGTGCAGCTTCA
 TCCAGACCAGCACTTTTGTGGTAATATTTATTTCTTACTTCTGCATCCTCATCACTGTGTTG
 AGCATCAAGTCCTCAGGTGGCAGAAGCAAAACATTCTCCACTTGTGCTTCCCACCTCATAG
 CAGTCACCTTATTCTATGGAGCGCTCCTGTTTATGTACTTACAGCCCACCACTAGCTATTCC
 35 CTAGACACTGATAAGGTGGTGGCAGTGTTTTATACTGTTGTATTTCCCATGTTTAATCCAA
 TAATTTATAGTTTCAGAAACAAGGATGTGAAAAATGCTCTCAAAAAGCTATTAGAAAGAA
 TTGGATATTCAAATGAATGGTATTTAAATCGTTTAAAGAATAGTCAATATCTAA (SEQ ID NO:
 364)

AOLFR197 sequences:

40 MCYLSQLCLSLGEHTLHMGMVRHTNESNLAGFILLGFSYDYPQLQKVLFLILLYLLTILGNTTI
 ILVSRLEPKLHMPMYFFLSHLSFLYRCFTSSVIPQLLVNLWEPMKTIAYGGCLVHLYNSHALGS
 TECVLLALMSCDRYVAVCRPLHYTVLMHIHLICMALASMAWLSGIATTLVQSTLTLQLPFCGH
 RQVDHFICEVPVLIKLACVGTTTFNEAELFVASILFLIVPVSFILVSSGYIAHAVLRIKSATRRQKAF
 45 GTCFSLTVVTIFYGTIFMYLQPAKSRSRDQKQFVSLFYTVVTRMLNPLIYTLRIKEVKGALKK
 VLAKALGVNII (SEQ ID NO: 365)

ATGTGTTATCTTTCTCAGCTATGCCTCAGCCTTGGGGAACACACTTTACATATGGGGATGG
 TGAGACATAACCAATGAGAGCAACCTAGCAGGTTTCATCCTTTTAGGGTTTTCTGATTATCC
 50 TCAGTTACAGAAGGTTCTATTTGTGCTCATATTGATTCTGTATTTACTAACTATTTGGGGA
 ATACCACCATCATTCTGGTTTCTCGTCTGGAACCCAAGCTTCATATGCCGATGTATTTCTTC
 CTTTCTCATCTCTCCTTCCTGTACCGCTGCTTCACCAGCAGTGTTATTTCCCAGCTCCTGGT
 AAACCTGTGGGAACCCATGAAAATATCGCCTATGGTGGCTGTTTGGTTACCTTTACAAC
 TCCCATGCCCTGGGATCCACTGAGTGCGTCTCTTGGCTCTGATGTCTGTGACCGCTATGT
 55 GGCTGTCTGCCGTCCTCTCCATTACACTGTCTTAATGCATATCCATCTCTGCATGGCCTTGG
 CATCTATGGCATGGCTCAGTGGAATAGCCACCACCTGGTACAGTCCACCCTCACCTGCA

GCTGCCCTTCTGTGGGCATCGCCAAGTGGATCATTTTCATCTGCGAGGTCCCTGTGCTCATC
 AAGCTGGCTTGTGTGGGCACACGTTTAAACGAGGCTGAGCTTTTTGTGGCTAGTATCCTTT
 TCCTTATAGTGCCTGTCTCATTTCATCCTGGTCTCCTCTGGCTACATTGCCACGCAGTGTG
 AGGATTAAGTCAGCTACCAGGAGACAGAAAGCATTGGGACCTGCTTCTCCACCTGACA
 5 GTGGTCACCATCTTTTATGGAACCATCATCTTCATGTATCTGCAGCCAGCCAAGAGTAGAT
 CCAGGGACCAAGGCAAGTTTGTCTCTCTTCTACACTGTGGTAACCCGCATGCTTAACCC
 TCTTATTTATACCTTGAGGATCAAGGAGGTGAAAGGGGCATTAAAGAAAGTTCTAGCAAA
 GGCTCTGGGAGTAAATATTTTATGA (SEQ ID NO: 366)

10 **AOLFR198 sequences:**

MENCTEVTKFILLGLTSVPELQIPLFILFTFIYLLTLCGNLGMMLLILMDSCLHTPMYFFLSNLSL
 VDFGYSSAVTPKVMAGFLRGDKVISYNACAVQMFFVALATVENYLLASMAFYDRAA VCKP
 LHYYYYMTASVGACALGSYVCGFLNASFHIGGIFSLFCKSNLVHHFFCDVPAVMALSCSDKH
 TSEVILVFMSSFNIFVLLVIFISYLFIFITILKMHSAGHQAALSTCASHFTAVSVFYGTIVIFYLQ
 15 PSSSHSMDTDKMASVFYAMIPMLNPVVYSLRNREVQNAFKKVLRRQKFL (SEQ ID NO: 367)

ATGGAGAATTGTACGGAAGTGACAAAGTTCATTCTTCTAGGACTAACCAGTGTCCCAGAAC
 TACAGATCCCCCTCTTTATCTTGTTACCTTCATCTACCTCCTCACTCTGTGTGGGAACCTG
 GGGATGATGTTGCTGATCCTGATGGACTCTTGCTCCACACCCCCATGTACTTTTCTCAG
 20 TAACCTGTCTCTGGTGGACTTTGGATACTCCTCAGCTGTCACTCCCAAGGTCATGGCTGGG
 TTCCTTAGAGGAGACAAGGTCATCTCCTACAATGCATGTGCTGTTCAAGATGTTCTTCTTGT
 AGCCTTGGCCACGGTGGAAAATTACTTGTGGCCTCAATGGCCTATGACCGCTATGCAGCA
 GTGTGCAAACCCCTACACTACACCACCACCATGACGGCCAGTGTAGGTGCCTGTCTGGCCC
 TAGGCTCATATGTCTGTGGCTTCTAAATGCCTCATTCCACATTGGGGGCATATTCACTCTC
 25 TCTTTCTGTAAATCCAATCTGGTACATCACTTTTCTGTGATGTTCCAGCAGTCATGGCTCT
 GTCTTGCTCTGATAAACACACTAGTGAGGTGATTCTGGTTTTTATGTCAAGCTTTAATATCT
 TTTTGTCTTCTAGTTATCTTTATCTCCTACTTGTTCATATTTCATCACCATCTTGAAGATGC
 ATTCAGCTAAGGGACACCAAAAAGCATTGTCCACCTGTGCCTCTCACTTCACTGCAGTCTC
 CGTCTTCTATGGGACAGTAATCTTCATCTACTTGCAGCCAGCTCCAGCCACTCCATGGAC
 30 ACAGACAAAATGGCATCTGTGTTCTATGCTATGATCATCCCCATGCTGAACCCTGTGGTCT
 ACAGCCTGAGGAACAGAGAAGTCCAGAATGCATTCAAGAAAGTGTGAGAAGGCAAAAAT
 TTCTATAA (SEQ ID NO: 368)

AOLFR199 sequences:

35 MDTGNKTL PQDFLLLGFPQSQTQLSLFMLFLVMYILTVSGNVAILMLVSTSHQLHTPMYFFLS
 NLSFLEIWTYTTAAVPKALAILLGRSQTISFTSCLLQMYFVFSLGCTEYFLLAAMAYDRCLAICY
 LHYGAIMSSLLSAQLALGSWVCGFVAIAVPTALISGLSFCGPRAINHHFCDIAPWIALACTNTQA
 VELVAFVIAVVILSSCLITFVSYYIISTILRIPSASGRSKAFSTCSSHLTVVLIWYGSTVFLHVR
 TSKDALDLIKA VHVLTNTVTPVLNPFITLRLNKEVRETLKKWK GK (SEQ ID NO: 369)

40 ATGGACACAGGCAACAAAACCTCTGCCCCAGGACTTTCTCTTACTGGGCTTTCTGTTCTC
 AAACCTCTTCAGCTCTCTCTCTTTATGCTTTTTCTGGTGATGTACATCCTCACAGTTAGTGGT
 AATGTGGCTATCTTGATGTTGGTGAGCACCTCCCATCAGTTGCATACCCCATGTACTTCTT
 TCTGAGCAACCTCTCCTTCTGGAGATTGGTATACCACAGCAGCAGTGCCCAAAGCACTG
 45 GCCATCCTACTGGGGAGAAGTCAGACCATATCATTTACAAGCTGTCTTTTGAGATGTACT
 TTGTTTTCTCATTAGGCTGCACAGAGTACTTCTCCTGGCAGCCATGGCTTATGACCGCTGT
 CTTGCCATCTGCTATCCTTTACACTACGGAGCCATCATGAGTAGCCTGCTCTCAGCGCAGC
 TGGCCCTGGGCTCCTGGGTGTGTGGTTTCGTGGCCATTGCAGTGCCACAGCCCTCATCAG
 TGGCCTGTCTTCTGTGGCCCCCGTCACATCAACCACTTCTTCTGTGACATTGCACCTTGA
 50 TTGCCCTGGCCTGCACCAACACACAGGCAGTAGAGCTTGTGGCCTTTGTGATTGCTGTTGT
 GGTATCCTGAGTTCATGCCTCATCACCTTTGTCTCCTATGTGTACATCATCAGCACCATCC
 TCAGGATCCCCTCTGCCAGTGGCCGGAGCAAAGCCTTCTCCACGTGCTCCTCGCATCTCAC
 CGTGGTGCTCATTTGGTATGGGTCCACAGTTTTCTTCCAGTCCGCACCTCTATCAAAGAT
 GCCTTGATCTGATCAAAGCTGTCCACGTCTGAACACTGTGGTGACTCCAGTTTTAAACC
 55 CCTCATCTATACGCTTCGTAATAAGGAAGTAAGAGAGACTCTGCTGAAGAAATGGAAGG
 GAAAATAA (SEQ ID NO: 370)

AOLFR200 sequences:

MTRKNYTSLETFVLLGLADTLELQILFFLVITYTLTVLGNLGMILLIRIDSQ LHTPMYFFLANL
 SFVDVCNSTTTTPKMLADLLSEKKTISFAGCFLQMYFFISLATTECILFGLMAYDRYAAICRPLL
 5 YSLIMSRTVYLKMAAGAFAGLLNFMVNTSHVSSLSFCDSNVIIHFFCDSPPLFKLSCSDTILKE
 SISSILAGVNIVGTLVLSSYSYVLFISFMSHSGEGRHRAFSTCASHLTAILFYATCIYTYLRPSS
 SYSLNQDKVASVFYTVVPMNLNPLIYSLRSKEVKKALANVISRKRTSSFL (SEQ ID NO: 371)

ATGACCAGAAAAAATTATACCTCACTGACTGAGTTCGTCCTATTGGGATTAGCAGACACGC
 10 TGGAGCTACAGATTATCCTCTTTTTGTTTTTCTTGTGATTATACACTTACAGTACTGGGA
 AATCTCGGGATGATCCTCTTAATCAGGATCGATTCCCAGCTTCACACACCCATGTATTTCTT
 CCTGGCTAACCTGTCTTTGTGGACGTTTGTAACCTCAACTACCATCACCCCAAAGATGCTG
 GCAGATTTATTATCAGAGAAGAAAACCATCTCTTTGCTGGCTGCTTCCTACAGATGTACT
 TCTTTATCTCCCTGGCGACAACCGAATGCATCCTCTTTGGGTAAATGGCCTATGACAGGTA
 15 TGCGGCCATATGTCGCGCGCTGCTTTACTCCTTGATCATGTCCAGGACCGTCTACCTAAAA
 ATGGCAGCCGGGGCTTTTGTGTCAGGGTGTGTAACCTTCATGGTCAACACAAGCCATGTCA
 GCAGCTTGTCATTCTGTGACTCCAATGTCATCCATCACTTCTTCTGTGACAGTCCCCCACTT
 TTCAAGCTCTCTTGTCTGACACAATCCTGAAAGAAAGCATAAGTTCTATTTTGGCTGGTG
 TGAATATTGTGGGACTCTGCTTGTCTATCCTCTCCTCCTACTCCTACGTTCTCTTCTCCATT
 20 TTTTCTATGCATTGCGGGGAGGGGAGGCACAGAGCTTTCTCCACGTGTGCCTCTCACCTGA
 CAGCCATAATTCTGTTCTATGCCACCTGCATCTATACTTACCTGAGACCTAGTTCAGCTAC
 TCCCTGAATCAGGACAAAAGTGGCTTCTGTGTTCTACACAGTGGTGATTCCCATGTTGAATC
 CTCTGATCTACAGCCTCAGGAGTAAGGAAAGTAAGGCTTTAGCGAATGTAATTAGCA
 GGAAAAGGACCTCTTCTTTCTGTGA (SEQ ID NO: 372)

AOLFR201 sequences:

MEWENHTILVEFFLKGLSGHPRLELLFFVLIFIMYVILLGNGTLILISILDPHLHTPMYFFLGNL
 SFLDICYTTTSTPSTLVSFLSERKTISLSGCAVQMFLGLAMGTTECVLLGMMAFDRYVAICNPLR
 YPIIMSKDAYVPMAAGSWIIGAVNSAVQSVFVVLQPFRCRNNIINHFTCEILAVMKLACADISDN
 30 EFIMLVATTLFILTPLLLIIVSYTLIIVSIFKISSSEGRSKASSTCSAHLTVVIIIFYGTILFMYMKPKS
 KETLNSDDL DATDKIISMFYGVMTMPMMNPLIYSLRNKDVKEAVKHLLNRRFFSK (SEQ ID NO:
 373)

ATGGAATGGGAAAACACACCATTTCTGGTGGAATTTTTTCTGAAGGGACTTTCTGGTCACC
 35 CAAGACTTGAGTTACTCTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG
 AATGGTACTCTCATTTTAATCAGCATCTTGGACCTCACCTTCACACCCCTATGTACTTCTT
 TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACGCTAG
 TGAGCTTCCTTTCAGAAAGAAAGACCATTTCCCTTTCTGGCTGTGCAGTGCAGATGTTCTT
 CGGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTAT
 40 GTGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA
 TGGCAGCTGGGTCTGGATCATAGGAGCTGTCAATTCTGCAGTACAATCAGTGTTTGTGGT
 ACAATTGCCTTTCTGCAGGAATAACATCATCAATCATTTTCACCTGTGAAATTCTGGCTGTC
 ATGAAACTGGCCTGTGCTGACATCTCAGACAATGAGTTCATCATGCTTGTGGCCACAACAT
 TGTTTCATATTGACACCTTTGTTATTAATCATTTGTCTCTTACACGTTAATCATTGTGAGCATC
 45 TTCAAAATTAGCTCTTCCGAGGGGAGAAGCAAAGCTTCCCTCTACCTGTTACGCCCATCTGA
 CTGTGGTCATAATATTCTATGGGACCATCCTCTTCATGTACATGAAGCCCAAGTCTAAAGA
 GACACTTAATTCGGATGACTTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTG
 ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCA
 GTAAACACCTACTGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 374)

AOLFR202 sequences:

MEWENHTILVEFFLKGLSGHPRLELLFFVLIFIMYVILLGNGTLILISILDPHLHTPMYFFLGNL
 SFLDICYTTTSTPSTLVSFLSERKTISLSGCAVQMFLSLAMGTTECVLLGVMAFDRYVAICNPLR
 YPIIMSKDAYVPMAAGSWIIGAVNSAVQTVFVVLQPFRCRNNIINHFTCEILAVMKLACADISGN
 55 EFILLVTTLFLLTPLLLIIVSYTLIILSIFKISSSEGRSKPSSTCSARLTVVITFCGTIFLMYMKPKSQ

CACATTTTGGTGCTACTGAGATCATCCTGCTGACAGTGATGGCCTGTGACTGCTATGTGG
CCATCTGCAAACCTCTGAACTACACAACCATTATGAGCCACAGCCTGTGCATTCTCCTGGT
GGCAGTGGCCTGGGTGGGAGGATTTCTTCATGCAACTATTTCAGATTCTCTTTACAGTATGG
5 CTGCCCTTCTGTGGCCCCAATGTCATAGGCCACTTCATGTGTGACTTGTACCCATTGTTAAA
ACTTGTTTGCATAGACACTCATACCCTTGGTCTCTTTGTTGCTGTGAACAGTGGGTTTATCT
GCTTATTAAACTTCCTTATCTTGGTGGTATCCTATGTGATCATCTTGAGATCTTTAAAGAAC
AATAGCTTGGAGGGGAGGTGTAAAGCCCTCTCCACCTGTATTTCTCATCATCATAGTAGTTG
TCTTATTCTTTGTGCCCTGTATTTTGTGTATCTGCGCTCAGTGACCACCTGTGCCATTGAT
AAAGCTGTTGCTGTATTTATACTATGGTGGTCCCAATGTTAAATCCCGTGGTCTACACAC
10 TCAGAAATGCTGAGGTAAAAAGTGCAATAAGGAAGCTTTGGAGAAAAAAAAGTGACTTCAG
ATAATGATTAA (SEQ ID NO: 380)

AOLFR205 sequences:

15 MESENRTVIREFILLGLTQSQDIQLLVFVLVLIFYFILPGNFLIIFTIKSDPGLTAPLYFFLGNLAFL
DASYSFTVAPRMLVDFLSAKKIISYRGCIQLFFLHFLGGGEGLLLVMAFDRYIAICRPLHYPT
VMNPRCTYAMMLALWLGGFVSHIIQVVLILRLPFCGPQNQLDNFFCDVPQVIKLACTDTFVVEL
LMVFNISGLMTLLCFLGLLASAYAVLCIRIGSSSEAKNKAMSTCITHIVFFMFGPGIFTYTRPFA
FPADKVVSLFHTVIFPLLNPVITYTLRNQEVKASMKKVFNKHIA (SEQ ID NO: 381)

20 ATGGAAGCGAGAACAGAAACAGTGTATAAGAGAATTCATCCTCCTTGGTCTGACCCAGTCT
CAAGATATTCAGCTCCTGGTCTTTGTGCTAGTTTTAATATTCTACTTCATCATCCTCCCTGG
AAATTTTCTCATTATTTTACCATAAAGTCAGACCCTGGGCTCACAGCCCCCTCTATTTCCT
TTCTGGGCAACTTGGCCTTCTGGATGCATCCTACTCCTTCACTGTGGCTCCCCGGATGTTG
25 GTGGACTTCCTCTCTGCGAAGAAGATAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTT
TCTTGCATTCCTTGGAGGAGGGGAGGGATTACTCCTTGTTGTGATGGCCTTTGACCGCTA
CATCGCCATCTGCCGGCCTCTGCACTATCCTACTGTCATGAACCCTAGAACCTGCTATGCA
ATGATGTTGGCTCTGTGGCTTGGGGGTTTGTGCCACTCCATTATCCAGGTGGTCCTCATCCT
CCGCTTGCTTTTTGTGGCCCAAACCAGCTGGACAACCTTCTTCTGTGATGTCCACAGGTC
ATCAAGCTGGCCTGCACCGACACATTTGTGGTGGAGCTTCTGATGGTCTTCAACAGTGGCC
30 TGATGACACTCCTGTGCTTTCTGGGGCTTCTGGCCTCCTATGCAGTCATTCTTTGTGCATA
CGAGGGCTCTTCTTGAGGCAAAAAACAAGGCCATGTCCACGTGCATCACCCATATCATTTG
TTATATTCTTCATGTTTGGACCTGGCATCTTCACTACACGCGCCCTTCAGGCGTTTCCCA
GCTGACAAGGTGGTTTCTCTCTTCCACACAGTGATTTTTCTTTGTGTAACCTGTGCATTTA
TACCTTTCGCAACCAGGAAGTGAAAGCTTCCATGAAAAAGGTGTTTAATAAGCACATAGC
35 CTGA (SEQ ID NO: 382)

AOLFR206 sequences:

MANRNNVTEFILLGLTENPKMQKIIFVVSFTYINAMIGNVLIVVTTITASPSLRSPMYFFLAYLSFI
40 DACYSSVNTPKLITDSLYENKTLFNGCMTQVFGHEFFRGVEVILLTVMAYDHYVAICKPLHYT
TIAMQKHVCSLLVGSWSVVGFLHATIQILFICQLPFCGPNVIDHMCGLYTLINLACTNTHTLGLF
IAANSFGICLLNCLLLVSCVILYSLKTHSLEARHEALSTCVSHITVVLSFIPCIFYMTRPPATL
PIDKAVAVFYTMITSMILNPLYTLRNAOMKNAIRKLCRKAISSVK (SEQ ID NO: 383)

45 ATGGCGAATAGAAACAATGTGACAGAGTTTATTCTATTGGGGCTTACAGAGAATCCAAAA
ATGCAGAAAATCATATTTGTGTGTTTTCTGTCATCTACATCAACGCCATGATAGGAAATG
TGCTCATTGTGGTCACCATCACTGCCAGCCCATCACTGAGATCCCCCATGTACTTTTCCCTG
GCCTATCTCTCCTTTATTGATGCCTGCTATTCCCTCTGTCAATACCCCTAAGCTGATCACAGA
TTCACCTCTATGAAAAACAAGACTATCTTATTCAATGGATGTATGACTCAAGTCTTTGGAGAA
CATTTTTTCAGAGGGTGTGAGGTACCTCTACTTAATGGCCTATGACCACATGTGG
50 CCATCTGCAAGCCCTTGACATATACCCACCATGTAAGCAGCATGTTTGTAGCCTGCTAGT
GGGAGTGTCAATGGGTAGGAGGCTTTCTTCATGCAACCATAAGATCCTCTTCATCTGTCAA
TTACCTTTCTGTGGTCCTAATGTGCATAGATCACTTTATGTGTGATCTCTACACTTTGATCAA
TCTTGCCCTGCACTAATACCCACACTCTAGGACTCTTCATTGCTGCCAACAGTGGGTTTCATAT
GCCTGTTAAAGTGCTCTTGCTCTGGTCTCTCGTGGTGCATCTGTACTCTCTTAAAGACC
55 CACAGCTTATGAGGCAAGGCATGAAGCCCTCTCACTGTGTCTCCCACTCAAGTTGTCA
TCTTATCCTTTATACCTGTCATATTTGTGTACATGAGACCTCCAGCTACTTTACCCATTGAT

AAAGCAGTTGCTGTATTCTACACTATGATAACTTCTATGTTAAACCCCTTAATCTACACCTT
GAGGAATGCTCAAATGAAAAATGCCATTAGGAAATTGTGTAGTAGGAAAGCTATTTCAAG
TGTCAAATAA (SEQ ID NO: 384)

5 **AOLFR207 sequences:**

MERTNDSTSTEFFLVGLSAHPKLQTVFFVLILWMYLMILLGNGVLISVIIFDSHLHTPMYFFLCN
LSFLDVCYTSSSVPLILASFLAVKKKVSFSGCMVQMFISFAMGATECMILGTMALDRYVAICYP
LRYPVIMSKGAYVAMAAGSWVTGLVDSVVQTAFAMQLPFCANNVIKHFVCEILAILKLACADI
SINVISMTGSNLIVLVIPLLVISISYIFIVATILRPSTEGKHKAFSTCSAHLTVVIIFYGTIFFMYACI
10 ESKASVDSGNEDIEALISLFYGVMTPLNPLIYSLRNKDVKA AVKNILCRKNFSDGK (SEQ ID
NO: 385)

ATGGAAAGGACCAACGATTCCACGTCGACAGAATTTTTCCTGGTAGGGCTTTCTGCCCACC
CAAAGCTCCAGACAGTTTCTTCGTTCTAATTTTGTGGATGTACCTGATGATCCTGCTTGGGA
15 AATGGAGTCCTTATCTCAGTTATCATCTTTGATTCTCACCTGCACACCCCATGTATTTCTT
CCTCTGTAATCTTTCTTCCTCGACGTTTGCTACACAAGTTCCTCTGTCCCACTAATTCTTG
CCAGCTTTCTGGCAGTAAAGAAAAAGGTTTCTTCTCTGGGTGTATGGTGAAATGTTTAT
TTCTTTTGCCATGGGGGCCACGGAGTGCATGATCTTAGGCACGATGGCACTGGACCGCTAT
GTGGCCATCTGCTACCACTGAGATAACCTGTCATCATGAGCAAGGGTGCCTATGTGGCCA
20 TGGCAGCTGGGTCTGGGTCACTGGGCTTGTGGACTCAGTAGTGCAGACAGCTTTTGCAAT
GCAGTTACCATTTCTGTGCTAATAATGTCATTAAACATTTTGTCTGTGAAATTTCTGGCTATCT
TGAAACTGGCCTGTGCTGATATTTCAATCAATGTGATTAGTATGACAGGGTGAATCTGAT
TGTTCTGGTTATTCATTGTTAGTAATTTCCATCTCTTACATATTTATTGTTGCCACTATTCT
GAGGATTCCTTCCACTGAAGGAAAACATAAGGCCTTCTCCACCTGCTCAGCCACCTGACA
25 GTGGTGATTATATTCTATGGAACCATCTTCTTCATGTACGCAAAGCCTGAGTCTAAAGCCT
CTGTTGATTCAGGTAATGAAGACATCATTTGAGGCCCTCATCTCCCTTTTCTATGCGAGTGAT
GACTCCCATGCTTAATCCTCTCATCTATAGTCTGCGAAACAAGGATGTAAAGGCTGCTGTC
AAAAACATACTGTGTAGGAAAAACTTTTCTGATGGAAAATGA (SEQ ID NO: 386)

30 **AOLFR208 sequences:**

MFPANWTSVKVFFFLGFFHYPKVQVIIFAVCLLMYLITLLGNIFLISITILDSHLHTPMYLFSLNL
SFLDIWYSSALSPMLANFVSGRNTISFSGCATQMYLSLAMGSTECVLLPMMAYDRYVAICNP
LRYPVIMNRRTCVQIAAGSWMTGCLTAMVEMMSVLPLSLCGNSIINHFTCEILAILKLVCVDTS
LVQLIMLVISVLLLPMPMLLICISYAFILASILRISSVEGRSKAFSTCTAHLMVVVLFGYGTALSMH
35 LKPSAVDSQEIDKFMA LVYAGQTPMLNPIIYSLRNKEVKVALKLLIRNHFNTAFISILK (SEQ
ID NO: 387)

ATGTTCCCGGCAAATTGGACATCTGTAAAAGTATTTTCTTCCTGGGATTTTTCCTACTACCC
CAAAGTTTCAAGTCATCATATTTGCGGTGTGCTTGCTGATGTACCTGATCACCTTGCTGGGC
40 AACATTTTCTGATCTCCATCACCATTCTAGATTCCCACCTGCACACCCCTATGTACCTCTT
CCTCAGCAATCTCTCCTTTCTGGACATCTGGTACTCCTCTCTGCCCTCTCTCCAATGCTGG
CAAACCTTTGTTTCAGGGAGAAACACTATTTTATTCTCAGGGTGCGCCACTCAGATGTACCT
CTCCCTTGCCATGGGCTCCACTGAGTGTGTGCTCCTGCCCATGATGGCATATGACCGGTAT
GTGGCCATCTGCAACCCCTGAGATAACCTGTCATCATGAATAGGAGAACCTGTGTGTCAGA
45 TTGCAGCTGGCTCCTGGATGACAGGCTGTCTCACTGCCATGGTGGAAATGATGTCTGTGCT
GCCACTGTCTCTGTGGTAATAGCATCATCAATCATTTCACTTGTGAAATTTCTGGCCATCT
TGAAATTGGTTTGTGTGGACACCTCCCTGGTGCAGTTAATCATGCTGGTGATCAGTGTACT
TCTTCTCCCATGCCAATGCTACTCATTTGTATCTCTTATGCATTTATCCTCGCCAGTATCC
TGAGAAATCAGCTCAGTGGAAGGTGGAAGTAAAGCCTTTTCAACGTGCACAGCCACCTGA
50 TGGTGGTAGTTTTGTTCTATGGGACGGCTCTCTCCATGCACCTGAAGCCCTCCGCTGTAGA
TTCACAGGAAATAGACAAATTTATGGCTTTGGTGTATGCCGGACAAACCCCATGTTGAAT
CCTATCATCTATAGTCTACGGAACAAAGAGGTGAAAGTGGCCTTGAAAAAATGCTGATTA
GAAATCATTTTAATACTGCCTTCATTTCATCCTCAAATAA (SEQ ID NO: 388)

AOLFR209 sequences:

- MDKINQTFVREFILLGLSGYPKLEIFFALILVMYVVILIGNGVLIASILDSRLHMPMYFFLGNLS
 5 FLDICYTTSSIPSTLVSLISKRNISFSGCAVQMFFGFAMGSTECFLLGMMAFDRYVAICNPLRY
 PIIMNKVVYVLLTSVSWLSGGINSTVQTSLAMRWPF CGNNIINHFLCEILAVLKLACSDISVNV
 TLAVSNIAFLVPLLVIFFSYMFILYTLRTNSATGRHKAFTSCSAHLTVVIIFYGTIFFMYAKPKS
 QDLLGKDNLQATEGLVSMFYGVVTPMLNPIIYSLRNKDVKAAIKYLLSRKAINQ (SEQ ID NO:
 389)
- 10 ATGGACAAGATAAACCAGACATTTGTGAGAGAATTCATTCTTCTGGGACTCTCTGGTTACC
 CCAAACCTTGAGATCATTTTCTTTGCTCTGATTCTAGTTATGTACGTAGTGATTCTAATTGGC
 AATGGTGTTCTGATCATAGCAAGCATCTTGGATTCTCGTCTTCACATGCCATGTACTTCTT
 CCTGGGCAACCTCTCTTTCTGGATATCTGCTATACAACCTCCTCCATCCCTCAACACTGG
 TGAGCTTAATCTCAAAGAAAAGAAACATTTCTTCTCTGGATGTGCAGTGCAGATGTTCTT
 15 TGGGTTTGCAATGGGGTCAACAGAATGTTTCTCTTGGCATGATGGCATTGATCGTTAT
 GTGGCCATCTGTAACCTCTGAGATACCCCATCATCATGAACAAGGTGGTGTATGTACTGC
 TGACTTCTGTATCATGGCTTTCTGGTGAATCAATTCAACTGTGCAAACATCACTTGCCAT
 GCGATGGCCTTTCTGTGGGAACAATATTATTAATCATTTCTTATGCGAGATCTTAGCTGTCC
 TAAAATTAGCTTGTTCTGATATATCTGTCAATATTGTTACCCTAGCAGTGTCAAATATTGCT
 20 TTCCTAGTTCTTCTCTGCTCGTGATTTTTTTCTCCTATATGTTTCATCCTCTACACCATCTTG
 CGAACGAACTCGGCCACAGGAAGACACAAGGCATTTTCTACATGCTCAGCTCACCTGACTG
 TGGTGATCATATTTTATGGTACCATCTTCTTTATGTATGCAAAACCTAAGTCCCAGGACCTC
 CTTGGGAAAAGACAACCTGCAAGCTACAGAGGGGCTTGTTCATGTTTTATGGGGTTGTGA
 CCCCCATGTTAAACCCATAATCTATAGCTTGAGAAATAAAGATGTAAAGCTGCTATAAA
 25 ATATTTGCTGAGCAGGAAAGCTATTAACAGTAA (SEQ ID NO: 390)

AOLFR210 sequences:

- MMGRRNDTNVADFILTGLSDSEEVQMALFMLFLLIYLTMLGNVGMILLIRLDLQLHTPMYFFL
 30 THLSFIDLSYSTVVPKTLANLLTSNYISFTGCF AQMFCFVFLGTAECYLLSSMAYDRYAAICSP
 LHYTVIMPKRLCLALITGPYVIGFMDSFVNVVSMRSLHFCDNSIIHHFFCDTSPILALSCTDTDN
 TEMPLIFLAGSTLMVSLITISASYVLSLTKINSTSGKQKAFSTCVSHLLGVTIFYGTMIIFYLKP
 RKSYSLGRDQVAPVFYTIIVPMLNPLIYSLRNREVKNALIRVMQRRQDSR (SEQ ID NO: 391)
- 35 ATGATGGGTAGAAGGAATGACACAAATGTGGCTGACTTCATCCTTACGGGACTGTCAGAC
 TCTGAAGAGGTCCAGATGGCTCTGTTTATGCTATTTCTCCTCATATACCTAATTACTATGCT
 GGGGAATGTGGGATGCTATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTAT
 TTTTCTTACTCACCTGTCAATTTATTGACCTCAGTTACTCAACTGTCGTCACACCTAAAAC
 CTTAGCGAACTTACTGACTTCCAACATATTTCTTTCACGGGCTGCTTTGCCAGATGTTCT
 40 GTTTTGTCTTCTTGGGTACTGCTGAATGTTATCTTCTCTCCTCAATGGCCTATGATCGCTAT
 GCAGCGATCTGCAGTCCTCTACACTACACAGTTATTATGCCAAAAGGCTCTGCCTCGCTC
 TCATCACTGGGCCTTATGTGATTGGCTTTATGGACTCCTTTGTCAATGTGGTTTCCATGAGC
 AGATTGCATTTCTGTGACTCAAACATAATTCATCACTTTTCTGTGACACTTCCCCAATTTT
 AGCTCTGTCTGCACTGACACAGACAACACTGAAATGCTGATATTCATTATCGCTGGTTCC
 ACCCTGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTCTACCATCCT
 45 GAAAATTAATTCACCTCAGGAAAGCAGAAAGCTTTCTCTACTTGCGTCTCTCATCTCTTG
 GGAGTCACCATCTTCTATGGAACATGATTTTTACTTACTTAAAGCCAAGAAAGTCTTATT
 CCTTGGGAAGAGATCAAGTGGCTCCTGTGTTTTATACTATTGTGATTCCCATGCTGAATCC
 ACTCATTTATAGTCTTAGAAACAGAGAAGTGAAAAATGCTCTCATTAGAGTCATGCAGAG
 AAGACAGGACTCCAGGTAG (SEQ ID NO: 392)

50

AOLFR211 sequences:

- MMGRRNNTNVADFILMGLTSLSEEIQMALFMLFLLIYLTMLGNVGMILLIRLDLQLHTPMYFFL
 55 THLSFIDLSYSTVVPKTLANLLTSNYISFTGCF AQMFFFAFLGTAECYLLSSMAHRYAAICSP
 LHYTVIMSKRLCLALITGPYVIGFIDSFVNVVSMRSLHFYDSNVIIHHFFCDTSPILALSCTDTYNT
 EILIFIIVGSTLMVSLFTISASYVLFILTKINSTSGKQKAFSTCVSHLLGVTIFYSTLIFTYLYLKP
 SYSLGRDQVASVFYTIIVPVLNPLIYSLRNKEVKNAVIRVMQRRQDSR (SEQ ID NO: 393)

ATGATGGGTAGAAAGGAATAACACAAATGTGGCTGACTTCATCCTTATGGGACTGACACTTT
 CTGAAGAGATCCAGATGGCTCTGTTTATGCTATTTCTCCTGATATACCTAATTACTATGCTG
 GGAATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTATT
 5 TTTTCCTTACTCACCTGTCATTTATTGACCTCAGTTACTCAACTGTCGTCACACCTAAAACC
 TTAGCGAACTTACTGACTTCCAACATATTTCCCTTTACGGGCTGCTTTGCCAGATGTTCTT
 TTTTGCCTTCTTGGGTACTGCTGAATGTTACCTTCTCTCCTCAATGGCCCATGATCGCTATG
 CAGCGATCTGCAGTCTCTACACTACACAGTTATTATGTCCAAAAGGCTCTGCCTCGCTCT
 CATCACTGGGCCTTATGTGATTGGCTTTATAGACTCCTTTGTCAACGTGGTTTCCATGAGCA
 10 GATTGCATTTCTACGACTCAAACGTAATTCATCACTTTTTCTGTGACACTTCCCCAATTTTA
 GCTCTGTCTGCACTGATACATAACAACCCGAAATCCTGATATTCATTATTGTTGGTTCCAC
 CCTGATGGTGTCCCTTTTCACAATATCTGCATCCTATGTGTTCACTTCTCTTACCATCCTGA
 AAATTAATTCCACTTCAGGAAAGCAGAAAGCTTTCTCTACTTGGCTCTCATCTCTTGGG
 AGTCACCATCTTTTATAGCACTCTGATTTTACTTATTTAAAACCAAGAAAGTCTTATTCCT
 15 TGGGAAGAGATCAAGTGGCTTCTGTTTTTATACTATTGTGATTCCCGTGCTGAATCCACT
 CATTATAGTCTTAGAAACAAAGAGGTGAAAAATGCTGTCATCAGAGTCATGCAGAGAAG
 ACAGGACTCCAGGTAA (SEQ ID NO: 394)

AOLFR212 sequences:

20 MAGNNFTEVTVFILSGFANHPQLVSLFLMFLFTYLFVTLGNLGLITLIRMDSQLHTPMYFFLSN
 LAFIDIFYSTVTPKALVNFQSNRRSISFVGCQVQMYFFVGLVCCECFLLGSMAYNRYIAICNPL
 LYSVMSQKVSNNWLGVMFYVIGFTSSLISVWVISSLAFCDSINHHFCDTALLALSCVDTFGT
 EMVSFVLGFTLLSLLITVTYIIISAILRQSAAGRQKAFSTCASHLMAVTIFYGSLIFTYLQPD
 NTSSLTQAQVASVFYTVIPMLNPLIYSLRNKDVKNALLRVIHRKLFP (SEQ ID NO: 395)

25 ATGGCTGGCAACAATTTCACTGAGGTTACCGTCTTCATCCTCTCTGGATTTGCAAATCACC
 CTGAATTACAAGTCAGTCTTTCTTGATGTTTCTCTTCACTTATCTATTCAGTCTTTTGGGA
 AACCTGGGACTGATCACGTTAATCAGAATGGATTCTCAGCTTCACACCCCTATGTACTTTT
 TCCTGAGCAATTTAGCATTTATTGACATATTTTACTCCTCTACTGTAACACCTAAGGCATTG
 30 GTGAATTTCCAATCCAATCGGAGATCCATCTCCTTTGTTGGCTGCTTTGTTCAAATGTACTT
 TTTTGTGGATTGGTGTGTTGTGAGTGTTCCTTCTGGGATCAATGGCCTACAATCGCTACA
 TAGCAATCTGCAATCCCTTACTGTATTCACTAGTATGTCCTCAAAAAGTGTCCAACCTGGCT
 GGGAGTAATGCCATATGTGATAGGCTTCACAAGCTCGCTGATATCTGTCTGGGTGATAAGC
 AGTTTGGCGTTCTGTGATTCCAGCATCAATCATTTTTTTTGTGACACCACAGCTCTTTTAGC
 35 ACTCTCCTGTGTAGATACATTCCGGCACAGAAATGGTGAGCTTTGTCTTAGCTGGATTCACT
 CTTCTTAGCTCTCTCCTTATCATCACAGTCACTTATATCATCATCTCAGCCATCCTGAG
 GATCCAGTCAGCAGCAGGCAGGCAGAAAGCCTTCTCCACCTGCGCATCCCACCTCATGGCT
 GTAACCTATCTTTATGGGTCTCTGATTTTACCTATTTGCAACCTGATAACACATCATCGCT
 GACCCAGTCAGGAGGTGGCATCTGTATTCTATACGATTGTGATTCCCATGTAATCCACTC
 40 ATCTACAGTCTGAGGAACAAAGATGTGAAAAATGCTCTTCTGAGAGTCATACATAGAAAA
 CTTTTTCCATGA (SEQ ID NO: 396)

AOLFR213 sequences:

45 MNSLGKLVSMILSAHVFCYSKFNCFCGCTHSIPALGADPPGGMGLGNESSLMDFILLGFSHPRL
 EAVLFVFLFFYLLTLVGNFTIIISYLDPLHTPMYFFLSNLSLLDICFTTSLAPQTLVNLQRPKK
 TITYGGCVAQLYISLALGSTECILLADMALDRYIAVCKPLHYVVMNPRLCQQLASISWLSGLA
 SSLIHATFTLQLPLCGNHRLDHFICEVPALLKLACVDTTVNELVLFVSVLFPVIPPALISISYGF
 TQAVLRIKSVEARHKAFSTCSSHLTVVIIFYGTIIYVYLQPSDSYAQDQGKFISLFYTMVTPILNP
 IYTLRNKDMKEALRKLLSGKL (SEQ ID NO: 397)

50 ATGAATAGTTTGGGAAAGTTGGTCTCCATGATCCTCTCAGCTCATGTGTTCTGTTATTTCTAA
 ATTTAATTGTTTTGGATGTACCCATTCCATTCTGCCTTAGGTGCGGATCCCCCTGGAGGG
 ATGGGATTGGGCAATGAGAGTTCCCTAATGGATTTTCATCCTTCTAGGCTTCTCAGACCACC
 CTCGTCTGGAGGCTGTTCTCTTTGTATTTGTCTTTTCTTCTACCTCCTGACCCCTGTGGGA
 55 AACTTCACCATAATCATCATCTCATATCTGGATCCCCCTCTTCATACCCCAATGTACTTTTT
 TCTCAGCAACCTCTCTTACTGGACATCTGCTTCACTACTAGCCTTGCTCCTCAGACCTTAG

TTAACTTGCAAAGACCAAAGAAGACGATCACTTACGGTGGTTGTGTGGCGCAACTCTATAT
 TTCTCTGGCACTGGGCTCCACTGAATGTATCCTCTTGGCTGACATGGCCTTGGATCGGTAC
 ATTGCTGTCTGCAAACCCCTCCACTATGTAGTCATCATGAACCCACGGCTTTGCCAACAGC
 TGGCATCTATCTCTGGCTCAGTGGTTTGGCTAGTTCCCTAATCCATGCAACTTTTACCTTG
 5 CAATTGCCTCTCTGTGGCAACCATAGGCTGGACATTTTATTTGCGAAGTACCAGCTCTTCT
 CAAGTTGGCTTGTGTGGACACCACTGTCAATGAATTGGTGTCTTTTGTGTAGTGTCTGT
 TTGTGTGTCATTCCACCAGCACTCATCTCCATCTCCTATGGCTTCATAACTCAAGCTGTGCTG
 AGGATCAAATCAGTAGAGGCAAGGCATAAAGCCTTCAGCACCTGCTCCTCCCACCTTACAG
 TGGTGATTATATTCTATGGCACCATAATCTACGTGTACCTGCAACCTAGTGACAGCTATGC
 10 CCAGGACCAAGGGAAGTTTATCTCCCTCTTCTACACCATGGTGACCCCCACTTTAAATCCT
 ATCATCTATACTTTAAGGAACAAGGATATGAAAGAGGCTCTGAGGAAACTTCTCTCGGA
 AAATTGTGA (SEQ ID NO: 398)

AOLFR214 sequences:

15 MDKSNSSVVSEFVLLGLCSSQKLQLFYCFSSVLYTVIVLGNLLIILTVTSDTSLHSPMYFLLGN
 LSFVDICQASFA TP KMIADFLSAHETISFSGCIAQIFFIHLFTGGEMVLLVSMAYDRYVAICKPLY
 YVVMISRRCTCTVLMISWAVSLVHTLSQLSFTVNLPFCGPNVDSFFCDLPRVTKLACLD SYIIE
 ILIVVNSGILSLSTFSLLVSSYIILVTWVKSSAAMAKAFSTLASHIAVVILFFGPCIFYVWPFTIS
 20 PLDKFLAIFYTVFTPVLPNIYTLNRNMDKA A VRKIVNHYLRPRRISEMSLVVRTSFH (SEQ ID
 NO: 399)

ATGGATAAGTCCAATTCTTCAGTGGTGTCTGAATTTGTA CTGTTGGGACTCTGTAGTTCTC
 AAAA ACTCCAGCTTTTCTATTTTGTCTTCTCTGTGTTGTATACAGTCAITGTGCTGGGA
 AATCTTCTCATTATCCTCACAGTGACTTCTGATACCAGCCTGCACTCCCCTATGTACTTTCT
 25 CTGGGAAACCTTTCTTTGTTGACATTTGTCAGGCTTCTTTTGCTACCCCTAAAATGATTG
 CAGATTTTCTGAGTGACACGAGACCATATCTTTCAGTGGCTGCATAGCCCCAAATTTTCTT
 ATTCACCTTTTACTGGAGGGGAGATGGTGCTACTTGTTCGATGGCCTATGCAGGATG
 TAGCCATATGCAAACCCCTTATACTATGTGGTCATCATGAGCCGAAGGACATGCACTGTCTT
 GGTAATGATCTCCTGGGCTGTGAGCTTGGTGACACATTAAGCCAGTTATCATTTACTGTG
 30 AACCTGCCCTTTTGTGGACCTAATGTAGTAGACAGCTTTTTTGTGATCTTCTCGAGTCAC
 CAAACTTGCTGCTGGACTCTTACATCATTGAAATACTAATTGTGGTCAATAGTGGAATT
 CTTTCCCTAAGCACTTTCTCTCTTGGTCAGCTCCTACATCATTATTCTTGTACAGTTTG
 GCTCAAGTCTTCAAGCTGCAATGGCAAAGGCATTTTCTACGCTGGCTTCCCATTATGCAGTA
 GTAATATTATTCTTTGGACCTTGCATCTTCATCTATGTGTGGCCCTTTACCATCTCTCCTT
 35 GGATAAATTTCTTGCCATATTTTACACTGTTTTCACCCCCGTCCTAAACCCATTATTTATA
 CACTAAGGAATAGGGATATGAAGGCTGCCGTAAGGAAAATTGTGAACCATTACCTGAGGC
 CAAGGAGAATTTCTGAAATGTCACTAGTAGTGAGAACTTCCTTTCATTAA (SEQ ID NO:
 400)

AOLFR215 sequences:

40 MAHTNESMVSEFVLLGLSNSWGLQLFFFAIFSIVYVTSVLGNVLIIVISFDSHLNSPMYFLLSNL
 SFIDICQSNFATPKMLVDFFIBERKTISFEGCMAQIFVLHSFVGSEMMLLVAMAYDRFIAICKPLH
 YSTIMNRRLCVIFVSISWAVGVLHVSVSHLAFTVDLPFCGPNEVDSFFCDLPLVIELACMDTYEM
 EIMTLTNSGLISLSCFLALHSYTHLIGVRCRSSSGSSKALSTLTAHITVVILFFGPCIFYFIWPPSRL
 45 PVDKFLSVFYTVCTPLNPIIYSLRNEDVKAAMWKLRNHHVNSWKN (SEQ ID NO: 401)

ATGGCTCACACAAATGAATCGATGGTGTCTGAGTTTGTACTTTTGGGACTCTCTAATTCCT
 GGGGACTTCAACTTTTCTTTTCGCCATCTTCTCTATAGTCTATGTGACATCAGTGCTAGGC
 AATGTCTTAATTATTGTCAATTATTTCTTTGACTCCCATTTGAACTCTCCTATGTACTTCTG
 50 CTCAGTAATCTTTCTTTTCATTGATATCTGTGACTCACTTGGCCACCCCAAGATGCTTGT
 AGACTTTTTTATTGAGCGCAAGACTATCTCCTTTGAGGGTTGCATGGCCCAGATATTCGTT
 CTTACAGTTTTTGTGGGAGTGAGATGATGTTGCTTGTAGCTATGGCATATGACAGATTTA
 TAGCCATATGTAAGCCTCTGCACTACAGTACAATTATGAACCGGAGGCTCTGTGTAATTTT
 TGTGTCTATTTCTGGGCGGTGGGCGTTCTTCATTCTGTGAGCCACTTGGCTTTTACAGTGG
 55 ACCTGCCATTCTGTGGTCCCAATGAGGTGGATAGCTTCTTTTGTGACCTTCCCTTGGTGATA
 GAGCTGGCTTGCATGGATACATATGAAATGGAAATTATGACCCTAACGAACAGTGGCCTG

ATATCATTGAGCTGTTTCCTGGCTTTAATTATTTCTACACCATCATTTTGATCGGTGTCCG
 ATGCAGGTCTCCAGTGGGTCATCTAAGGCTCTTTCTACATTAAGTGGCCACATCAGATG
 GTCATTCTTTTCTTCGGGCTTGCATTTATTTCTATATATGGCCTTTTAGCAGACTTCTGT
 GGACAAATTTCTTTCTGTGTCTACACTGTTTGTACTCCCTTGTGAACCCCATCATCTACT
 5 CTTTGAGGAATGAAGATGTTAAAGCAGCCATGTGGAAGCTGAGAAACCATCATGTGAAC
 CTGGAAAACTAG (SEQ ID NO: 402)

AOLFR216 sequences:

MDVGNKSTMSEFVLLGLSNWELQMFFFMVFSLLYVATMVGNLIVITVIVDPHLHSPMYFLL
 10 TNLSIIDMSLASFATPKMITDYLTHKTSISFDGCLTQIFFLHLFTGTEILLMAMSFDRYIAICKPL
 HYASVISPPQVCVALVVASWIMGVMHSMQVIFALTFPCGPYEVDSEFFCDLPVVFLACVDY
 VLGLFMISTSGIILSCFIVLFNSYVIVLVTVKHSSRGSSKALSTCTAHFIVVFLFFGPCIFYMW
 PLSSFLTDKILSVFYTIFTPTLNPITYTLRNQEVKIAMRKLKNRFLNFKAMPS (SEQ ID NO: 403)

15 ATGGATGTGGGCAATAAGTCTACCATGTCTGAATTTGTTTTGCTGGGGCTCTCTAATTCCT
 GGGAACTACAGATGTTTTCTTTATGGTGTTCATTGCTTTATGTGGCAACAATGGTGGG
 TAACAGCCTCATAGTCATCACAGTTATAGTGGACCCTCACCTACACTCTCCTATGTATTTCC
 TGCTTACCAATCTTTCAATCATTGATATGTCTCTTGCTTCTTTTCGCCACCCCAAAGATGATT
 ACAGATTACCTAACAGGTCACAAAACCATCTCTTTGATGGCTGCCTTACCCAGATATTCT
 20 TTCTCCACCTTTTCACTGGAAGTGAATCATCTTACTCATGGCCATGTCTTTGATAGGTAT
 ATTGCAATATGCAAGCCCTGCACTATGCTTCTGTCTATTAGTCCCCAGGTGTGTGTGTCTCT
 CGTGGTGGCTTCTGGATTATGGGAGTTATGCATTCAATGAGTCAGGTCATATTTGCCCTC
 ACGTTACCATCTGTGGTCCCTATGAGGTAGACAGCTTTTTCTGTGACCTTCCTGTGGTGT
 CCAGTTGGCTTGTGTGGATACTTATGTTCTGGGCCTCTTTATGATCTCAACAAGTGGCATA
 25 ATTGCGTTGTCTGTTTTATTGTTTTATTTAATTCATATGTTATTGTCTGGTTACTGTGAA
 GCATATTCTTCCAGAGGATCATCTAAGGCCCTTTCTACTTGTACAGCTCATTTTCTCACA
 TCTTCTGTTCTTTGGGCCATGCATCTTCTCATCATGTGGCCACTAAGCAGCTTTCTCACA
 GACAAGATTCTGTCTGTGTTTTATACCATCTTTACTCCCACTCTGAACCCAATAATCTATAC
 TTTGAGGAATCAAGAAGTAAAGATAGCCATGAGGAACTGAAAAATAGGTTTCTAAATTT
 30 TAATAAGGCAATGCCTTCATAG (SEQ ID NO: 404)

AOLFR217 sequences:

MLESFQKSEQMAWSNQSAVTEFILRGLSSSLELQIFYFLFFSIVYAATVLGNLLIVVTIASEPHLH
 SPTYFLLGNLSFIDMSLASFATPKMIADFLREHKAI SFEGCMTQMFFLHLLGGAIEVLLISMSTF
 35 RYVAICKPLHYLTMSRRMCVGLVLSWVIGIFHALSQLAFTVNLPFCGPNEVDSEFFCDLPVVK
 LACVDYTYLGVFMISTSGMIALVCFILLVISYTHLVTVRQRSSGSSKALSTCSAHFTVTVLFFGP
 CTFIYVWPFTNFPIDKVLVSVFYTTYTPLLNPVIYTVRNKDVKYSMRKLSSHIFKSRKTDHTP
 (SEQ ID NO: 405)

40 ATGCTAGAGTCTTCCAGAAATCAGAGCAAAATGGCCTGGAGCAATCAGTCTGCGGTAACC
 GAATTCATACTACGGGGTCTGTCCAGTTCTTTAGAACTCCAGATTTTCTACTTCTGTTTTT
 CTCCATAGTCTATGCAGCCACTGTGCTGGGGAACCTTCTTATTGTGGTCACCATTGCATCA
 GAGCCACACCTTCATTCCCCTACGTACTTTCTGCTGGGCAATCTCTCCTTCATTGACATGTC
 CCTGGCCTCATTTGCCACCCCAAAATGATTGCAGACTTCTTAGAGAACACAAAGCCATC
 45 TCTTTTGAAGGCTGCATGACCCAGATGTTCTTCTACATCTCTTAGGGGGTGTGAGATTG
 TACTGCTGATCTCCATGTCTTTGATAGGTACGTGGCTATCTGTAAGCCTCTACATTACCTA
 ACAATCATGAGCCGAAGAATGTGTGTTGGGCTTGTGATACTTTCTGGATTGTGGGCATCT
 TCCATGCTCTGAGTCAGTTAGCATTTACAGTGAATCTGCCCTTCTGTGGACCCAATGAAGT
 AGACAGTTTCTTTGTGACCTCCCTTTGGTGATTAACCTTGCTTGTGTGCGACACATATATTC
 50 TGGGGGTGTTTCATGATCTCAACCAAGTGGCATGATTGCCCTGGTGTGCTTCACTCTTGGT
 GATCTCTTACACTATCATCTGGTCAACCGTTCGGCAGCGTTCTCTGGTGGATCCTCCAAA
 GCCCTCTCCACGTGCAGTGGCCACTTTACTGTTGTGACCCCTTTCTTTGGCCCATGCACTTT
 CATTTATGTGTGGCCTTTCAAAAATTTCCCAATAGACAAAGTACTCTCAGTATTTTATACCA
 TATACACTCCCCTCTTGAATCCAGTGATCTATACCGTTAGGAATAAAGATGTCAAGTATTC
 55 CATGAGGAACTAAGCAGCCATATCTTTAAATCTAGGAAGACTGATCATACTCCTTAA
 (SEQ ID NO: 406)

AOLFR218 sequences:

METANYTKVTEFVLTLGLSQTREVLVLFVIFLSFYLFILPGNLIICTIRLDPHLTSPMYFLLANLA
 LLDIWYSSITAPKMLIDFFVERKIIISFGGCIQLFFLHFVGAEMFLLIVMAYDRYAAICRPLHYA
 5 TIMNRRLLCCILVALSWMGGFIHSIIQVALIVRLPFCGPNELDSYFCDITQVVRIACANTFPEELVM
 ICSSGLISVVCFIALLMSYAFLLALLKKHSGSDENTNRAMSTCYSHITTVLVMFGPSIYIYARPF
 SFLDKVVSFHTVIFLLNPIIYTLRNKEVKAAMRKVVTKYILCEEK (SEQ ID NO: 407)

ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC
 10 GGGAGGTCCAACTAGTCCTATTTGTTATATTTCTATCCTTCTATTTGTTTCATCCTACCAGGA
 AATATCCTTATCATTTGCACCATCAGGCTAGACCCTCATCTGACTTCTCCTATGTATTTCT
 GTTGGCTAATCTGGCCCTCCTTGATATTTGGTACTCTTCCATTACAGCCCCATAAATGCTCA
 TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTGGTGGATGCATTGCACAGCTCTTCTT
 CTTACACTTTGTTGGGGCTTCGGAGATGTTCTTGCTCATAGTGATGGCCTATGACCGCTAT
 15 GCTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCGACGCTCTGCTGTATCCT
 GGTGGCTCTCTCCTGGATGGGGGGCTTCATTCTATAATACAGGTGGCTCTCATTGTT
 CGACTTCTTTCTGTGGGCCCAATGAGTTAGACAGTACTTCTGTGACATCACACAGGTG
 TCCGGATTGCCTGTGCCAACACCTTCCCAGAGGAGTAGTGATGATCTGTAGTAGTGGTCT
 GATCTCTGTGGTGTGTTTCATTGCTCTGTTAATGTCCTATGCCTTCCTTCTGGCCTTGCTCA
 20 AGAAACATTACAGGCTCAGATGAGAATACCAACAGGGCCATGTCCACCTGCTATTCCCACAT
 TACCATTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCCATTTGACTCAT
 TTTCCCTAGATAAAGTGGTGTCTGTGTTTCATACTGTAATATCCCTTTACTTAATCCCATT
 ATTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGGTGGTCACCAAATAT
 ATTTGTGTGAAGAGAAGTGA (SEQ ID NO: 408).

25

AOLFR219 sequences:

MLTSLTDLCSPIQVAEIKSLPKSMNETNHSRVTEFVLLGLSSSRELQPFLFLTFSLLYLAILLGNF
 LILTVTSDSRLHTPMYFLLANLSFIDVCVASFATPKMIADFLVERKTISFDACLAQIFVHLFTGS
 EMVLLVSMAYDRYVAICKPLHYMTVMSRRVCVVLVLISWVFGFIHTTSQLAFTVNLPCGPN
 30 KVDSEFCDLPLVTKLACIDTYVVSLLIVADSGFLSLSSFLLLVSYSYTVILVTVNRSSASMAKAR
 STLAHITVVTLFFGPCIFIYVWPSSYSVDKVLAVFYTIFTLILNPVIYTLRNKEVKAAMSKLKS
 RYLKPSQVSVVIRNVLFLETK (SEQ ID NO: 409).

ATGCTCACTTCATTAAGTATCTCTGTTTCTCTCCTATTCAGGTAGCTGAAATTAAGTCCCT
 35 TCCAAAATCGATGAATGAGACAAATCATTCTCGGGTGACAGAATTTGTGTTGCTGGGACTG
 TCTAGTTCAAGGGAGCTCCAACCTTTCTGTTTCTTACATTTTCACTACTTTATCTAGCAAT
 TCTGTTGGGCAACTTTCTCATCATCTCATCTGACCTCAGATTCCCGCCTTCACACCCCCA
 TGTACTTTCTGCTTGCAAACCTGTCATTTATAGACGATGTGTTGCCTCTTTTGCTACCCCT
 AAAATGATTGCAGACTTTCTGGTTGAGCGCAAGACTATTTCTTTTGATGCCTGCCTGGCCC
 40 AGATTTTCTTTGTTTCATCTCTTCACTGGCAGTGAAATGGTGCTCCTAGTTTCCATGGCCTAT
 GACCGTTATGTTGCTATATGCAAACCTCTCCACTACATGACAGTCATGAGCCGTCGTGTAT
 GTGTTGTGCTCGTCCTCATTTTCATGGTTTGTGGGCTTCATCCATACTACCAGCCAGTTGGCA
 TTCACTGTTAATCTGCCATTTTGTGGTCTTAATAAGGTAGACAGTTTTTCTGTGACCTTCC
 TCTAGTGACCAAGTTAGCCTGCATAGACACTTATGTTGTGACGTTACTAATAGTTGCAGAT
 45 AGTGGCTTTCTTTCTCTGAGTTCTTTCTCCTCTTGTTGTCTCCTACACTGTAATACTTGT
 ACAGTTAGGAATCGCTCCTCTGCAAGCATGGCGAAGGCCCGCTCCACATTGACTGCTCACA
 TCACTGTGGTCACTTTATTCTTTGGACCATGCATTTTCATCTATGTGTGGCCCTTCAGCAGT
 TACTCAGTTGACAAAGTCTTGCTGTATTCTACACCATCTTCACGCTTATTTTAAACCTGT
 AATCTACACGCTAAGAAACAAAGAGTGAAGGCAGCTATGTCAAAACTGAAGAGTCGGTA
 50 TCTGAAGCCTAGTCAGGTTTCTGTAGTCATAAGAAATGTTCTTTTCTAGAAACAAAGTAA
 (SEQ ID NO: 410).

AOLFR220 sequences:

MKQYSVGNQHSNYRSLFPFLCSQMTQLTASGNQTMVTEFLFSMPHAHRGGLLFIPLLLIYG
 55 FILTGNLIMFIVIQVGMALHTPLYFFISVLSEICYYTTTTIPKMLSCLISEQKSISVAGCLLQMYFF
 HSLGITESCVLTAIDRYIAICNPLRYPTIMPKLCIQLTVGSCFCGFLVLPEIAWISTLPFCGS

NQIHQIFCDFTPVLSLACTDTFLVVIVDAIHAAEIVASFLVIALSYIRIIIVILGMHSAEGHHKAFST
CAAH LAVFLFFGSAVMYLRFSATYSVFWDTALAVTFVILAPFFNPIIYSLKNKDMKEAIGRLF
HYQKRAGWAGK (SEQ ID NO: 411).

5 ATGAAGCAATATTCAGTGGGTAATCAACATTCCAATTATAGGAGTCTCTTGTTTCCTTTTCT
GTGTTACAGATGACACAGTTGACGGCCAGTGGGAATCAGACAATGGTGACTGAGTTCCT
CTTCTCTATGTTCCCGCATGCGCACAGAGGTGGCCTCTTATTCTTTATTCCTTGCTTCTCA
TCTACGGATTTATCCTAACTGGAAACCTAATAATGTTTCATTGTCATCCAGGTGGGCATGGC
10 CCTGCACACCCCTTTGTATTTCTTTATCAGTGTCTCTCTCTTCTGGAGATCTGCTATACCA
CAACCACCATCCCCAAGATGCTGTCTGCCTAATCAGTGAGCAGAAGAGCATTTCGGTGGC
TGGCTGCCTCCTGCAGATGTACTTTTTCCACTCACTTGGTATCACAGAAAGCTGTGTCTG
ACAGCAATGGCCATTGACAGGTACATAGCTATCTGCAATCCACTCCGTTACCCAACCATCA
TGATTCCCAAACCTTTGTATCCAGCTGACAGTTGGATCCTGCTTTTGTGGCTTCCTCCTTG
15 CTTCTGAGATTGCATGGATTTCACCTTGCTTTCTGTGGCTCCAACCAGATCCACCAGAT
ATTCTGTGATTTACACCTGTGCTGAGCTTGGCCTGCACAGATACATTCTAGTGGTCATT
GTGGATGCCATCCATGCAGCGGAAATTGTAGCCTCCTTCCTGGTCATTGCTCTATCCTACA
TCCGGATTATTATAGTGATTCTGGGAATGCACTCAGCTGAAGGTCATCACAAGGCCTTTTC
CACCTGTGCTGCTACCTTGCTGTGTTCTTGCTATTTTTGGCAGTGTGGCTGTCTGATTT
TGAGATTCTCAGCCACCTACTCAGTGTTTGGGACACAGCAATTGCTGTCACTTTTGTTATC
20 CTTGCTCCCTTTTCAACCCCATCATCTATAGCCTGAAAAACAAGGACATGAAAGAGGCTA
TTGGAAGGCTTTTCCACTATCAGAAGAGGGCTGGTTGGGCTGGGAAATAG (SEQ ID NO:
412).

AOLFR221 sequences:

25 MRNLSGGHVBEFVLVGFPPTPPLQLLLFVLFIAIYLLTLENALIVFTIWLAPSLHRPAMYFFLGH
LSFLELWYINVTIPRLAAFLTQDGRVSYVGCMTQLYFFIALACTECVLLAVMAYDRYLACGP
LLYPSLMPSSLATRLAAASWGSFFSSMMKLLFISQLSYCGPNINHHFFCDISPLLNLTCSDKEQA
ELVDLFLALVMILLPLLAVVSSYTAIAAILRIPTSRGRHKAFSTCAAH LAVVVIYSSSTLFTYAR
PRAMYTFNHNKIIISVLYTHVPPFNPAIYCLRNKEVKEAFRKTVMGRCHYPRDVQD (SEQ ID
30 NO: 413).

ATGAGAAATTTGAGTGGAGGCCATGTCGAGGAGTTTGTCTTGGTGGGTTTCCCTACCACGC
CTCCCTCCAGCTGCTCCTCTTTGTCCTTTTTTTTGCAATTTACCTTCTGACATTGTTGGAGA
ATGCACTTATTGTCTTCACAATATGGCTTGCTCCAAGCCTTCATCGTCCCATGTACTTTTC
35 CTTGGCCATCTCTTTCTGGAGCTATGGTACATCAATGTCACCATTCTCGGCTCTTGGC
AGCCTTTCTTACCCAGGATGGTAGAGTCTCCTACGTAGGTTGCATGACCCAAGTACTTC
TTTATTGCCTTAGCCTGTACTGAATGTGTGCTGTTGGCAGTTATGGCCTATGATCGCTACCT
GGCCATCTGTGGACCCCTCCTTTACCTAGTCTCATGCCTTCCAGTCTGGCCACTCGCCTTG
CTGCTGCCTCTTGGGGCAGTGGCTTCTTCAGCTCCATGATGAAGCTTCTTTTATTTCCCAA
40 TTGTCCTACTGTGGACCCAACATTATCAACCACTTTTTCTGTGATATTTCCCACTACTCAA
CCTCACCTGCTCTGACAAGGAGCAAGCAGAGCTAGTAGACTTCCTTCTGGCCCTGGTGATG
ATTCTACTCCCTCTATTGGCTGTGGTTTCATGATACACTGCCATCATTGCAGCCATCCTGAG
GATCCCTACGTCCAGGGGACGCCACAAAGCCTTTTCCACTTGTGCCGCTCATCTGGCAGTG
GTTGTTATCTACTACTCCTCCACTCTCTTACCTATGCACGGCCCCGGGCCATGTACACCTT
45 CAACCACAACAAGATTATCTGTGCTCTACACTATCATTGTACCATTCTTCAACCCAGCCA
TCTACTGCCTGAGGAACAAGGAGGTGAAGGAGGCCTTCAGGAAGACAGTGATGGGCAGAT
GTCATATCCTAGGGATGTTTCCAGGACTGA (SEQ ID NO: 414).

AOLFR222 sequences:

50 MGQTNVTSWRDFVFLGFSSSGELQLLLFALFLSLYLVTLSNVFIHAIRLDLSHLHTPMYFLSFL
SFSETCYTLGIIPRLSGLAGGDQAIYSYVGCQAQMFFSASWACTNCFLLAAMGFDRYVAICAPL
HYASHMNP TLCAQLVTSFLTGYLFGLMTLVIFHLSFCSSHEIQHFFCDTPPVLSLACGDTGPS
ELRIFILSLVLLVSFFFITISYAYILAAILRPSAEGQKKAFTSCASHLTVVIIHYGCASFVYLRPK
ASYSLERDQLIAMTYTVVTPLLNPIVYSLRTRAIQTALRNAFRGRLLGKG (SEQ ID NO: 415).

55

ATGGGGCAGACCAACGTAACCTCCTGGAGGGATTTTGTCTTCCTGGGCTTCTCCAGTTCTG
 GGGAGTTGCAGCTCCTTCTCTTGCCTTGTTCTCTCTGTATCTAGTCACTCTGACCAGC
 AATGTCTTCATTATCATAGCCATCAGGCTGGATAGCCATCTGCACACCCCATGTACCTCTT
 CCTTTCCTTCCTATCCTTCTCTGAGACCTGCTACACTTTGGGCATCATCCCTAGAATGCTCT
 5 CTGGCCTGGCTGGGGGGGACCAGGCTATCTCCTATGTGGGCTGTGCTGCCAGATGTTCTT
 TTCTGCCTCATGGGCCTGTACTAACTGCTTCCTTCTGGCTGCCATGGGCTTTGACAGATATG
 TGGCCATCTGTGCTCCACTCCACTATGCCAGCCACATGAATCCTACCCTCTGTGCCAGCT
 GGTCACTTACTTCTTCTGACTGGATACTCTTTGGACTGGGAATGACACTAGTTATTTTCC
 ACCTCTCATTCTGCAGCTCCCATGAAATCCAGCACTTTTTTTGTGACACGCCACCTGTGCTG
 10 AGCCTAGCCTGTGGAGATACAGGCCCGAGTGAGCTGAGGATCTTTATCCTCAGTCTTTTGG
 TCCTCTTGGTCTCCTTCTTCTTCATCACCATCTCCTACGCCTACATCTTGGCAGCAATACTG
 AGGATCCCCTCTGCTGAGGGGCAGAAGAAGGCCTTCTCCACTTGTGCCTCGCACCTTACAG
 TGGTCATTATTATTATGGCTGTGCTTCCTTCGTGTACCTGAGGCCCAAAGCCAGCTACTCT
 CTTGAGAGAGATCAGCTTATTGCCATGACCTATACTGTAGTGACCCCCCTCCTTAATCCCA
 15 TTGTTTATAGTCTAAGGACTAGGGCTATACAGACAGCTCTGAGGAATGCTTTCAGAGGGAG
 ATTGCTGGGTAAAGGATGA (SEQ ID NO: 416).

AOLFR223 sequences:

MEAANESSEGISFVLLGLTTPSPGQQRPLFVLFLLLYVASLLGNGLIVAAIQASPALHAPMYFLLA
 20 HLSFADLCFASVTVPKMLANLLAHDHSISLAGCLTQMYFFFALGVTDSCLLAAMAYDCYVAIR
 HPLPYATRMSRAMCAALVGMWL VSHVHSLLYLLMARLSFCASHQVPHFFCDHQPLRLRSC
 SDTHIQLLIFTEGA VVVTPFLLILASYGAIAAAVLQLPSASGRRLRAVSTCGSHLAVVSLFYGT
 VIAVYFQATSRREA EWGRVATVMYTVVTPMLNPIIYSLWNRDVQGALRALLIGRRISASDS
 (SEQ ID NO: 417).

25 ATGGAGGCTGCCAATGAGTCTTCAGAGGGAATCTCATTCGTTTTATTGGGACTGACAACAA
 GTCCTGGACAGCAGCGGCCTCTCTTGTGCTGTTCTTGCTCTTGATGTGGCCAGCCTCCTG
 GGTAATGGACTCATTGTGGCTGCCATCCAGGCCAGTCCAGCCCTTCATGCACCCATGTACT
 TCCTGCTGGCCACCTGTCTTTGCTGACCTCTGTTTCGCCTCCGTCAGTGTGCCAAGATG
 30 TTGGCCAACTTGTGGCCCATGACCACTCCATCTCGCTGGCTGGCTGCCTGACCCAAATGT
 ACTTCTTCTTTGCCCTGGGGGTAAGTATAGCTGTCTTCTGGCGGCCATGGCCTATGACTG
 CTACGTGGCCATCCGGCACCCCTCCCCTATGCCACGAGGATGTCCCGGGCCATGTGCGCA
 GCCCTGGTGGGAATGGCATGGCTGGTGTCCACGTCCACTCCCTCCTGTATATCCTGCTCA
 TGGCTCGCTTGTCTTCTGTGCTTCCACCAAGTGCCCCACTTCTTCTGTGACCACCAGCCT
 35 CTCTTAAGGCTCTCGTGCTCTGACACCCACCACATCCAGCTGCTCATCTTACCGAGGGCG
 CCGCAGTGGTGGTCACTCCCTTCTGCTCATCTCGCCTCCTATGGGGCCATCGCAGCTGC
 CGTGCTCCAGCTGCCCTCAGCCTCTGGGAGGCTCCGGGCTGTGTCCACCTGTGGCTCCCAC
 CTGGCTGTGGTGAGCCTCTTCTATGGGACAGTCACTTGCAGTCTACTTCCAGGCCACATCCC
 GACGCGAGGCAGAGTGGGGCCGTGTGGCCACTGTCTGTACACTGTAGTCACCCCATGTC
 40 TGAACCCCATCATCTACAGCCTCTGGAATCGCGATGTACAGGGGGCACTCCGAGCCCTTCT
 CATTGGGCGAAGGATCTCAGCTAGTGACTCCTGA (SEQ ID NO: 418).

AOLFR224 sequences:

MGSFNSTFEDGFILVGFSDWPQLEPILVFIFIFYSLTLFGNTIIALS WLDLRLHTPMYFFLSHL
 45 LDLCFTTSTVPQLLINL CGVDRITITRGGCVAQLFIYLALGSTECVLLVVMFAFDRYAAVCRPLHY
 MAIMHPHLCQTLAIASWGAGFVNSLIQTGLAMAMPLCGHRLNHFFCEMPVFLKLACADTEGT
 EAKMFVARVIVVAVPAALILGSYVHIAHAVLRVKSTAGRRKAFGTGSHLLVFLFYGSAIYT
 YLQSIHNYSEREGKFVALFYTITPILNPLIYTLRNKDVKGALWKVLWRGRDSG (SEQ ID NO:
 419).

50 ATGGGAAGTTTCAACACCAGTTTTGAAGATGGCTTCATTTTGGTGGGATTCTCAGATTGGC
 CGCAACTGGAGCCCATCCTGTTTGTCTTTATTTTATTTTCTACTCCCTAACTCTCTTTGGC
 AACACCATCATCATCGCTCTCTCTGGCTAGACCTTCGGCTGCACACACCTATGTACTTCTT
 TCTCTCTCATCTGTCCCTCCTGGACCTCTGCTTACCAACCAGCACCCTGCCCCAGCTCCTGA
 55 TCAACCTTTGCGGGGTGGACCGCACCATCACCCGTGGAGGGTGTGTGGCTCAGCTCTTCAT
 CTACCTAGCCCTGGGCTCCACAGAGTGTGTGCTCCTGGTGGTGATGGCCTTTGACCGCTAT

GCTGCTGTCTGTCTGCTCCACTCCACTACATGGCCATCATGCACCCCCATCTCTGCCAGACCCCT
 GGCTATCGCCTCCTGGGGTGC GG GTTTCGTGAACCTCTCTGATCCAGACAGGTCTCGCAATG
 GCCATGCCTCTCTGTGGCCATCGACTGAATCACTTCTTCTGTGAGATGCCTGTATTCTGAA
 GTTGGCTTGTGCGGACACAGAAGGAACAGAGGCCAAGATGTTTGTGGCCCGAGTCATAGT
 5 CGTGGCTGTTCTGCGACACTTATTCTAGGCTCCTATGTGCACATTGCTCATGCAGTGCTG
 AGGGTGAAGTCAACGGCTGGGCGCAGAAAGGCTTTTGGGACTTGTGGGTCCCACCTCCTA
 GTAGTTTTCTTTTTTATGGCTCAGCCATCTACACATATCTCCAATCCATCCACAATTATTC
 TGAGCGTGAGGGAAAATTTGTTGCCCTTTTTTATACTATAATTACCCCCATTCTCAATCCTC
 TCATTTATACACTAAGAAACAAGGACGTGAAGGGGGCTCTGTGGAAGTACTATGGAGGG
 10 GCAGGGACTCAGGGTAG (SEQ ID NO: 420).

AOLFR225 sequences:

MENYNQSTDFILLGLFPPSIIDLFFFILVFI FL MALIGNLSMILLIFLDTHLHTPMYFLLSQLSLID
 LNYISTIVPKMASDFLHGNKSISFTGCGIQSFFFLALGGAEALLASMA YDRYIAICFPLHYLIRM
 15 SKRVCVLMITGSWIGSINACAHTVYVLHIPYCRSRAINHFFCDVPAMVTLACMDTWVYEGTV
 FLSATIFLVFPFIGISCSYGQVLFVYHMKSAEGRKKAYLTCSTHLTVVTFYYAPFVYTYLRPRS
 LRSPTEDKVLAVFYTILTPMLNPIIYSLRNKEVMGALTRVSQRICSVKM (SEQ ID NO: 421).

ATGGAAAATTACAATCAAACATCAACTGATTTTCATCTTATTGGGGCTGTTTCCACCATCAA
 20 TAATTGACCTTTTCTTCTTCATTCTCATTGTTTTTCATTTTCTGATGGCTCTAATTGGAAACC
 TGTCCATGATTCTTCTCATCTTCTTGGACACCCATCTCCACACACCCATGTATTTCCTACTG
 AGTCAGCTCTCCCTCATTGACCTAAATTACATCTCCACCATTGTTCTTAAGATGGCATCTGA
 TTTTCTGCATGGAAACAAGTCTATCTCCTTCACTGGGTGTGGGATTGAGAGTTTCTTCTTCT
 TGGCATTAGGAGGTGCAGAAGCACTACTTTTGGCATCTATGGCCTATGATCGTTACATTGC
 25 TATTTGCTTTCTCTCCACTATCTCATCCGCATGAGCAAAAGAGTGTGTGTGCTGATGATA
 ACAGGGTCTTGGATCATAGGCTCGATCAATGCTTGTGCTCACA CTGTATATGTACTCCATA
 TTCCTTATTGCCGATCCAGGGCCATCAATCATTTCTTCTGTGATGTCCCAGCAATGGTGACT
 CTGGCCTGCATGGACACCTGGGTCTATGAGGGCACAGTGTTTTTGAGTGCCACCATCTTTC
 TCGTGTTCCTTTCATTGGTATTTTCATGTTCTCTATGGCCAGGTTCTCTTTGCTGTCTACCAC
 30 ATGAAATCTGCAGAAGGGAGGAAGAAAGCCTATTTGACCTGCAGCACCCACCTCACTGTA
 GTAACCTTTCTACTATGCACCTTTTGTCTACACTTATCTACGTCCAAGATCCCTGCGATCTCC
 AACAGAGGACAAGGTTCTGGCTGTCTTCTACACCATCCTCACCCCAATGCTCAACCCCATC
 ATCTATAGCCTGAGGAACAAGGAGGTGATGGGGGCCCTGACACGAGTGAGTCAGAGAATC
 TGCTCTGTGAAAATGTAG (SEQ ID NO: 422).

35

AOLFR226 sequences:

MEWRNHSGRVSEFVLLGFPAPAPLQVLLFALLLLAYVLVTENTLIIMAIRNHSTLHKPMYFFL
 ANMSFLEIYWVTVTIPKMLAGFVGSQDHDGQLISFEGCMTQLYFFLGLGCTECVLLAVMAYD
 RYMAICYPLHYPVIVSGRLCVQMAAGSWAGGFGISMVKVFLISGLSYCGPNIINHFFCDVSPLL
 40 NLSCDTMSTAELTDFILAIFILLGPLSVTGASYVAITGAVMHISAAAGRYKAFSTCASHLT VVIIF
 YAASIFTYARPKALS AFDTNKLVS VLYAVIVPLNPIIYCLRNQEVKRALCCTLHLYQHQPDP
 KKASRNV (SEQ ID NO: 423).

ATGGAGTGGCGGAACCATAGTGGGAGAGTGAGTGAGTTTGTGTTGCTGGGCTTCCCTGCT
 45 CCTGCGCCACTACAGGTACTATTGTTTGCCCTTTTGGCTGCTGGCCTATGTGTTGGTGCTGAC
 TGAGAACACACTCATCATTATGGCAATTAGGAACCATCTACCCTCCACAAACCCATGTAC
 TTTTTCTAGCTAATATGTCCTTTCTGGAGATCTGGTATGTCACTGTCACTATTCCCAAGAT
 GCTTGCTGGCTTTGTTGGATCCAAACAGGATCATGGACAGCTAATCTCCTTTGAGGGATGC
 ATGACACAGCTCTACTTTTCTTGGCTTGGGCTGCACTGAGTGTGCTCTTCTCGCTGTTAT
 50 GGCCTATGATCGCTATATGGCCATCTGCTATCCTCTCCACTACCCAGTCATTGTCACTGGCC
 GGCTGTGTGTCAGATGGCTGCTGGCTCTTGGGCTGGAGGTTTTGGCATCTCCATGGTCAA
 AGTTTTCTTATTTCTGGCCTCTCTTACTGTGGCCCCAACATCATCAACCACTTTTCTGTG
 ATGTCTCTCCATTGCTCAACCTCTCATGCACTGATATGTCCACAGCAGAGCTTACAGATTTT
 ATCCTGGCCATTTTTATTCTTCTAGGGCCACTCTCTGTCACTGGGGCCTCCTATGTGGCCAT
 55 TACTGGTGCTGTGATGCACATATCTTCGGCTGCTGGACGCTATAAGGCCTTTTCCACCTGT
 GCCTCTCATCTCACTGTTGTGATAATCTTCTATGCAGCCAGTATCTTCATCTATGCTCGGCC

AAAGGCACTCTCAGCTTTTGACACCAACAAGTTGGTCTCTGTACTGTATGCTGTCATTGTA
CCATTGCTCAATCCCATCATTTACTGCCTGCGCAATCAAGAGGTCAAGAGAGCCCTATGCT
GTACTCTGCACCTGTACCAGCACCAGGATCCTGACCCCAAGAAAGCTAGCAGAAATGTATA
G (SEQ ID NO: 424).

5

AOLFR227 sequences:

MEPQNTSTVTNFQLLGFQNLLEWQALLFVIFLLIYCLTIIGNVVIITVVSQGLRLHSPMYMFLQH
LSFLEVWYTSTTVPLLLANLLSWGQAISFSACMAQLYFFVFLGATECFLLAFMAYDRYLAICSP
LRYPFMLHRGLCARLVVSWCTGVSTGFLHSMMSRLDFCGRNQINHFFCDLPPLMQLSCSR
10 YITEVTIFILSLAVLCICFFLTGPHYVFISSILRIPSTSGRRKTFSTCGSHLAVVTLYYGTMISMYV
CPSPHLLPEINKIISVFYTVVTPLLNPVIYSLRNKDFKEAVRKVMRRKCGILWSTSKRKF
LY (SEQ ID NO: 425).

ATGGAGCCCCAAAATACCTCCACTGTGACTAACTTTCAGCTGTTAGGATTCCAGAACCTTC
15 TTGAATGGCAGGCCCTGCTCTTTGTCAATTTCTGCTCATCTACTGCCTGACCATTATAGGG
AATGTTGTCAATCACCGTGGTGAGCCAGGGCCTGCGACTGCACTCCCCTATGTACATGT
TCCTCCAGCATCTCTCTTTCTGGAGGTCTGGTACACGTCCACCACTGTGCCCTTCTCCTA
GCCAACCTGCTGCTCCTGGGGCCAAAGCATCTCCTTCTCTGCTGCATGGCACAGCTCTACT
TCTTCGTATTCTCGGCGCCACCGAGTGCTTTCTCTGCTGCGCTTCATGGCCTATGACCGTTAC
20 CTGGCCATCTGCAGCCCACTCCGCTACCCCTTTCTCATGCATCGTGGGCTATGTGCCAGGTT
GGTGGTGGTCTCATGGTGCACAGGGGTGACGACAGGCTTTCTGCATTCCATGATGATTTC
AGGTTGGACTTCTGTGGGCGCAATCAGATTAACCATTTCTTCTGCGACCTCCCGCCACTCA
TGCAGCTCTCCTGTTCCAGAGTTTATATACCGAGGTGACCATCTTCATCTGTCAATTGCC
GTGCTGTGCATTTGTTTTTTCTGACACTGGGGCCCTATGTTTTTCATTGTGTCTCCATATT
25 GAGAATCCCTTCCACCTCTGGCCGGAGAAAGACCTTTTCCACATGTGGCTCCACCTGGCT
GTTGTCACTCTCTACTACGGGACCATGATCTCCATGTATGTGTGTCCAGTCCCCACCTGTT
GCCTGAAATCAACAAGATCATTTCTGTCTTCTACACTGTGGTCACACCACTGCTGAACCCA
GTTATCTACAGCTTGAGGAACAAAGACTTCAAAGAAGCTGTTAGAAAGGTCATGAGAAGG
AAATGTGGTATTCTATGGAGTACAAGTAAAGGAAGTTCCCTTTATTAG (SEQ ID NO: 426).

30

AOLFR229 sequences:

MFYVNVQIPFQLYHISFVYPTELWSRAIIPCMTLSFWVCSATPVSPGFFALILLVFVTSIASNVVK
IILIHDSRLHTPMYFLLSQLSLRDILYISTVPMKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAE
FLLGLMSCDRYVAICNPLHYPDLMRSRKICWLIVAAAWLGGSIDGFLTPVTMQFPFCASREIN
35 HFFCEVPALLKLSCTDTSAYETAMYVCCIMMLLIPFSVISGSYTRILITVYRMSEABGRRKAVAT
CSSHMVVVSLFYGAAMYTYVLPHSYHTPEQDKAVSAFYTILTPMLNPLIYSLRNKDVGTALQK
VVGRCVSSGKVTTT (SEQ ID NO: 427).

ATGTTTTATGTAAATCAGATACCTTTCCAACCTTTATCATATCTCTTTCGTGTACCCTACAGA
40 GCTATGGAGCAGAGCAATTATCCGTGTATGCCGACTTTATCCTTCTGGGTTTGTTCAGCA
ACGCCCCGTTTCCCCTGGCTTCTTTGCCCTCATCTCCTGGTCTTTGTGACCTCCATAGCCAG
CAACGTGGTCAAGATCATTCTCATCCACATAGACTCCCGCCTCCACACCCCCATGTACTTC
CTGCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTTCCACCATTGTGCCCAAAATGCT
GGTGCAGCAGGTGATGAGCCAGAGAGCCATTTCTTTGCTGGATGCACTGCCCAACACTTC
45 CTCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCCTAGGACTCATGTCTGTGATCGCTA
CGTAGCCATCTGCAACCCTCTGCACTATCCTGACCTCATGAGCCGCAAGATCTGCTGGTTG
ATTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTCACCCCCGTCACCA
TGCAATTCCCCCTTCTGTGCCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCCTGCCCTT
CTGAAGCTCTCCTGCACGGACACATCAGCCTACGAGACAGCCATGTATGTCTGCTGTATTA
50 TGATGCTCCTCATCCCTTTCTCTGTGATCTCGGGCTCTTACACAAGAATTCTCATTACTGTT
TATAGGATGAGCGAGGCAGAGGGGAGGCGAAAGGCTGTGGCCACCTGCTCCTCACACATG
GTGGTTGTGAGCCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCA
CACCCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTCACTCCCATGCTCAAT
CCTCATTTTACAGCCTTAGGAACAAGGATGTACAGGGGGCCCTACAGAAGGTTGTTGGG
55 AGGTGTGTGCTCCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 428).

AOLFR230 sequences:

MGMEGLLQNSTNFVLTGLITHPAFPGLLFAIVFSIFVVAITANLVMILLIHMD SRLHTPMYFLLS
 QLSIMDTIYICITVPKMLQDLLSKDKTISFLGCAVQIFLYLTLIGGEFFLLGLMAYDRYVAVCNP
 LRYPLLMNRRVCLFMVVGSWVGGSLDGFMLTPVTMSFPFCRSREINHFFCEIPAVLKLSDTDS
 5 LYETLMYACCVLMLLPLSVISVSYTHILLTVHRMNSAEGRRKAFATCSSHIMVVS VFYGAIFY
 TNVLPHSYHTPEKDKVVS AFYTILTPMLNPLIYSLRNKDVAALRKVLGRCGSSQSIRVATVIR
 KG (SEQ ID NO: 429).

ATGGGCATGGAGGGTCTTCTCCAGAACTCCACTAACTTCGTCCTCACAGGCCTCATCACCC
 10 ATCTGCGCTTCCCCGGGCTTCTCTTTGCAATAGTCTTCTCCATCTTTGTGGTGGCTATAACA
 GCCAACTTGGTCATGATTCTGCTCATCCACATGGACTCCCGCTCCACACACCCATGTACTT
 CTGCTCAGCCAGCTCTCCATCATGGATACCATCTACATCTGTATCACTGTCCCCAAGATGC
 TCCAGGACCTCCTGTCCAAGGACAAGACCATTTCCTTCCTGGGCTGTGCAGTTCAGATCTT
 CCTCTACCTGACCCTGATTGGAGGGGAATTCTTCCTGCTGGGTCTCATGGCCTATGACCGC
 15 TATGTGGCTGTGTGCAACCCTCTACGGTACCCTCTCCTCATGAACCGCAGGGTTTGCTTATT
 CATGGTGGTTCGGCTCCTGGGTGGTGGTTCCTTGGATGGGTTTCATGCTGACTCCTGTCACT
 ATGAGTTTCCCTTCTGTAGATCCCGAGAGATCAATCACTTTTTCTGTGAGATCCAGCCGT
 GCTGAAGTTGTCTTGACAGACACGTCACCTCTATGAGACCCTGATGTATGCCTGCTGCGTG
 CTGATGCTGCTTATCCCTCTATCTGTCTCTGTCTCCTACACGCACATCCTCCTGACTGT
 20 CCACAGGATGAACCTCTGCTGAGGGCCGGCGCAAAGCCTTTGCTACGTGTTCTCCACATT
 ATGGTGGTGAGCGTTTTCTACGGGGCAGCCTTCTACACCAACGTGCTGCCCACTCCTACC
 AACTCCAGAGAAAGATAAAGTGGTGTCTGCCTTCTACACCATCCTCACCCCCATGCCTCAA
 CCCACTCATCTACAGCTTGAGGAATAAAGATGTGGCTGCAGCTCTGAGGAAAGTACTAGG
 GAGATGTGGTTCCTCCAGAGCATCAGGGTGGCGACTGTGATCAGGAAGGGCTAG (SEQ ID
 25 NO: 430).

AOLFR231 sequences:

MERANHSSVSEFILLGLSKSQNLQILFLGFVSFVGVIVLGNLLILVTVTFDLSLHTPMYFLLSNL
 SCIDMILASFATPKMIVDFLRERKTISWWGCYSQMFFMHLLGGSEMMLLVAMADRYVAICKP
 30 LHYMTIMSPRVL TGLLLSSYAVGVFVHSSQMAFMLTLPFCGPNVIDSFFCDLPLVKLACKDITY
 LQLLVIADSGLLSLVCFLLLLVSYGVIIFSVRYRAASRSSKAFSTLSAHITVVTLFFAPCVFIYVW
 PFSRYSVDKILSVFYTIFTPLLNPIIYTLRNQEVKAAIKKRLCI (SEQ ID NO: 431).

ATGGAAAGAGCAAACCATTCAGTGGTATCGGAATTTATTTGTGGGACTTTCCAAATCTC
 35 AAAATCTTCAGATTTTATTCTTCTTGGGATTCTCTGTGGTCTTCGTGGGGATTGTGTTAGGA
 AACCTGCTCATCTTGGTGACTGTGACCTTTGATTGCTCCTTCACACACCAATGTATTTCT
 GCTTAGCAACCTCTCCTGCATTGATATGATCCTGGCTTCTTTGCTACCCCTAAGATGATTG
 TAGATTTCTCCTCCGAGAACGTAAGACCATCTCATGGTGGGGATGTTATCCCAGATGTTCTT
 TATGCACCTCCTGGGTGGGAGTGAGATGATGTTGCTTGTAGCCATGGCAATAGACAGGTAT
 40 GTTGCCATATGCAAACCCCTCCATTACATGACCATCATGAGCCACGGGTGCTCACTGGGC
 TACTGTTATCCTCCTATGCAGTTGGATTTGTGCACTCATCTAGTCAAATGGCTTTTCATGTTG
 ACTTTGCCCTTCTGTGGTCCCAATGTTATAGACAGCTTTTTCTGTGACCTTCCCCTTGTGAT
 TAAACTTGCCCTGCAAGGACACCTACATCCTACAGCTCCTGGTCATTGCTGACAGTGGGCTC
 CTGTCACTGGTCTGCTTCTCCTCTTGTCTCCTATGGAGTCATAATATTCTCAGTTAG
 45 GTACCGTGCTGCTAGTCGATCCTCTAAGGCTTTCTCCACTCTCTCAGCTCACATCACAGTTG
 TGACTCTGTTCTTTGCTCCGTGTGTCTTTATCTACGTCTGGCCCTTCAGCAGATACTCGGTA
 GATAAAATTCTTTCTGTGTTTACACAATTTTCACACCTCTCTTAAATCCTATTATTTATAC
 ATTAAGAAATCAAGAGGTAAAAGCAGCCATTAAGGAGACTCTGCATATAA (SEQ ID NO:
 432).

50

AOLFR232 sequences:

MDNITWMAHTGWSDFILMGLFRQSKHPMANITWMANHTGWSDFILLGLFRQSKHPALLCV
 VIFVFLMALSGNAVLILLIHCD AHLHTPMYFFISQLSLMDMAYISVTVPKMLLDQVMGVNKS
 APEGCMQMFYVTLAGSEFFLLATMAYDRYVAICHPLRYPVLMNHRVCLFSSGCWFLGSVD
 55 GFTFTPTMTFPFRGSREIHFFCEVPAVLNLSCSDTSLYEIFMYLCCVLMMLIPVVISSYLLILL

TIHGMNSAEGRKKAFATCSSHLTVVILFYGAAIYTYMLPSSYHTPEKDMMVSVFYTLTPVNVN
LIYSLRNKDVGMGALKKMLTVEPAFQKAME (SEQ ID NO: 433).

5 ATGGACAACATCACCTGGATGGCCAGCCACACTGGATGGTCGGATTTTCATCCTGATGGGAC
TCTTCAGACAATCCAAACATCCAATGGCCAATATCACCTGGATGGCCAACCACACTGGATG
GTCGGATTTTCATCCTGTTGGGACTCTTCAGACAATCCAAACATCCAGCACTACTTTGTGTG
GTCATTTTTGTGGTTTTCTGATGGCGTTGTCTGGAAATGCTGTCTGATCCTTCTGATACA
CTGTGACGCCCCACCTCCACACCCCCATGTACTTTTTTCATCAGTCAATTGTCTCTCATGGACA
10 TGGCGTACATTTCTGTCACTGTGCCCAAGATGCTCCTGGACCAGGTCATGGGTGTGAATAA
GATCTCAGCCCCCTGAGTGTGGGATGCAGATGTTCTTCTACGTGACACTAGCAGGTTCAAGAA
TTTTTCCTTCTAGCCACCATGGCCTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTA
CCCTGTCTCATGAACCATAGGGTGTGTCTCTTCTGTCTCATCAGGCTGCTGGTTCCTGGGCT
CAGTGGATGGCTTCACATTCACTCCCATCACCATGACCTTCCCCTTCCGTGGATCCCGGGA
GATTCATCATTTCTTCTGTGAAGTTCCTGCTGTATTGAATCTCTCCTGCTCAGACACCTCAC
15 TCTATGAGATTTTCATGTACTTGTGCTGTGTCTCATGCTCCTCATCCCTGTGGTGATCATT
TCAAGCTCCTATTTACTCATCTCCTCACCATCCACGGGATGAACTCAGCAGAGGGGCCGGA
AAAAGGCCCTTTGCCACCTGCTCCTCCCACCTGACTGTGGTCATCCTCTTCTATGGGGCTGCC
ATCTACACCTACATGCTCCCCAGCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTG
TCTTCTATACCATCCTCACTCCAGTGGTGAACCCCTTTAATCTATAGTCTTAGGAATAAGGAT
20 GTCATGGGGGCTCTGAAGAAAATGTTAACAGTGGAACCTGCCTTTCAAAAAGCTATGGAG
TAG (SEQ ID NO: 434).

AOLFR233 sequences:

25 MANITRMANHTGKLDFFILMGLFRRSKHPALLSVVIFVFLKALSGNAVILLIHCD AHLHSPMY
FFISQLSLMDMAYISVTVPKMLLDQVMGVNKVSAPECGMQMFLYLTLAGSEFFLLATMAYDR
YVAICHPLRYPVLMNHRVCLFLASGCWFLGSVDGFMLTPITMSFPFCRSWEIHHFFCEVPAVTI
LSCSDTSLYETLMYLCCVLMLLIPVTIHSYLLILLTVHRMNSAEGRKKAFATCSSHLTVVILFY
GAAVYTYMLPSSYHTPEKDMMVSVFYTLTPVLNPLIYSLRNKDVGMGALKKMLTVRFVL
(SEQ ID NO: 435).

30 ATGGCCAACATCACCAGGATGGCCAACCACACTGGAAAGTTGGATTTTCATCCTCATGGGAC
TCTTCAGACGATCCAAACATCCAGCTCTACTTAGTGTGGTCATCTTTGTGGTTTTCTGAAAG
GCGTTGTCTGGAAATGCTGTCTGATCCTTCTGATACACTGTGACGCCCCACCTCCACAGCC
CCATGTACTTTTTTCATCAGTCAATTGTCTCTCATGGACATGGCGTACATTTCTGTCACTGTG
35 CCAAGATGCTCCTGGACCAGGTCATGGGTGTGAATAAGGTCTCAGCCCCCTGAGTGTGGG
ATGCAGATGTTCTCTATCTGACACTAGCAGGTTCCGGAATTTTTCTTCTAGCCACCATGGC
CTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTACCCTGTCCTCATGAACCATAGG
GTCTGTCTTTTCTGGCATCGGGCTGCTGGTTCTGGGCTCAGTGGATGGCTTCATGCTCAC
TCCCATCACCATGAGCTTCCCCTTCTGCAGATCCTGGGAGATTCATCATTTCTTCTGTGAAG
40 TCCCTGCTGTAACGATCCTGTCTGCTCAGACACCTCACTCTATGAGACCCCTCATGTACCTA
TGCTGTGTCTCATGCTCCTCATCCCTGTGACGATCATTTCAAGCTCCTATTTACTCATCCT
CCTCACCGTCCACAGGATGAACTCAGCAGAGGGCCGGAAGGCGCTTTGCCACCTGCTC
CTCCACCTGACTGTGGTCATCCTCTTCTATGGGGCTGCCGTCTACACCTACATGCTCCCCA
GCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTGTCTTCTATACCATCCTCACTCC
45 GGTGCTGAACCCCTTAATCTATAGTCTTAGGAATAAGGATGTCATGGGGGCTCTGAAGAAA
ATGTTAACTGTGAGATTCGTCCTTTAG (SEQ ID NO: 436).

AOLFR234 sequences:

50 MPNSTTVMEFLLMRFSVDVWTLQILHSASFFMLYLVTLMGNILIVTVTTCDSSLHMPMYFFLRN
LSILDACYISVTVPTSCVNSLLDSTTISKAGCVAQVFLVFFVYVELLFLTIMAHDYVAVCQPL
HYPVIVNSRICQMTLASLLSGLVYAGMHTGSTFQLPFCRSNVIHQFFCDIPSLLKLSCSDTFSNE
VMIVVSALGVGGGCFIFIRSYIHIFSTVLGFPRGADRTKAFSTCIPHILVVSFLSSCSSVYLRRP
AIPAATQDLILSGFYSIMPLFNPIIYSLRNKQIKVAIKKIMKRIFYSENV (SEQ ID NO: 437).

55 ATGCCCAATTCAACCACCGTGATGGAATTTCTCCTCATGAGGTTTTCTGATGTGTGGACAC
TACAGATTTTACATTCTGCATCCTTCTTATGTTGTATTGTTGGTAACTCTAATGGGAAACATC

CTCATTGTGACCGTCACCACTGTGACAGCAGCCTTCACATGCCCATGTACTTCTTCCTCAG
 GAATCTGTCTATCTTGGATGCCTGCTACATTTCTGTTACAGTCCCTACCTCATGTGTCAATT
 CCCTACTGGACAGCACCACCATTTCTAAGGCGGGATGTGTAGCTCAGGTCTTCCTCGTGGT
 TTTTTTTGTATATGTGGAGCTTCTGTTTCTCACCATTATGGCTCATGACCGCTATGTGGCTG
 5 TCTGCCAGCCACTTCACTACCTGTGATCGTGAACCTCTCGAATCTGCATCCAGATGACACT
 GGCCTCCCTACTCAGTGGTCTTGTCTATGCAGGCATGCACACTGGCAGCACATTCCAGCTG
 CCCTTCTGTCCGTCCAACGTTATTCATCAATTCTTCTGTGACATCCCCCTCTCTGCTGAAGCT
 CTCTTGCTCTGACACCTTCAGCAATGAGGTCATGATTGTTGTCTCTGCTCTGGGGGTAGGT
 GCGGGCTGTTTCATCTTTATCATCAGGTCTTACATTCACATCTTTTCGACCGTGCTCGGGTT
 10 TCCAAGAGGAGCAGACAGAACAAAGGCCTTTCCACCTGCATCCCTCACATCCTGGTGGTG
 TCAGTCTTCCTCAGTTCATGCTCTTCTGTGTACCTCAGGCCACCTGCGATACCTGCAGCCAC
 CCAGGATCTGATCCTTTCTGGTTTTTATTCCATAATGCCTCCCCCTCTTTAACCCTATTATTTA
 CAGTCTTAGAAATAAGCAAATAAAGGTGGCCATCAAGAAAATCATGAAGAGAATTTTTTA
 TTCAGAAAATGTGTAA (SEQ ID NO: 438).

15

AOLFR235 sequences:

MDGVNDSSLQGFVLMGISDHPQLEMIFFIALLFSYLLTLLGNSTILLRLEARLHTPMYFFLSNL
 SSLDLAFATSSVPQMLNLWGPKTISYGGCTQLYVFLWLGATECILLVMAFDRYVAVCRPL
 RYTAIMNPQLCWLLAVIACLGGLGNSVIQSTFTLQLPLCGHRRVEGFLCEVPAMIKLACGDTSL
 20 NQAVLNGVCTFFTA VPLSIIVISYCLIAQAVLKIRSAEGRRKAFNTCLSHLLVFLFYGSASYGY
 LLPAKNSKQDQKFISLFYSLVTPMVNPLIYTLRNMEVKGALRRLGKGREVG (SEQ ID NO:
 439).

ATGGACGGGGTGAATGATAGCTCCTTGCAGGGCTTTGTTCTGATGGGCATATCAGACCATC
 25 CCCAGCTGGAGATGATCTTTTTATAGCCATCCTCTTCTCCTATTTGCTGACCCTACTTGGG
 AACTCAACCATCATCTTGCTTTCCCGCTGGAGGCCCGGCTCCATACACCCATGTACTTCTT
 CCTCAGCAACCTCTCCTCCTTGGACCTTGCTTTTCGCTACTAGTTCAGTCCCCAAATGCTGA
 TCAATTTATGGGGACCAAGCAAGACCATCAGCTATGGTGGCTGCATAACCCAGCTCTATGT
 CTTCCTTTGGCTGGGGGCCACCGAGTGCATCCTGCTGGTGGTGATGGCATTGACCGCTAC
 30 GTGGCAGTGTGCCGGCCCCCTCCGCTACACCGCCATCATGAACCCCCAGCTCTGCTGGCTGC
 TGGCTGTGATTGCCTGCCTGGGTGGCTTGGGCAACTCTGTGATCCAGTCAACATTCACTCT
 GCAGCTCCCATTTGTGTGGGCACCGGAGGGTGGAGGGATTCTCTGCGAGGTGCCTGCCAT
 GATCAAACCTGGCCTGTGGCGACACAAGTCTCAACCAAGGCTGTGCTCAATGGTGTCTGCACC
 TTCTTCACTGCAGTCCCACTAAGCATCATCGTGATCTCCTACTGCCTCATTGCTCAGGCAGT
 35 GCTGAAAATCCGCTCTGCAGAGGGGAGGCGAAAGGCGTTCAATACGTGCCTCTCCCCTCT
 GCTGGTGGTGTCTCTTCTATGGCTCAGCCAGCTATGGGTATCTGCTTCCGGCCAAGAAC
 AGCAAACAGGACCAGGGCAAGTTCATTTCCCTGTTCTACTCGTTGGTCACACCCATGGTGA
 ATCCCCTCATCTACACGCTGCGGAACATGGAAGTGAAGGGCGCACTGAGGAGGTTGCTGG
 GGAAAGGAAGAGAAGTTGGCTGA (SEQ ID NO: 440).

40

AOLFR236 sequences:

MTSQRDTAIYSINVSFVAKGMTSRVCEKMTMTTENPNQTVVSHFFLEGLRYTAKHSSLFFL
 LFLLIYSITVAGNLLILLTVGSDSHLSLPMYHFLGHLSFLDACLSTVTVPKVMAGLLTLDGKVIS
 FEGCAVQLYCFHFLASTEFLYTVMAYDRYLAICQLHYPVAMNRRMCAEMAGITWAIGATH
 45 AAIHTSLTFRLLYCGPCHIA YFFCDIPPVLKLACTDTTINELVMLASIGIVAAGCLILIVISYIFIVA
 AVLRI RTAQQRQRAFSPTAQLTGVLVYVPPVCYILQPRSSEAGAGAPAVFYTIVTPMLNPFYI
 TLRNKEVKHALQRLLCSSFRESTAGSPPP (SEQ ID NO: 441).

ATGACATCTCAGGAAAGGGATACAGCTATTTATTCCATTAATGTCAGTTTTGTTGCAAAGG
 50 GGATGACTAGCCGCTCTGTGTGTGAGAAGATGACCATGACAACGGAGAACCCCAACCGA
 CTGTGGTGAGCCACTTCTTCTGGAGGGTTTGAAGGTACACCGCTAAACATTCTAGCCTCTT
 TCTCTCTCTTCTCTCTCATCTACAGCATCACTGTGGCTGGGAATCTCCTCATCCTCTCTAA
 CTGTGGGCTCTGACTCTCACCTCAGCTTACCCATGTACCACTTCTCTGGGGCACCTCTCCTTC
 CTGGATGCCTGTTTGTCTACAGTGACAGTGCCCAAGGTCATGGCAGGCCTGCTGACTCTGG
 55 ATGGGAAGGTGATCTCCTTTGAGGGCTGTGCCGTACAGCTTTATTGCTTCCACTTTCTGGC
 CAGCACTGAGTGCTTCTGTACACAGTCATGGCCTATGACCGCTATCTGGCTATCTGTCAA

CCCCTGCACTACCCAGTGGCCATGAACAGAAGGATGTGTGCAGAAATGGCTGGAATCACC
 TGGGCCATAGGTGCCACGCACGCTGCAATCCACACCTCCCTCACCTTCCGCCTGCTCTACT
 GTGGGCCCTTGCCACATTGCCTACTTCTTCTGCGACATAACCCCTGTCTAAAGCTCGCCTGT
 ACAGACACCACCATTAATGAGCTAGTCATGCTTGCCAGCATTGGCATCGTGGCTGCAGGCT
 5 GCCTCATCCTCATCGTTATTTCTACATCTTCATCGTGGCAGCTGTGTTGCGCATCCGCACA
 GCCAGGGCCGGCAGCGGGCCTTCTCCCCCTGCACTGCCAGCTCACTGGGGTGCTCCTGT
 ACTACGTGCCACCTGTCTGTATCTACCTGCAGCCTCGCTCCAGTGAGGCAGGAGCTGGGGC
 CCCTGCTGTCTTCTACACAATCGTAACTCCAATGCTCAACCCATTCAATTTACACTTTGCGGA
 ACAAGGAGGTGAAGCATGCTCTGCAAAGGCTTTTGTGCAGCAGCTTCCGAGAGTCTACAG
 10 CAGGCAGCCCCACCCCATAG (SEQ ID NO: 442).

AOLFR237 sequences:

MDQRNYTRVKEFTFLGITQSRELSQVLFITFLVYMTTLMGNFLIMVTVTCESHLHTPMYFLL
 RNLSILDICFSSITAPKVLIDLLSETKTISFSGCVTQMFFFHLLGGADVFSLSVMAFDRIAISKPL
 15 HYMTIMSRGRCTGLIVGFLGGGLVHSIAQISLLPLPVCNPNVLDTFYCDVPQVLKLACTDFT
 LELLMISNGLVSWFVFFLLISYTVILMMLRSHTGEGRRKAISTCTSHITVVTLHFVPCIVVYA
 RPFALTPTDAISVTFTVISPLNPIIYTLRNQEMKLMRKLKRRRLGQSERILIQ (SEQ ID NO:
 443).

20 ATGGATCAGAGAAATTACACCAGAGTGAAAGAATTTACCTTCCTGGGAATTACTCAGTCCC
 GAGAACTGAGCCAGGTCTTATTTACCTTCCTGTTTTTGGTGTACATGACAACTCTAATGGG
 AAACCTTCCTCATCATGGTTACAGTTACCTGTGAATCTCACCTTCATACGCCCATGTACTTCC
 TGCTCCGCAACCTGTCTATTCTTGACATCTGCTTTTCTCCATCACAGCTCCTAAGGTCCTG
 ATAGATCTTCTATCAGAGACAAAAACCATCTCCTTCAGTGGCTGTGTCACTCAAATGTTCT
 25 TCTTCCACCTTCTGGGGGGAGCAGACGTTTTTCTCTCTGTGTATGGCGTTTGACCGCTAT
 ATAGCCATCTCCAAGCCCCTGCACTATATGACCATCATGAGTAGGGGGCGATGCACAGGCC
 TCATCGTGGGCTTCTTGGGTGGGGGGCTTGTCCTCCATAGCGCAGATTTCTCTATTGCT
 CCCACTCCCTGTCTGTGGACCCAATGTTCTTGACACTTTCTACTGCGATGTCCCCAGGTCC
 TCAAACITGCTGCACTGACACCTTCACTCTGGAGCTCCTGATGATTTCAAATAATGGGTT
 30 AGTCAGTTGGTTGTATTCTTCTTCTCTCATATCTTACACGGTCATCTTGATGATGCTGA
 GGTCTCACACTGGGGAAGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCACATCACCG
 TGGTGACCCTGCATTTCTGTCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCC
 ACAGACACTGCCATCTCTGTACCTTCACTGTCTATCTCCCTTTGCTCAATCTATAATTTA
 CACGCTGAGGAATCAGGAAATGAAGTTGGCCATGAGGAAACTGAAGAGACGGCTAGGAC
 35 AATCAGAAAGGATTTTAATTCAATAA (SEQ ID NO: 444).

AOLFR238 sequences:

MAPENFTRVTEFILTGVSSPELQIPLFLVFLVLYVLTMAGNLIITLTSVDSRLQTPMYFFLRHL
 AIINLGNSTVIAPKMLMNFVKKKTTSFYECATQLGGFLFFIVSEVMMLAVMAYDRYVAICNP
 40 LLYMVVVSRRCLLLVSLTYLYGFSTAIVVSPCIFSVSYCSSNIINHFCYDIAPLLALSCSDTYIPE
 TTVFISAATNLFFSMITVLVSFYFNIVLSILRIRSPGRKKAFSTCASHMLAVTVFYGTMLFMYLQP
 QTNHSLDTDKMASVFYTLVIPMLNPLIYSLRNNDVNVALKKFMENPCYSFKSM (SEQ ID NO:
 445).

45 ATGGCTCCTGAAAATTCACCAGGGTCACTGAGTTTATTCTCACAGGTGTCTCTAGCTGTC
 CAGAGCTCCAGATTCCCCTCTTCCCTGGTCTTCTAGTGCTCTATGTGCTGACCATGGCAGG
 GAACCTGGGCATCATCACCTCACCAGTGTTGACTCTCGACTTCAAACCCCATGTACTTTT
 TCCTGAGACATCTAGCTATCATCAATCTTGGCAACTCTACTGTCAATTGCCCTAAATGCTG
 50 ATGAACTTTTAGTAAAGAAGAAAACCTACCTATTCTATGAATGTGCCACCAACTGGGAG
 GGTTCTTGTTCTTTATTGTATCGGAGGATGATGCTGGCTGTGATGGCCTATGACCGCTA
 TGTGGCCATTTGTAACCTCTGCTCTACATGGTGGTGGTGTCTCGCGGCTCTGCCTCCTGC
 TGGTGTCCCTCACGTACCTCTATGGCTTTTCTACAGCTATTGTGGTTTACCTTGTATATTC
 TCTGTGTCTTATTGCTCTTCTAATAATCAATCATTTTTACTGTGATATTGCACCTCTGTT
 AGCATTATCTTGCTCTGATACTTACATACCAGAAACAATAGTCTTTATATCTGCAGCAACA
 55 AATTTGTTTTTTTCCATGATTACAGTTCTAGTATCTTATTTCAATATTGTTTGTCCATTCTA
 AGGATACGTTACACCAGAAGGAAGGAAAAAGCCTTTTCCACCTGCGCTTCGCATATGATA

GCAGTCACGGTTTTCTATGGGACAATGCTATTTATGTATTTGCAGCCCCAAACCAACCACT
 CACTGGATACTGATAAGATGGCTTCTGTGTTTTACACATTGGTGATTCCCTATGCTGAATCC
 CTTGATCTACAGCCTGAGGAATAATGATGTAAATGTTGCCTTAAAGAAATTCATGGAAAAT
 CCATGTTACTCCTTTAAATCAATGTAA (SEQ ID NO: 446).

5

AOLFR239 sequences:

MDPQNYSLVSEFVLHGLCTSRHLQNFFIFFFGVYVAIMLGNLLILVTVISDPCLHSSPMYFLLG
 NLAFLDMWLASFATPKMIRDFLSDQKLISFGGCMAQIFFLHFTGGAEMVLLVSMAYDRYVAIC
 KPLHYMTLMSWQTCIRLVLASWVVG FVHSISQVAFVNLPYCGPNEVDSFFCDLPLVIKLACM
 10 DTYVLGIIMISDSGLLSLSCFLLLLISYTVILLAIRQRAAGSTSKALSTCSAHIMVVTLFFGPCI FV
 YVRPFSRFSVDKLLSVFYTIFTPLLNPIYTLRNEEMKAAMKKLQNRRTVTFQ (SEQ ID NO: 447).

ATGGACCCACAGAACTATTCCTTGGTGTCAGAAATTTGTGTTGCATGGACTCTGCACTTCAC
 GACATCTTCAAAATTTTTCTTTATATTTTTCTTTGGGGTCTATGTGGCCATTATGCTGGGT
 15 AACCTTCTCATTITGGTCACTGTAATTTCTGATCCCTGCCCTGCACTCCTCCCCTATGTACTT
 CCGTCTGGGGAACCTAGCTTTCCCTGGACATGTGGCTGGCCTCATTTGCCACTCCCAAGATG
 ATCAGGGATTTCCCTTAGTGATCAAAACTCATCTCCTTTGGAGGATGTATGGCTCAAATCT
 TCTTCTGCACTTTACTGGTGGGGCTGAGATGGTGCTCCTGGTTTCCATGGCCTATGACAG
 ATATGTGGCCATATGCAAACCTTGCAATTACATGACTTTGATGAGTTGGCAGACTTGCATC
 20 AGGCTGGTGCTGGCTTCATGGGTCTGGATTGTGCACTCCATCAGTCAAGTGGCTTTCA
 CTGTAAATTTGCCTTACTGTGGCCCCAATGAGGTAGACAGCTTCTTCTGTGACCTCCCTCTG
 GTGATCAAACTTGCCCTGCATGGACACCTATGTCTTGGGTATAATTATGATCTCAGACAGTG
 GGTGCTTTTCTTGAGCTGTTTTCTGCTCCTCCTGATCTCCTACACCGTGATCCTCCTCGCT
 ATCAGACAGCGTGCTGCCGGTAGCACATCCAAAGCACTCTCCACTTGCTCTGCACATATCA
 25 TGGTAGTGACGCTGTTCTTTGGCCCTTGCAATTTTTGTTTATGTGCGGCCTTTCACTAGGTTT
 TCTGTGGACAAGCTGCTGTCTGTGTTTTATACCATTTTTACTCCACTCCTGAACCCCATAT
 CTACACATTGAGAAATGAGGAGATGAAAGCAGCTATGAAGAACTGCAAAACCGACGGGT
 GACTTTTCAATGA (SEQ ID NO: 448).

30 **AOLFR240 sequences:**

MAGENHTTLPEFLLLGFSDLKALQGFLFWVLLVYLVTLLGNSLIILLTQVSPALHSPMYFFLR
 QLSVVELFYTTDIVPRTLNLGSPHPQAISFQGCQAQMYVFIVLGISECCLLTAMAYDRYVAIC
 QPLRYSTLLSPRACLAMVGSSWLTGHTATTHASLIFSLPFRSHPIPHFLCDILPVLRLASAGKHR
 SEISVMTATIVFIMIPFSLIVTSYRILGAILAMASTQSRRKVFSTCSSHLLVVS LFFGTASITYIRPQ
 35 AGSSVTTDRVLSLFYTVITPMLNPIYTLRNDVRRALRHLVKRQRPS (SEQ ID NO: 449).

ATGGCTGGGGAAAACCATACTACACTGCCTGAATTCCTCCTTCTGGGATTCTCTGACCTCA
 AGGCCCTGCAGGGCCCCCTGTTCTGGGTGGTGCTTCTGGTCTACCTGGTCACCTTGCTGGG
 TAACTCCCTGATCATCCTCCTCACACAGGTCAGCCCTGCCCTGCACTCCCCCATGTACTTCT
 40 TCCTGCGCCAACCTCTCAGTGGTGGAGCTCTTCTACACCACTGACATCGTGCCAGGACCT
 GGCCAATCTGGGCTCCCCGCATCCCCAGGCCATCTCTTCCAGGGCTGTGCAGCCCAGATG
 TACGTCTTCATTGTCTGGGCATCTCGGAGTGCTGCCTGCTCACGGCCATGGCCTATGACC
 GATATGTTGCCATCTGCCAGCCCCTACGCTATTCCACCCTCTTGAGCCCACGGCCCTGCTT
 GGCCATGGTGGGGTCTCCTGGCTCACAGGCATCATCACGGCCACCACCCATGCCTCCCTC
 45 ATCTTCTCTACCTTTTCGAGCCACCCGATCATCCCGCACTTTCTCTGTGACATCCTGCC
 AGTACTGAGGCTGGCAAGTGCTGGGAAGCACAGGAGCGAGATCTCCGTGATGACAGCCAC
 CATAGTCTTCATTATGATCCCCTTCTCTGATTGTACCTCTTACATCCGCATCCTGGGTG
 CCATCCTAGCAATGGCCTCCACCCAGAGCCGCCGCAAGGTCTTCTCCACCTGCTCCTCCCA
 TCTGCTCGTGGTCTCTCTCTTTGGAACAGCCAGCATCACCTACATCCGCCGACAGGCA
 50 GGCTCCTCTGTTACCACAGACCGCTCCTCAGTCTCTTCTACACAGTCATCACCCATGTG
 CAACCCCATCATCTACACCCCTCGGAACAAGGACGTGAGGAGGGCCCTGCGACACTTGGT
 GAAGAGGCAGCGCCCCCTCACCTGA (SEQ ID NO: 450).

AOLFR241 sequences:

MPQILIFTYLNMFYFFPLQILAENLTMVTEFLLGFSSLGELQALFVVFLLFLYLVLSGNVTHS
 55 VIHLDKSLHTPMYFFLGILSTSETFYTFVILPKMLINLLSVARTISFNCCALQMFFFLGFAITNCLL

LGVMGYDRYAAICHPLHYPTLMSWQVCGKLAACAIGGFLASLTVVNLVFSLPFCSANKVNH
YFCDISAVILLACTNTDVNEFVIFICGVLVLVVPFLFICVSYLCILRTLKIPSAEGRRKAFSTCAS
HLSVVIVHYGCASFYLRPTANYVSNKDRLVTVTYTIVTPLNPMVYSLRNKDVQLAIRKVLG
KKGSLKLYN (SEQ ID NO: 451).

5
ATGCCCCAAATTCTTATATTCACATACCTGAATATGTTTTACTTCTTTCCCCCTTTGCAGAT
CTTGGCAGAAAAACCTCACCATGGTCACCGAATTCCTGTTGCTGGGTTTTTCCAGCCTTGGT
GAAATTCAGCTGGCCCTCTTGTAGTTTTTCTTTTCTGTATCTAGTCATTCTTAGTGGCAA
TGTCACCATATCAGTGTCACTCCACCTGGATAAAAAGCCTCCACACACCAATGTACTTCTTCC
10 TTGGCATTCTCTCAACATCTGAGACCTTCTACACCTTTGTCACTTCTACCCAAGATGCTCATC
AATCTACTTTCTGTGGCCAGGACAATCTCCTTCAACTGTTGTGCTCTTCAAATGTTCTTCTT
CCTTGGTTTTTGGCATTACCAACTGCCTGCTATTGGGTGTGATGGGTTATGATCGCTATGCTG
CCATTTGTCAACCTCTGCATTACCCCACTCTTATGAGCTGGCAGGTGTGTGGAAAAGTGGC
AGCTGCCTGTGCAATTGGTGGCTTCTTGGCCTCTCTTACAGTAGTAAATTTAGTTTTTCAGCC
15 TCCCTTTTTGTAGCGCCAACAAAGTCAATCACTTCTGTGACATCTCAGCAGTCATTCTT
CTGGCTTGTACCAACACAGATGTTAACGAATTTGTGATATTCAATTTGTGGAGTTCTTGTAC
TTGTGGTTCCCTTTCTGTTTATCTGTGTTTCTTATCTCTGCATTCTGAGGACTATCCTGAAG
ATTCCCTCAGCTGAGGGCAGACGGAAGCGTTTTCCACCTGCGCCTCTCACCTCAGTGTG
TTATTGTTTCAATATGGCTGTGCTTCTTCTCATCTACCTGAGGCCTACAGCAAACTATGTGTCC
20 AACAAAGACAGGCTGGTGACGGTGACATACACGATTGTCACTCCATTACTAAACCCCATG
GTTTATAGCCTCAGAAACAAGGATGTCCAACCTGCTATCAGAAAAGTGTGGGCAAGAAA
GGTCTCTAAACTATATAATTGA (SEQ ID NO: 452).

AOLFR242 sequences:

25 MNTTLFHPYFLLGIPGLESMHLWVGPFPAVFLTAVLGNITILFVIQTDSSLHHPMFYFLAILS
SIDPGLSTSTIPKMLGTFWFTLREISFEGCLTQMFFIHLCTGMESAVLVAMAYDCYVAICDPLCY
TLVLNKNVSVMALAIFLRPLVFVIFVLFILRLPFCGHQIIPHTYGEHMGARLSCASIRVNIY
LCAISILVFDIAIVISYVQILCAVFLSSHDARLKAFSTCGSHVCVMLTFYMPAFFSFMTHRFGR
NIPHFHILLANFYVIPPALNSVIYGVRTKQIRAQVLKMFFNK (SEQ ID NO: 453).

30
ATGAATACCACTCTATTTTCATCCTTACTCTTTCTTCTTCTGGAATTCCTGGGCTGGAAAG
TATGCATCTCTGGGTTGGTTTTCTTTCTTGTGCTGTGTTCTGACAGCTGCTCTGGGAATA
TCACCATCCTTTTTGTGATTGAGACTGACAGTAGTCTCCATCATCCCATGTTCTACTTCTG
GCCATTCTGTCTATTGACCCGGGCTGTCTACATCCACCATCCCTAAAATGCTTGGCAC
35 CTTCTGGTTTACCCTGAGAGAAATCTCCTTTGAAGGATGCCTTACCCAGATGTTCTTCATCC
ACCTGTGCACTGGCATGGAATCAGCTGTGCTTGTGGCCATGGCCTATGATTGCTATGTGGC
CATCTGTGACCCCTTTTGTACACGTTGGTGTGACAAACAAGGTGGTGTGAGTTATGGCA
CTGGCCATCTTTCTGAGACCCCTAGTCTTTGTCTATACCCCTTGTCTATTTATCCTAAGGCT
TCCATTTTGTGGACACCAAAATTATTCCTCATACTTATGGTGAGCATGGGCATTGCCCCG
40 CTGCTTGTGCGCAGCATCAGGGTTAACATCATCTATGGCTTATGTGCCATCTCTATCCTGGT
CTTTGACATCATAGCAATTGTCAATTCCTATGTACAGATCCTTTGTGCTGTATTCTACTCT
CTTCACATGATGCACGACTCAAGGCATTGACACCTGTGGCTCTCATGTGTGTGTCATGTT
GACTTTCTATATGCCTGCATTTTTCTCATTCTATGACCCATAGGTTTGGTCGGAATATACCTC
ACTTTATCCACATTCTTCTGGCTAATTTCTATGTAGTCATTCCACCTGCTCTCAACTCTGTA
45 ATTTATGGTGTGAGAACCAACAGATTAGAGCACAAAGTGCTGAAAATGTTTTCAATAAAT
AA (SEQ ID NO: 454).

AOLFR243 sequences:

50 MEQVNTVTVREFVVLGFSSLARLQQLLFVIFLLLYLFTLGTNMIISTIVLDRALHTPMYFFLAIL
SCSEICYTFVIVPKMLVDLLSQKKTISFLGCAIQMFSFLFFGSSHSFLLAAMGYDRYMAICNPLR
YSVLMGHGVCMGLMAAACACGFTVSLVTTSLVFHLPFHSSNQLHHFFCDISPVKLASQHS
SQLVIFMLGVFALVPLLLILVSYIRIISAILKIPSSVGRYKTFSTCASHLIVTVHYSCASFYLRPK
TNYTSSQDTLISVSYTILTPLFNPMIYSLRNKEFKSALRRITIGQTFYPLS (SEQ ID NO: 455).

55 ATGGAGCAAGTCAATAAGACTGTGGTGAGAGAGTTCGTCGTCCTCGGCTTCTCATCCCTGG
CCAGGCTGCAGCAGCTGCTCTTTGTTATCTTCTGCTCCTCTACCTGTTCACTCTGGGCACC

AATGCAATCATCATTTCCACCATTGTGCTGGACAGAGCCCTTCATACTCCCATGTACTTCTT
 CCTTGCCATCCTTTCTTGCTCTGAGATTTGCTATACCTTTGTCATTGTACCCAAGATGCTGG
 TTGACCTGCTGTCCCAGAAGAAGACCATTTCTTTCTGGGCTGTGCCATCCAAATGTTTTCC
 TTCTCTTCTTTGGCTCCTCTCACTCCTTCTGCTGGCAGCCATGGGCTATGATCGCTATAT
 5 GGCCATCTGTAACCCACTGCGCTACTCAGTGCTCATGGGACATGGGGTGTGTATGGGACTA
 ATGGCTGCTGCCTGTGCCTGTGGCTTCACTGTCTCCCTGGTCACCACCTCCCTAGTATTTCA
 TCTGCCCTTCCACTCCTCCAACCAGCTCCATCACTTCTTCTGTGACATCTCCCTGTCTTA
 AACTGGCATCTCAGCACTCCGGCTTCACTCAGCTGGTCATATTCATGCTTGGTGTATTTGC
 CTTGGTCATTCTCTGCTACTTATCTAGTCTCTACATCCGCATCATCTCTGCCATTCTAA
 10 AAATCCCTTCCCTCCGTTGGAAGATACAAGACCTTCTCCACCTGTGCCTCCCATCTCATTGTG
 GTAACCTGTTCACTACAGTTGTGCCTCTTTCATCTACTTAAGGCCCAAGACTAATTACACTTC
 AAGCCAAGACACCCTAATATCTGTGTCATACACCATCCTTACCCCATTTGTTCAATCCAATG
 ATTTATAGTCTGAGAAATAAGGAATTCAAATCAGCCCTACGAAGAACAATCGGCCAACT
 TTCTATCCTCTTAGTTAA (SEQ ID NO: 456).

15

AOLFR244 sequences:

MWQBYEYFLNVFFPLLKVCCLTINSHVVILLPWECYHLIWKILPYIGTTVGSMBEYNTSSTDFTF
 MGLFNRKETSGLIFAIISIFFTALMANGVMIFLIQTDLRLHTPMYFLLSHLSLIDMMYISTIVPKM
 LVNYLLDQRTISFVGCTAQHFLYLTLVGAEBFLLGLMAYDRYVAICNPLRYPVLMSSRRVCWMI
 20 IAGSWFGGSLDGFLLTPITMSFPFCNSREINHFFCEAPAVLKLACADTALYETVMYVCCVLMML
 IPFSVVLASYARILTTVQCMSSVEGRKKAFATCSSHMTTVVSLFYGAAMYTYMLPHSYHKPAQ
 DKVLSVFYTLTPMLNPLIYSLRNKDVGTALKRALGRFKGPQRVSGGVF (SEQ ID NO: 457).

ATGTGGCAAGAATACTATTTTTTAAATGTTTTCTTCCCACTTTTAAAAGTTTGCTGCCTAAC
 25 AATTAATTCACATGTTGTTATTTTACTGCCCTGGGAATGCTATCATCTTATTTGGAAGATAT
 TACCTTATATCGGCACAACCTGTAGGATCAATGGAAGAGTACAACACATCCTCTACAGACTT
 CACTTTATGCGGCTGTTCAACAGAAAGGAAACCTCAGGTCTTATTTTGGCATCATCTCT
 ATCATCTTCTTACCGCACTGATGGCCAATGGGGTTATGATCTTCTGATCCAAACAGATT
 TGCGCCTTCATACACCCATGTACTTCTCTCAGCCACCTTTCCTTAATTGACATGATGTAT
 30 ATTTCCACTATTGTGCCTAAGATGCTGGTTAATTACCTGCTGGATCAAAGGACCATTTCCTT
 TGTGGGGTGCACAGCTCAACACTTCTCTACCTTACCCTTGTGGGAGCTGAATTCTTCTG
 CTGGGCCTCATGGCCTATGACCGCTATGTGGCCATTTGCAACCCTCTGAGATACCCTGTCC
 TCATGAGCCGCCGGGTCTGTTGGATGATTATAGCAGGTTCTGGTTTGGGGGCTCTTTGGA
 TGGCTTCTCTCCTAACCCCATCACCATGAGCTTTCCTTCTGCAATTCGCCGGGAGATTAACC
 35 ACTTCTTCTGTGAGGCACCAGCAGTCCTGAAGTTGGCATGTGCAGACACAGCCCTCTACGA
 GACAGTGATGTATGTGTGCTGTGTTTTGATGCTGCTGATTCTTTCTCTGTAGTCCTTGCTT
 CCTATGCCGAATCCTGACTACAGTTCAGTGATGAGCTCAGTGGAGGGCAGGAAGAAGG
 CATTTGCCACTTGCTCATCCCATGACTGCTGGTGTCTTGTCTACGGGGCTGCCATGTAC
 ACCTACATGCTGCCACATTCTTACCACAAGCCAGCCAGGACAAAGTCCTCTCTGTGTTTT
 40 ACACCATTTCTCACACCCATGCTGAACCCCTCATCTACAGCCTTAGAAACAAGGATGTGAC
 TGGAGCTCTGAAGAGGGCCTTGGGGAGGTTCAAGGGTCTCAAAGGGTGTGAGGAGGTGT
 CTTTGA (SEQ ID NO: 458).

AOLFR245 sequences:

MDLKNGLSVTEFILLGFFGRWELQIFFVTFSLIYGATVMGNILIMVTVTCRSTLHSPYFLLGN
 45 LSFLDMCLSTATTPKMIIDLLTDHKTISVWGCVTQMFFMHFFGGAEMTLIIIMAFDRYVAICKP
 LHVRTIMSHKLLKGFAILSWIIGFLHSISQIVLTMINLPFCGHNVINNIFCDLPLVIKLCIETYLE
 LFVIADSGLLSFTCFILLVSYIVILVSVPKSSHGLSKALSTLSAHIVVTLFFGPCIFYVWPFFSL
 ASNKTLAVFYTVITPLNPSIYTLRNKKMQEAIKLRFYVSSAQNF (SEQ ID NO: 459).

50

ATGGATCTTAAAAATGGATCTCTAGTGACCGAGTTTATTTTACTAGGATTTTTTGGACGAT
 GGGAACTTCAAATTTTCTTCTTTGTGACATTTTCCCTGATCTACGGTGCTACTGTGATGGGA
 AACATTCTCATTATGGTCACAGTGACATGTAGGTCAACCCTTCACTTCTCCCTGTACTTTCT
 CCTTGGAAATCTCTCTTTTTTGGACATGTGTCTCTCCACTGCCACAACACCCAAGATGATCA
 55 TAGATTTGCTCACTGACCACAAGACCATCTCTGTGTGGGGCTGCGTGACCCAGATGTTCTT
 CATGCACTTCTTGGGGGTGCTGAGATGACTCTTCTGATAATCATGGCCTTTGACAGGTAT

GTAGCCATATGTAAACCCCTGCACTATAGGACAATCATGAGCCACAAGCTGCTAAAGGGG
 TTTGCGATACTTTTCATGGATAATTGGTTTTTACACTCCATAAGCCAGATAGTTTTAACAAAT
 GAACTTGCCTTTCTGTGGCCACAATGTCATAAACAACATATTTGTGATCTTCCCCTTGTGA
 TCAAGCTTGCCTTGCATTGAAACATACACCCTGGAATTATTTGTCATTGCTGACAGCGGGCT
 5 GCTCTCTTTCACCTGTTTCATCCTCTTGCTTGTTCCTTACATTGTCATCCTGGTCAGTGATACC
 AAAAAAATCATCACATGGGCTCTCCAAGGCGCTGTCCACATTGTCTGCCACATCATTGTG
 GTCATCTGTTCTTTGGACCTTGTATTTTATCTATGTTTGGCCATTGAGTAGTTTGGCAAG
 CAATAAAACTCTTGCCGTATTTTATACAGTTATCACACCCTTACTGAATCCGAGTATTTATA
 CCCTGAGAAATAAGAAAATGCAAGAGGCCATAAGAAAATTACGGTTCCAATATGTTAGTT
 10 CTGCACAGAATTTCTAG (SEQ ID NO: 460).

AOLFR246 sequences:

MSPENQSSVSEFLLGLPIRPEQAVFFTLFLGMYLTTVLGNLLIMLLIQLDLSHLHTPMYFFLSH
 LALTDISFSSVTVPKMLMDMRTKYKSILYEECISQMYFFIFFTDLDSFLITSMAYDRYVAICHPL
 15 HYTVIMREELCVFLVAVSWILSCASSLSHTLLLRLSFCAANTIPHVFCDLAALLKLSCSDIFLNE
 LVMFTVGVVITLPMFCILVSYGYIGATILRVPSTKGIHKALSTCGSHLSVSVSLYYGSIFGQYLF
 PTVSSSIDKD VIVALMYTVVTPMLNPFYISLRNRDMKEALGKLFSRATFFSW (SEQ ID NO:
 461).

ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCCTCCTTCTGGGCCTCCCCATCCGGC
 CAGAGCAGCAGGCTGTGTTCTTACCCTGTTCTGCGCATGTACCTGACCACGGTGCTGGG
 GAACCTGCTCATCATGCTGCTCATCCAGCTGGACTCTCACCTTCACACCCCCATGACTTCT
 TCCTCAGCCACTTGGCTCTCACTGACATCTCCTTTTCATCTGTCACTGTCCCTAAGATGCTG
 ATGGACATGCGGACTAAGTACAAATCGATCCTCTATGAGGAATGCATTTCTCAGATGTATT
 25 TTTTATATTTTACTGACCTGGACAGCTTCCTTATTACATCAATGGCATATGACCGATAT
 GTTGCCATATGTCACCCCTCTCCACTACACTGTATCATGAGGGAAGAGCTCTGTGTCTTCTT
 AGTGGCTGTATCTTGATTCTGTCTTGTGCCAGCTCCCTCTCTCACACCCCTCTCCTGACCC
 GGCTGTCTTTCTGTGCTGCGAACACCATCCCCCATGTCTTCTGTGACCTTGCTGCCCTGCTC
 AAGCTGTCTGCTCAGATATCTTCTCAATGAGCTGGTCATGTTTACAGTAGGGGTGGTGG
 30 TCATTACCCTGCCATTTCATGTGTATCCTGGTATCATATGGCTACATTGGGGCCACCATCCTG
 AGGGTCCCTTCAACCAAAGGGATCCACAAAGCATTGTCCACATGTGGCTCCCATCTCTCTG
 TGGTGTCTCTCTATTATGGGTCAATATTTGGCCAGTACCTTTTCCCGACTGTAAGCAGTTCT
 ATTGACAAGGATGTCATTGTGGCTCTCATGTACACGGTGGTCACACCCATGTTGAACCCCT
 TTATCTACAGCCTTAGGAACAGGGACATGAAAGARGCCCTTGGGAAACTCTTCAGTAGAG
 35 CAACATTTTTCTCCTTGGTGACATCTGACTTTTTAAAAAATTAG (SEQ ID NO: 462).

AOLFR247 sequences:

MGQHNLTVLTEFILMELTRPELQIPLFGVFLVYILITVVGNLTMILTKLDSHLHTPMYFSIRHL
 ASVDLGNSTVICPKVLANFVDRNTISYYACAAQLAFFLMFISEFFILSAMAYDRYVAICNPLL
 40 YYVIMSQRLCHVLVGIQYLYSTFQALMFTIKIFTLTFCGSNVISHFYCDDVPLLPMLCSNAQIE
 LLSILFSVFNLISSFLIVLVSYMLILLAICQMHSAGEGRKKAFASTCGSHLTVVVVFYGSLLFMVMQ
 PNSTHFFD TDKMASVFYTLVIPMLNPLIYSLRNEEVKNAFYKLFEN (SEQ ID NO: 463).

ATGGGCCAACACAATCTAACAGTGCTAACTGAATTCATTCTGATGGAAGTCAACAAGGCGGC
 45 CTGAGCTGCAGATTCCCCTTTTGGAGTCTTCTCGTCATCTACCTAATCACAGTGGTGGGC
 AACCTAACTATGATCATTTTGACCAAAGTGGACTCCCACTTACATACACCTATGTACTTTTC
 TATCAGACATTTGGCTTCTGTTGATCTTGGTAATTTCTACTGTCAATTTGTCCCAAGGTGCTGG
 CAAATTTTGTGTGGATCGAAATACTATTTCTTATTATGCATGTGCTGCACAGCTGGCATTCT
 TTCTTATGTTTATTATCAGTGAATTTTTCATCCTGTGAGCCATGGCCTATGACCGCTATGT
 50 GGCCATTTGTAACCCCTGCTCTATTATGTTATGTTCTGAGCGACTGTGCTCATGTATGTTG
 TGGGCATTCAATATCTCTACAGCACATTTTCAAGGCTCTGATGTTCACTATTAAAGATTTTACA
 TTGACCTTCTGTGGCTCTAATGTCATCAGTCATTTTACTGTGATGATGTTCTTTGCTACC
 TATGCTTTGCTCAAATGCACAGGAAATAGAATTGTTGAGCATACTATTTTCTGTATTTAATT
 TGATCTCCTCCTTTCTGATAGTCTTAGTGCTACATGTTGATTTTGTAGCTATATGTCAA
 55 ATGCATTCTGCAGAGGGCAGGAAAAAGGCTTTCTCCACATGTGGTTCCTATTTGACAGTGG
 TGGTTGTGTTCTATGGGTCTCTACTCTTCATGTACATGCAGCCCAATTCCACTCACTTCTTT

GATACTGATAAAATGGCTTCTGTGTTTTACACTTTAGTAATCCCCATGCTTAACCCCTTTGAT
TTACAGCTTAAGAAACGAAGAGGTGAAAAATGCCTTCTATAAGCTCTTTGAGAATTGA
(SEQ ID NO: 464).

5 **AOLFR248 sequences:**

MPCMPICALPTGGLLPHQHTMMEIANVSSPEVFLVLLGFSTRPSLETVLFIVVLSFYMVLSILNGNI
IILVSHTDVHLHTPMYFFLANLPFLDMSFTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWL
ATECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGGTTSVMVGSTLTMLPLCG
NNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFLVPLGLLVSYGHIARAVLKIRSAEGR
10 RKAFTNCSSHVAVVSLFYGSIIFMYLQPAKSTSHEQKFIALFYTVVTPALNPLIYTLRNTEVKS
ALRHMVLENC CGSAGKLAQI (SEQ ID NO: 465).

ATGCCCTGTATGCCCTGTGCTCTTCCACAGGTGGCCTTTTGCCCCACCCCCAGCATACAAT
GATGGAAATAGCCAATGTGAGTTCTCCAGAAGTCTTTGTCTCCTGGGCTTCTCCACACGA
15 CCCTCACTAGAACTGTCTCTTCATAGTTGTCTTGAGTTTTACATGGTATCGATCTTGGG
CAATGGCATCATCATTCTGGTCTCCCATACAGATGTGCACCTCCACACACCTATGTACTTCT
TTCTTGCCAACTCCCTTCTGGACATGAGCTTCAACACGAGCATTGTCCACAGCTCCTG
GCTAACCTCTGGGGACCACAGAAAACCATAAGCTATGGAGGGTGTGTGGTCCAGTTCTAT
ATCTCCCATTTGGCTGGGGGCAACCGAGTGTGTCTGCTGGCCACCATGTCCTATGACCGCT
20 ACGCTGCCATCTGCAGGCCACTCCATTACACTGTCATTATGCATCCACAGCTTTGCCTTGG
GCTAGCTTTGGCCTCCTGGCTGGGGGTCTGACCACCAGCATGGTGGGCTCCACGCTCACC
ATGCTCCTACCGCTGTGTGGGAACAATTGCATCGACCACTTCTTTGCGAGATGCCCTCA
TTATGCAACTGGCTTGTGTGGATACCAGCCTCAATGAGATGGAGATGTACCTGGCCAGCTT
TGTCTTTGTTGTCTGCCTCTGGGGCTCATCTGGTCTCTTACGGCCACATTGCCCCGGGCGG
25 TGTTGAAGATCAGGTCAGCAGAAAGGGCGGAGAAAGGCATTCAACACCTGTTCTTCCACG
TGGCTGTGGTGTCTCTGTTTTACGGGAGCATCATCTTCATGTATCTCCAGCCAGCCAAGAG
CACCTCCCATGAGCAGGGCAAGTTCATAGCTCTGTTCTACACCGTAGTCACTCCTGCGCTG
AACCCACTTATTTACACCCTGAGGAACACGGAGGTGAAGAGCGCCCTCCGGCACATGGTA
TTAGAGAACTGCTGTGGCTCTGCAGGCAAGCTGGCGCAAATTTAG (SEQ ID NO: 466).

30

AOLFR249 sequences:

MKSQIEKSDLKYRAILLQKVTRMFLFWVLLLVLSRLLVVMGRGNSTEVTEFHLLGFGVQHEF
QHVLFIVLLLIYVTSIGNIGMILLIKTDSRLQTPMYFFPQHAFVDICYTSAITPKMLQSFTEEN
NLITFRGCVIQLVYATFATSDCYLLAIMAMDCYVAICKPLRYPMIMSQTVYIQLVAGSYIIGSI
35 NASVHTGFTFSLFCKSNKINHFFCDGLPILALSCSNIDINILDVVFVGFDMFTLVIFSYTYIM
VTILKMSSTAGRKKSFTCSHLTAVTIFYGTLSYMYLQPPQSNNSQENMKVASIFYGTVIPMLN
PLIYSLRNKEGK (SEQ ID NO: 467).

ATGAAAAGTCAAATTGAAAAAAGTGACTTAAAATATAGAGCCATTTTATTGCAAAAAGTC
40 ACAAGGATGTTCTGCTTTTCTGGGTCTTCTCTTGGTCCTTTCTAGACTTTTGGTAGTCAT
GGGTGAGGAAACAGCACTGAAAGTGAATTCATCTTCTGGGATTGGTGTCCAACAC
GAATTTGAGCATGTCCTTTTTCATTGTAATCTTCTTATCTATGTGACCTCCCTGATAGGAAA
TATTGGAATGATCTTACTCATCAAGACCGATTCCAGACTTCAAACACCCATGTACTTTTTTC
CACAACATTTGGCTTTTGTGATATCTGTTATACTTCTGCTATCACTCCCAAGATGCTCCAA
45 AGCTTCACAGAAGAAAATAATTTGATAACATTTGCGGGCTGTGTGATACAATTCTTAGTTT
ATGCAACATTTGCAACCAGTGACTGTTACCTCCTAGCTATTATGGCAATGGATTGTTATGT
TGCCATCTGTAAGCCCCCTTCGCTATCCCATGATCATGTCCCAAACAGTCTACATCCAACTCG
TAGCTGGCTCATATATTATAGGCTCAATAAATGCCTCTGTACATACAGGTTTTACATTTTCA
CTGTCCTTCTGCAAGTCTAATAAAATCAATCACTTTTTCTGTGATGGTCTCCCAATTCTTGC
50 CCTTTCTGCTCCAACATTGACATCAACATCTTAGATGTTGTCTTTGTGGGATTTGACT
TGATGTTCACTGAGTTGGTCATCATCTTTTCTACATCTACATTATGGTACCATGCTGAAG
ATGTCTTCTACTGCTGGGAGGAAAAATCCTTCTCCACATGTGCCTCCACCTGACAGCAG
TAACCATTTTCTATGGGACACTCTCTTACATGTACTTACAGCCTCAGTCTAATAATTCTCAG
GAGAATATGAAAGTAGCCTCTATTTTTATGGCACTGTTATCCCATGTTGAATCCTTTAAT
55 CTATAGCTTGAGAAATAAGGAAGGAAAAATAA (SEQ ID NO: 468).

AOLFR250 sequences:

MENQSSISEFFLRGISAPPEQQQSLFGIFLCMYLVTLTGNLLILAIGSDLHLHTPMYFFLANLSFV
 DMGLTSSTVTKMLVNIQTRHHTISYTGCLTQMYFFLMFGDLDSFFLAAMAYDRYVAICHPLCY
 STVMRPQVCALMLALCWVLTNIVALTHTFLMARLSFCVTGEIAHFFCDITPVKLKSCSDTHINE
 5 MMVFLVGGTVLIVPFLCIVTSYIHVPAILRVTRGGVGKAFSTCSSHLCVVCFYGTLFSAYL
 PPSIASEEKDIAAAAMYTTVTPMLNPFYISLRNKDMKGALKRFLSHRSIVSS (SEQ ID NO: 469).

ATGGAACCAATCCAGCATTTCTGAATTTTCTCCGAGGAATATCAGCGCCTCCAGAGC
 AACAGCAGTCCCTCTTCGGAATTTTCTGTGTATGTATCTTGTACCTTGACTGGGAACCTG
 10 CTCATCATCTGGCCATTGGCTCTGACCTGCACCTCCACACCCCATGTACTTTTCTTGGC
 CAACCTGTCTTTTGTGACATGGGTAAACGTCTCCACAGTTACCAAGATGCTGGTGAAT
 ATACAGACTCGGCATCACACCATCTCCTATACGGGTTGCCTCACGCAAATGTATTTCTTTCT
 GATGTTTGGTGATCTAGACAGCTTCTTCTGGCTGCCATGGCGTATGACCGCTATGTGGCC
 ATTTGCCACCCCTCTGCTACTCCACAGTCATGAGGCCCAAGTCTGTGCCCTAATGCTTGC
 15 ATTGTGCTGGGTCTCACCAATATCGTTGCCCTGACTCACACGTTCTCATGGCTCGGTTGT
 CCTTCTGTGTGACTGGGAAATTGCTCACTTTTCTGTGACATCACTCCTGTCTGAAGCTG
 TCATGTTCTGACACCCACATCAACGAGATGATGGTTTTTGTCTTGGGAGGCACCGTACTCA
 TCGTCCCTTTTATGCATTGTCACTCCTACATCCACATTGTGCCAGCTATCCTGAGGGTC
 CGAACCCGTGGTGGGGTGGGCAAGGCCTTTCCACCTGCAGTTCCACCTCTGCGTTGTTT
 20 GTGTGTTCTATGGGACCTCTTCAGTGCCTACCTGTGTCTCCTCCCTCCATTGCCTCTGAAGAG
 AAGGACATTGCAGCAGCTGCAATGTACACCATAGTGACTCCCATGTTGAACCCCTTTATCT
 ATAGCCTAAGGAACAAGGACATGAAGGGGCCCTAAAGAGGCTCTTCAGTCACAGGAGTA
 TTGTTTCTCTTAG (SEQ ID NO: 470).

AOLFR251 sequences:

MEGNKTWITDITLPRFQVGPALAILLCGLFSAFYTLTLLGNGVIFGHCILDCKLHTPMYFFLSHLA
 IVDISYASNYVPKMLTNLMNQESTISFFPCIMQTFLYLAFHVECLILVVMYSYDRYADICHPLRY
 NILMSWRVCTVLAVASWVFSLLALVPLVLILRPFPCGPHENHFCEILSVLKLACADTWLNQV
 VIFAACVFILVGPLCLVLVSYLRLAAILRIQSGEGRRKAFSTCSSHLCVVGLFFGSAIVTYMAPK
 30 SRHPEEQKVLSLFYSLFNPMLNPLIYSLRNAEVKGALRRALRKERLT (SEQ ID NO: 471).

ATGGAAGGCAACAAGACATGGATCACAGACATCACCTTGCCGCGATTCCAGGTTGGTCCA
 GCAGTGGAGATTCTCTCTGTGGACTTTTCTCTGCCTTCTATACACTCACCTGCTGGGGAA
 TGGGTCATCTTTGGGATTATCTGCCTGGACTGTAAGCTTCACACACCCATGTACTTCTTCC
 35 TCTCACACTGGCCATTGTTGACATATCCTATGCTTCCAATATGTCCCAAGATGCTGACG
 AATCTTATGAACCAGGAAAGCACCATCTCCTTTTTTCCATGCATAATGCAGACATTCTTGT
 ATTTGGCTTTTGCTACGTAGAGTGTCTGATTTTGGTGGTGATGTCCTATGATCGCTATGCG
 GACATCTGCCACCCCTTACGTTACAATATCCTCATGAGCTGGAGAGTGTGCACTGTCCTGG
 CTGTGGCTTCTGGGTGTTCACTTCTCCTGGCTCTGGTCCCTTTAGTTCTCATCCTGAGG
 40 CTGCCCTTCTGCGGGCCTCATGAAATCAACCACTTCTGTGAAATCCTGTCTGTCTCAAGTT
 GGCCTGTGCTGACACCTGGCTCAACCAGGTGGTCATCTTTGCAGCCTGCGTGTTCATCCTG
 GTGGGGCACTCTGCCTGGTGTGCTGCTCCTACTTGCGCATCCTGGCCGCCATCTTGAGGA
 TCCAGTCTGGGGAGGGCCGAGAAAGGCCCTTCCACCTGCTCCTCCACCTTTGCGTGGT
 GGGACTCTTCTTTGGCAGCGCCATTGTCACGTACATGGCCCCCAAGTCCCGCCATCCTGAG
 45 GAGCAGCAGAAAGTTCTTTCCCTGTTTTACAGCCTTTTCAATCCAATGCTGAACCCCTGA
 TATATAGCCTAAGGAATGCAGAGGTCAAGGGCGCCCTGAGGAGGGCACTGAGGAAGGAG
 AGGCTGACGTGA (SEQ ID NO: 472).

AOLFR252 sequences:

MRLANQTLGGDFLLGIFSQISHPGRLCLLIFSIFLMAVSWNITLILLIHIDSSLHTPMYFFINQLSL
 IDLTYSVTVPKMLVNQLAKDKTISVLGCGTQMYFYLLQGGAECCLLAAMAYDRYVAICHPLR
 YSVLMSHRVCLLLASGCWFVGSVDGFMLTPIAMSFPCRSHIEIQHFFCEVPAVLKLSCDTSLY
 KIFMYLCCVIMLLIPVTVISVSYYYILTIHKMNSVEGRKKAFTTCSHITVVSFLFYGAATYNYML
 PSSYQTPEKDMMSFFYTILTPVLNPIIYSFRNKDVTRALKKMLSVQKPPY (SEQ ID NO: 473).

55

ATGCGGCTGGCCAACCAGACCCTGGGTGGTGACTTTTTCTGTTGGGAATCTTCAGCCAGA
 TCTCACACCCTGGCCGCTCTGCTTGCTTATCTTCAGTATATTTTGATGGCTGTGTCTTGG
 AATATTACATTGATACTTCTGATCCACATGACTCCTCTCTGCATACTCCCATGTACTTCTT
 TATAAACAGCTCTCACTCATAGACTTGACATATATTTCTGTCACTGTCCCCAAAATGCTG
 5 GTGAACCAGCTGGCCAAAGACAAGACCATCTCGGTCCTTGGGTGTGGCACCAGATGTAC
 TTCTACCTGCAGTTGGGAGGTGCAGAGTGCTGCCTTCTAGCCGCCATGGCCTATGACCGCT
 ATGTGGCTATCTGCCATCCTCTCCGTTACTCTGTGCTCATGAGCCATAGGGTATGTCTCCTC
 CTGGCATCAGGCTGCTGGTTTGTGGGCTCAGTGGATGGCTTCATGCTCACTCCCATCGCCA
 TGAGCTTCCCCTTCTGCAGATCCCATGAGATTACAGCACTTCTTCTGTGAGGTCCCTGCTGTT
 10 TTGAAGCTCTCTTGCTCAGACACCTCACTTTACAAGATTTTCATGTACTTGTGCTGTGTCAT
 CATGCTCCTGATACCTGTGACGGTCATTTACAGTGTCTTACTACTATATCATCCTCACCATCC
 ATAAGATGAACTCAGTTGAGGGTCGGAAGGCCTTACCACTGCTCCTCCACATTAC
 AGTGGTCAGCCTCTTCTATGGAGCTGCTATTTACAACTACATGCTCCCCAGCTCCTACCAA
 ACTCCTGAGAAAGATATGATGTCATCCTTTTTCTACACTATCCTTACACCTGTCTTGAATCC
 15 TATCATTACAGTTTTCAGGAATAAGGATGTCAACAAGGGCTTTGAAAAAATGCTGAGCGT
 GCAGAAACCTCCATATTAA (SEQ ID NO: 474).

AOLFR253 sequences:

MTFSSGGNCEPVMCSGNQTSQNQTASTDFLTGLFAESKHAALLYTVTFLLFLMALTGNALL
 20 ILLIHSEPRLHTPMYFFISQLALMDLMLYLCVTPKMLVGQVTGDDTISPSGCGIQMFFHLTLAG
 AEFVLLAAMAYDRYAAVCRPLHYPLLMNQVRVCQLLVSAWVLMVMDGLLTPITMSFPFCQS
 RKILSFFCETPALKLSCSDVSLYKMLTYLCCILMLLTPIMVISSYTLHLHHRMNSAAGRKA
 LATCSSHMIIVLLLFGASFYTYMLRSSYHTAEQDMMVSAFYTIFTPVLNPLIYSLRNKDVTAL
 RSMQMQRMNQEK (SEQ ID NO: 475).

25 ATGACTTTTTTTTCTCAGGGGGAAACTGTGAGCCAGTCATGTGCTCAGGGAATCAGACTT
 CTCAGAATCAAACAGCAAGCACTGATTTACCCCTCACGGGACTCTTTGCTGAGAGCAAGCA
 TGCTGCCCTCCTCTACACCGTGACCTTCTTCTTTCTTGATGGCCCTCACTGGGAATGCC
 TCCTCATCCTCCTCATCCACTCAGAGCCCCGCTCCACACCCCATGTACTTCTTCATCAGC
 30 CAGCTCGCGCTCATGGATCTCATGTACCTATGCGTGACTGTGCCCAAGATGCTTGTGGGCC
 AGGTCACTGGAGATGATAACATTTCCCCGTGAGGCTGTGGGATCCAGATGTTCTTCCACCT
 GACCCTGGCTGGAGCTGAGGTTTTCTCCTGGCTGCCATGGCCTATGACCGATATGCTGCT
 GTTTGCAGACCTCTCCATTACCACTGCTGATGAACCAGAGGGTGTGCCAGCTCCTGGTGT
 CAGCCTGCTGGGTTTTGGGAATGGTTGATGGTTTGTGCTCACCCCCATTACCATGAGCTT
 35 CCCCTTTTGCCAGTCTAGGAAAATCCTGAGTTTTTCTGTGAGACTCCTGCCCTGCTGAAGC
 TCTCCTGCTCTGACGTCTCCCTCTATAAGATGCTCACGTACCTGTGCTGCATCCTCATGCTT
 CTCACCCCATCATGGTCATCTCCAGCTCATACACCCTCATCCTGCATCTCATCCACAGAT
 GAATTTCTGCGCGCGCCGAGGAAGGCCTTGGCCACCTGCTCCTCCACATGATCATAGTG
 CTGCTGCTCTTCGGTGCTTCCTTCTACACCTACATGCTCCGGAGTTCTACACACAGCTGA
 40 GCAGGACATGATGGTGTCTGCCTTTTACACCATCTTCACTCCTGTGCTGAACCCCTCATTT
 ACAGTCTCCGCAACAAAGATGTCACCAGGGCTCTGAGGAGCATGATGCAGTCAAGAATGA
 ACCAAGAAAAGTAG (SEQ ID NO: 476).

AOLFR254 sequences:

45 MTNTSSSDFLLGLLVNSEAAGIVFTVILAVFLGAVTANLVMIFLIQVDSRLHTPMYFLLSQLSI
 MDTLFICTTVPKLLADMVSKEKISFVACGIQIFLYLTMIGSEFFLLGLMAYDCYVAVCNPLRYP
 VLMNRKKCLLAAGAWFGGSLDGFLTPITMNVPCGSRINHHFCEIPAVLKLACADTSLEYET
 LMYICCVLMMLIPISIISTSYSLILLTIHRMPAEGRKAFTTCSHLTVVSIFYGAAFYTYVLPQS
 FHTPEQDKVVSAFYTIVTPMLNPLIYSLRNKDVGAFKKVFACSSAQKVATSDA (SEQ ID NO:
 50 477).

55 ATGACGAACACATCATCCTCTGACTTCACCCTCCTGGGGCTTCTGGTGAACAGTGAGGCTG
 CCGGGATTGTATTTACAGTGATCCTTGCTGTTTTCTTGGGGGCGTGACTGCAAATTTGGT
 CATGATATTCTTGATTCAGGTGGACTCTCGCCTCCACACCCCATGTACTTCTGCTCAGTC
 AGCTGTCCATCATGGACACCCTTTTCATCTGTACCACTGTCCCAAACTCCTGGCAGACAT
 GGTCTTCTAAAGAGAAGATCATTTCTTTGTGGCCTGTGGCATCCAGATCTTCTCTACCTG

ACCATGATTGGTTCTGAGTTCTTCCTCCTGGGCCTCATGGCCTATGACTGCTACGTGGCTGT
 CTGTAAACCCTCTGAGATACCCAGTCCTGATGAACCGCAAGAAGTGTCTTTTGCTGGCTGCT
 GGTGCCTGGTTTGGGGGCTCCCTCGATGGCTTTCTGCTCACTCCCATCACCATGAATGTCC
 CTTACTGTGGCTCCCGAAGTATCAACCATTTTTCTGTGAGATCCCAGCAGTTCTGAAACT
 5 GGCCTGTGCAGACACGTCCTTGTATGAAACTCTGATGTACATCTGCTGTGTCCTCATGTTG
 CTCATCCCCATCTCTATCATCTCCACTTCCTACTCCCTCATCTTGTTAACCATCCACCGCAT
 GCCCTCTGCTGAAGGTCGCAAAAAGGCCTTCACCACTTGTTCCTCCACTTGACTGTAGTT
 AGCATCTTCTATGGGGCTGCCTTCTACACATACGTGCTGCCCCAGTCCTTCCACACCCCCG
 AGCAGGACAAAGTAGTGTACAGCCTTCTATACCATTTGTACGCCCATGCTTAATCCTCTCAT
 10 CTACAGCCTCAGAAACAAGGACGTCATAGGGGCATTTAAAAAGGTATTTGCATGTTGCTCA
 TCTGCTCAGAAAGTAGCAACAAGTGATGCTTAG (SEQ ID NO: 478).

AOLFR255 sequences:

MEQSNYSVYADFILLGLFSNARFPWLLFALILLVFLTSIASNVVKIILIHDSRLHTPMYFLLSQLS
 15 LRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAEFFLLGLMSYDRYVAICNPLH
 YPVLMSRKICWLIVAAAWLGGSIDGFLLPVTMQFPFCASREINHFFCEVPALLKLSCTDTSAY
 ETAMYVCCIMMLLPFSVISGSYTRILITVYRMSEAEGRGKAVATCSSHMVVVSLFYGAAMYT
 YVLPHSYHTPEQDKAVSAFYTILTPMLNPLIYSLRNKDVGTALQKVVGRCVSSGKVTF (SEQ
 ID NO: 479).
 20
 ATGGAGCAGAGCAATTATTCCGTGTATGCCGACTTTATCCTTCTGGGTTTGTTCAGCAACG
 CCCGTTTCCCCTGGCTTCTCTTTGCCCTCATTCTCCTGGTCTTTTGACCTCCATAGCCAGC
 AACGTGGTCAAGATCAATTCTCATCCACATAGACTCCCGCCTCCACACCCCCATGTACTTCCT
 GCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTTCCACCATTGTGCCCAAAATGCTG
 25 GTCGACCAGGTGATGAGCCAGAGAGCCATTTCCCTTGGCTGGATGCACTGCCCAACACTTCC
 TCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCCTAGGACTCATGTCCTATGATCGCTAC
 GTAGCCCTGCAACCCTCTGCACTATCCTGTCTCATGAGCCGCAAGATCTGCTGGTTGA
 TTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTCACCCCCGTCACCAT
 GCAGTTCCCCCTTCTGTGCCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCCTGCCCTTC
 30 TGAAGCTCTCCTGCACGGACACATCAGCCTACGAGACAGCCATGTATGTCTGCTGTATTAT
 GATGCTCCTCATCCCTTTCTCTGTCTATCTCGGGCTCTTACACAAGAATTCTCATTACTGTTT
 ATAGGATGAGCGAGGCAGAGGGGAGGGGAAAGGCTGTGGCCACCTGCTCCTCACACATGG
 TGGTTGTACAGCCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCAC
 ACCCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTTACTCCCATGCTCAATC
 35 CACTCATTTACAGCCTTAGGAACAAGGATGTACAGGGGCCCTACAGAAGGTTGTGGGGA
 GGTGTGTGTCCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 480).

AOLFR256 sequences:

MGGKQPWVTEFILVGFQVGPALAILLCGLFSVFYTLTLLGNGVIFGIIICLDSKLHTPMYFFLSHL
 40 AIIDMSYASNNVPKMLANLMNQKSTISFVPCIMQTFLYLAFVTECLILVVMYSYDRYVAICHPF
 QYTVIMSWRVCTILASTCWIISFLMALVHITHILRPPFCGPOKINHFIQIMSVFKLACAGPRLNQ
 VVLYAGSAFIVEGPLCLELVSNLHILSRHLEDPMGRAADRLTLPAPSHLCMVGLLFGSTMVM
 YMAPKSRHPBEEQQKVLFLFSLFNPMLNPLIYSLRNAEVKGALKRVLWKQRSK (SEQ ID NO:
 481).
 45
 ATGGGAGGCAAGCAGCCCTGGGTCACAGAATTCATCCTGGTGGGATTCCAGGTTGGTCCA
 GCACTGGCGATTCTCCTCTGTGGACTCTTCTCTGTCTTCTATACACTCACCTGCTGGGGAA
 TGGGGTCATCTTTGGGATTATCTGCCTGGACTCTAAGCTTCACACACCCATGTACTTCTTCC
 TCTCACACCTGGCCATCATTGACATGTCCTATGCTTCCAACAATGTTCCCAAGATGTTGGC
 50 AAACCTAATGAACCAGAAAAGCACCATCTCCTTTGTTCCATGCATAATGCAGATCTTTTGT
 TATTTGGCTTTTGTGTTACAGAGTGCCTGATTTTGGTGGTGATGTCCTATGATAGGTATGT
 GGCCATCTGCCACCCCTTTCCAGTACACTGTCATCATGAGCTGGAGAGTGTGCACGATCCTG
 GCCTCAACATGCTGGATAATTAGCTTTCTCATGGCTCTGGTCCATATAACTCATATTCTGAG
 GCCGCTTTTGTGGCCCAAAAAGATCAACCACTTATCTGTCAAATCATGTCCGTATTCA
 55 AATTGGCCTGTGCTGGCCCTAGGCTCAACCAGGTGGTCTATATGCGGGTTCTGCGTTCAT
 CGTAGAGGGGCCGCTCTGCCTGGAGCTGGTCTCCAACCTGCACATCCTGTCGCGCCATCTT

GAGGATCCAGTAATGGGGAGGGCCGACACCGACTTACTCTTCCTGCTCCTTCCACCTTT
GCATGGTGGGACTCCTTTTGGCAGCACCATGGTCATGTACATGGCCCCAAGTCCCGCCA
CCCTGAGGAGCAGCAGAAGGTCCTTTCCTGTTTTACAGCCTTTTCAACCCGATGCTGAAC
CCCTTGATCTACAGCCTGAGGAACGCAGAGGTCAAGGGTGCCCTGAAAAGAGTGTTGTGG
5 AACAGAGATCAAAGTGA (SEQ ID NO: 482).

AOLFR257 sequences:

MESNQTWITEVILLGFQVDPALBLFLFGFFLLFYSLTLMGNGHILGLIYLD SRLHTPMYVFLSHL
AIVDMSYASSTVPKMLANLVMHKKVISFAPCILQTFLYLAFATECLILVMMCYDRYVAICHPL
10 QYTLIMNWRVCTVLA STCWIFSLLALVHITLILRPF CGPQKINHFFCQIMSVFKLACADTRLN
QVVLFA GSAFILVGPLCLVLVSYLHLVAILRIQSGEGRRKAFSTCSSHL CVVGLFFGSAIVMYM
APKSSHSQERRKILSLFYSLFNPLNPLIYSLRNAEVKGALKRVLWKQRSM (SEQ ID NO: 483).

ATGGAAAGCAATCAGACCTGGATCACAGAAGTCATCCTGTTGGGATTCCAGGTGGACCCA
15 GCTCTGGAGTTGTTCTCTTTGGGTTTTTCTTGCTATTCTACAGCTTAACCCTGATGGGAAA
TGGGATTATCCTGGGGCTCATCTACTTGGACTCTAGACTGCACACACCCATGTATGTCTTC
CTGTACACCTGGCCATTGTGGACATGTCCTATGCCTCGAGTACTGTCCCTAAGATGCTAG
CAAATCTTGTGATGCACAAAAAGTCATCTCCTTTGCTCCTTGCATACCTCAGACTTTTTTG
TATTTGGCGTTTGTCTATTACAGAGTGTCTGATTTTGGTGATGATGTGCTATGATCGGTATG
20 TGGCAATCTGTCAACCCCTTGCAATACACCCTCATTATGAAGTGGAGAGTGTGCACTGTCT
GGCCTCAACTTGGTGGATATTTAGCTTTCTCTGGCTCTGGTCCATATTACTCTTATTCTGA
GGCTGCCTTTTTGTGGCCCAAAAAGATCAACCACTTTTTCTGTCAAATCATGTCCGTATTC
AAATTGGCCTGTGCTGACACTAGGCTCAACCAGGTGGTCCATTTTGGCGGTTCTGCGTTCA
TCTTAGTGGGGCCGCTCTGCCTGGTGTCTGCTCTCTACTTGCACATCCTGGTGGCCATCTTG
25 AGGATCCAGTCTGGGGAGGGCCGACAGAAAGGCCTTCTCTACCTGCTCCTCCACCTCTGCG
TGGTGGGGCTTTTCTTTGGCAGCGCCATTGTCATGTACATGGCCCCAAGTCAAGCCATTG
TCAAGAACGGAGGAAGATCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATCCTGAACCCC
CTCATCTACAGCCTTAGGAATGCAGAGGTGAAAGGGGCTCTAAAGAGAGTCCTTTTGAAA
CAGAGATCAATGTGA (SEQ ID NO: 484).

30

AOLFR259 sequences:

MGDNQSRVTEFILVGFQLSVEMEVLFWIFSLLYLFSLLANGMILGLICLDPRLRTPMYFFLSHL
AVIDIYYASSNLLNMLENLVKHKKTISFISCIMQMALYLTFAAAVCMILVVMYSYDRFVAICHPL
HYTVIMNWRVCTVLAITSWACGFSALINLILLRLPFCGPQEVNHFFGEILSVLKLACADTRLN
35 EIFVFAGGVFVLVGPLSLMLISYMRILLAILKIQSKEGRKKAFTSCSSHL CVVGLYFGMAMVVY
LVPDNSQRQKQKILTLFYSLFNPLNPLIYSLRNAQVKALYRALQKKRTM (SEQ ID NO:
485).

ATGGGGGACAACCAATCACGGGTCACAGAATTCATCCTGGTTGGATTCCAGCTCAGTGTG
40 GAGATGGAAGTGCTCCTCTTCTGGATCTTCTCCCTGTTATATCTCTTCAGCCTGCTGGCAAA
TGGCATGATCTTGGGGCTCATCTGTCTGGATCCAGACTGCGCACCCCATGTACTTCTTCC
TGTCACACTTGGCCGTCATTGACATATACTATGCTTCCAGCAATTTGCTCAACATGCTGGA
AAACCTAGTGAAACACAAAAAACTATCTCGTTCATCTCTTGCATTATGCAGATGGCTTTG
TATTTGACTTTTGTCTGCTGCAGTGTGCATGATTTTGGTGGTGATGTCCTATGACAGATTGT
45 GGCATCTGCCATCCCTGCATTACACTGTCATCATGAAGTGGAGAGTGTGCACAGTACTG
GCTATTACTTCTGGGCATGTGGATTTTCCCTGGCCCTCATAAATCTAATTCTCCTTCTAAG
GCTGCCCTTCTGTGGGCCCCAGGAGGTGAACCACTTCTTCGGTGAAATTTCTGTCTGTCTC
AAACTGGCCTGTGCAGACACCTGGATTAATGAAATTTTGTCTTTGCTGGTGGTGTGTTTG
TCTTAGTCGGGCCCCCTTCTTGTGCTGATCTCCTACATGCGCATCCTCTTGCCCATCCTG
50 AAGATCCAGTCAAAGGAGGGCCGCAAAAAGCCTTTTCCACCTGCTCCTCCCATCTGTG
TGTTTGGGCTTTACTTTGGCATGGCCATGGTGGTTTACCTGGTCCCAGACAACAGTCAACG
ACAGAAGCAGCAGAAAATTCTCACCTGTTTTACAGCCTTTTCAACCCATTGCTGAACCCC
CTCATCTACAGCCTGCGGAATGCTCAAGTGAAGGGTGCTTATACAGAGCACTGCAGAAA
AAGAGGACCATGTGA (SEQ ID NO: 486).

55

AOLFR24B sequences:

MPSINDTHFYPPFFLLLGIPGLDTLHIWISFPFCIVYLIAIVGNMTILFVIKTEHSLHQPMFYFLAM
 LSMIDLGLSTSTIPKMLGIFWFNLQEISFGGCLLMFFIHMFTGMETVLLVVMAYDRFVAICNP
 LQYTMILTNKTISILASVVVGRNLVLVTPFVFLRLPFCGHNIVPHTYCEHRGLAGLACAPIKIN
 5 IYGLMVISYIIVDVILIASSYVLILRAVFRLP SQDVRLKAFNTCGSHVCVMLCFYTPAFFSFMTH
 RFGQNPHYIHILLANLYVVVPPALNPVIYGVRTKQIREQIVKIFVQKE (SEQ ID NO: 487)

ATGCCTTCTATCAATGACACCCACTTCTATCCCCCTTCTTCCTCCTGCTAGGAATACCAGG
 ACTGGACACTTTACATATCTGGATTCTTTCCCATTTCTGTATTGTGTACCTGATTGCCATTG
 10 TGGGGAATATGACCATTTCTTTGTGATCAAAACTGAACATAGTCTACACCAGCCCATGTT
 CTACTTCCTGGCCATGTTGTCTATGATTGATCTGGGTCTGTCCACATCCACTATCCCCAAAA
 TGCTAGGAATCTTCTGGTTCAACCTCCAAGAGATCAGCTTTGGGGGATGCCTTCTTCAGAT
 GTTCTTTATTACATGTTTACAGGCATGGAGACTGTTCTGTTGGTGGTTCATGGCTTATGACC
 GCTTTGTTGCCATCTGCAACCTCTCCAGTACACCATGATCCTCACCAATAAAACCATCAG
 15 TATCCTAGCTTCTGTGGTTGTTGGAAGAAATTTAGTTCTTGTAAACCCATTTGTGTTTCTCA
 TTCTGCGTCTGCCATTCTGTGGGCATAACATCGTACCTCACACATACTGTGAGCACAGGGG
 TCTGGCCGGGTTGGCCTGTGCACCCATTAAGATCAACATAATCTATGGGCTCATGGTGATT
 TCTTATATTATTGTGGATGTGATCTTAATTGCCTCTTCCTATGTGCTTATCCTTAGAGCTGT
 TTTTCGCCCTTCCCTCTCAAGATGTCCGACTAAAGGCCCTCAATACCTGTGGTTCTCATGTCT
 20 GTGTTATGCTGTGCTTTTACACACCAGCATTTTTTTCTTTTATGACACATCGTTTTGGCCAA
 AACATTCCTCCACTATATCCATATTCTTTTGGCTAACCTGTATGTGGTTGTCCACCTGCCCT
 TAACCTGTCAATTATGGAGTCAGGACCAAGCAGATCCGAGAGCAAATTGTGAAAATATTT
 GTACAGAAAGAATAA (SEQ ID NO: 488)

AOLFR33B sequences:

MLHTNNTQFHPSTFLVVGVPGLDVHVWIGFPPFAVYLTALLGNIIILFVIQTEQSLHQPMFYFL
 AMLAGTDLGLSTATIPKMLGIFWFNLGEIAFGACITQMYTIHICTGLESVVLTVTGIDRYIAICNP
 LRYSMILTNKVIAILGIVIVRTL VFVTPFTFLTLRLPFCGVRIIPHTYCEHMGLAKLACASINVIY
 GLIAFSVGYIDISVIGFSYVQILRAVFHLPWDARLKALSTCGSHVCVMLAFYLPALFSFMTHRF
 30 GHNPVHYIHILLANLYVVVPPALNSVIYGVKTKQIREQVLRILNPKSFWHFDPKRIFHNNSVRQ
 (SEQ ID NO: 489)

ATGCTTCATACCAACAATACACAGTTTCACCCCTCCACCTTCCTCGTAGTGGGGGTCCCAG
 GGCTGGAAGATGTGCATGTATGGATTGGCTTCCCTTCTTTGCGGTGTATCTAACAGCCCT
 35 TCTAGGGAACATCATTATCCTGTTGTGATACAGACTGAACAGAGCCTCCACCAACCCATG
 TTTTACTTCCTAGCCATGTTGGCCGGCACTGATCTGGGCTTGTCTACAGCAACCATCCCCA
 AGATGCTGGGAATTTTCTGGTTAATCTTGGAGAGATTGCATTTGGTGCCTGCATCACACA
 GATGTATACCATTCATATATGCACTGGCCTGGAGTCTGTGGTACTGACAGTCACGGGCATA
 GATCGCTATATTGCCATCTGCAACCCCTGAGATATAGCATGATCCTTACCAACAAGGTAA
 40 TAGCCATTCTGGGCATAGTCATCATTTGTCAGGACTTTGGTATTTGTGACTCCATTCACATTT
 CTCACCCTGAGATTGCCTTTCTGTGGTGTCCGGATTATCCCTCATACCTATTGTGAACACAT
 GGGCTTGGCAAAGTTAGCTTGTGCCAGTATTAATGTTATATATGGATTGATTGCCTTCTCA
 GTGGGATACATTGACATTTCTGTGATTGGATTTTCCTATGTCCAGATCCTCCGAGCTGTCTT
 CCATCTCCCAGCCTGGGATGCCCGGCTTAAGGCACTCAGCACATGTGGCTCTCACGTCTGT
 45 GTTATGTTGGCTTTCTACCTGCCAGCCCTCTTTTCCTTCATGACACACCGCTTTGGCCACAA
 CATCCCTCATTACATCCACATTCTTCTGGCCAATCTGTATGTGGTTTTTCCCCCTGCTCTTA
 ACTCTGTTATCTATGGGGTCAAAACAAAACAGATACGAGAGCAGGTACTTAGGATACTCA
 ACCCTAAAAGCTTTTGGCATTTTGACCCCAAGAGGATCTTCCACAACAATTCAGTTAGACA
 ATAA (SEQ ID NO: 490)

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AOLFR112B sequences:

MKNKTVLTFEILLGLTDVPELQVAVFTFLFLAYLLSILGNLTILITLLDLSHLQTPMYFFLRNFSF
 LEISFTNIFIPRVLISITTGNKISIFAGCFTQYFFAMFLGATEFYLLAAMSVDYVAICKPLHYTTI
 MSSRICIQLIFCSWLGGLMAIIPITITLMSQQDFCASNRLNHYFCDYEPLLELSCSDTSLIEKVVFL
 55 VASVTLVTVLVLVLSYAFIITLKLPSAQQRKAFSTCSSHMVISLSYGSCMFMYINPSAKEG
 DTFNKGVALITSVAPLLNPFYITLNRQVQKQPFKDMVKLLNL (SEQ ID NO: 491)

ATGAAAAATAAAACCGTGTTAACTGAGTTTATCCTTCTGGGTCTAACAGATGTCCTGAAC
 TCCAGGTGGCAGTTTTACCTTTCTTTTCCCTTGCCTATTACTCAGCATCCTTGGAATCTG
 ACTATCCTCATCCTCACCTTGCTGGACTCCCACTTCAGACTCCCATGTATTTCTTTCTCCG
 5 GAACTTCTCCTTCTTGAAATTTCCCTTCAAAACATCTTCATTCCAAGGGTCTGATTAGCA
 TCACAACAGGGAACAAGAGTATCAGCTTTGCTGGCTGCTTCACTCAGTATTTCTTTGCCAT
 GTTCTTGGGGCTACAGAGTTTTACCTTCTGGCTGCCATGTCCTATGACCGCTATGTGGCC
 ATCTGCAAACCTCTGCATTACACCACCATCATGAGCAGCAGAATCTGCATCCAGCTGATTT
 TCTGCTCTTGGCTGGGTGGGCTAATGGCTATTATACCAACAATCACCTGATGAGTCAGCA
 10 GGACTTTTGTGCATCCAACAGACTGAATCATTACTTCTGTGACTATGAGCCTCTTCTGGAA
 CTCTCATGTTTCAGACACAAGCCTCATAGAGAAGGTTGTCTTTCTTGTGGCATCTGTGACCC
 TGGTGGTCACTCTGGTGTAGTGATTCTCTCCTATGCATTATTATCAAGACTATTCTGAAG
 CTCCCCTCTGCCCAACAAAGGACAAAAGCCTTTCCACATGTTCTTCCCACATGATTGTCAT
 CTCCCTCTCTTACGGAAGCTGCATGTTTATGTACATTAATCCCTCTGCAAAAGAAGGGGAT
 15 ACATTCAACAAGGGAGTAGCTCTACTACTTTCAGTTGCTCCTTTGTTGAACCCCTTAT
 TTACACCCTAAGGAACCAACAGGTAAACAACCCCTCAAGGATATGGTCAAAAAGCTTCT
 GAATCTTTAA (SEQ ID NO: 492)

AOLFR130B sequences:

20 MEGKNQTAPSEFILGFDHLNELQYLLFTIFFLTYICTLGGNVFIIVVTIADSHLHTPMYYFLGNL
 ALIDICYTTTNPVQMMVHLLSEKKIISYGGCVTQLFAFIFVVGSECLLLAAMAYDRYIAICKPLR
 YSFIMNKALCSWLAASCWTCGFLNSVLHTVLTFLHPFCGNNQINYYFFCDIPLLILSCGDTSLNE
 LALLSIGILISWTPFLCILSYLYIISTILRIRSEGRHKAFTSCASHLLIVLYYGSIFTYVRPISSYS
 LEKDRLISVLYSVVTPMLNPVIYTLRNKDIKEAVKAIGRKWQPPVFSSDI (SEQ ID NO: 493)

25 ATGGAAGGAAAGAATCAAACAGCTCCATCTGAATTCATCATCTTGGGGTTCGACCACCTGA
 ATGAATTGCAGTATTTACTCTTCAACCATCTTCTTTCTGACCTACATATGCACCTTAGGAGGC
 AATGTTTTTATCATTGTGGTGACCATAGCTGATTCCACCTACACACACCCATGTATTATTT
 CCTAGGAAATCTTGCCCTTATTGACATCTGCTACACTACTACTAATGTCCCCCAGATGATG
 30 GTGCATCTTCTGTGAGAGAAGAAAATCATTTCCTATGGAGGCTGTGTGACCCAGCTCTTTG
 CATTCAATTTCTTTGTTGGCTCAGAGTGTCTCCTCCTGGCAGCAATGGCATATGATCGATAT
 ATTGCTATCTGTAAGCCGTTAAGGTACTCATTATATTATGAACAAGGCCCTGTGCAGCTGGT
 TAGCAGCCTCATGCTGGACATGTGGGTTTCTCAACTCAGTGTTGCACACCGTTCTGACCTT
 CCACCTGCCCTTCTGTGGTAACAATCAGATCAATTATTTCTTCTGTGACATACCTCCCTTGC
 35 TCATCTTGTCTTGTGGTGATACTTCCCTCAATGAACTGGCTTTGCTGTCCATTGGGATCCTC
 ATAAGCTGGACTCCTTTCTGTGCATCATCCTTTCTACCTTTACATCATCTCCACCATCCT
 GAGGATCCGTTCTCTGAGGGGAGGCACAAAGCCTTTTCCACCTGTGCCTCCCACCTGCTC
 ATTGTTATTCTCTATTATGGCAGTGCTATCTTACAGTATGTGAGGCCCATCTCATCTTACTC
 TCTAGAGAAAAGATAGATTGATCTCAGTGCTGTATAGTGTGTGACACCCCATGCTGATCACTC
 40 GTAATTTATACGCTAAGGAATAAGGACATCAAAGAGGCTGTGAAGGCCATAGGGAGAAAG
 TGGCAGCCACCAGTTTTCTTCTGATATATAA (SEQ ID NO: 494)

AOLFR142B sequences:

45 MARKDMAHINCTQATEFILVGLTDHQELKMPLFVLFSLIYLFVVGNLGLILLIRADTSLNTPM
 YFFLSNLAFFVDFCYSSVITPKMLGNFLYKQNVISFDACATQLGCFLTFMISESLLASMAVDYR
 VAICNPLLYMVVMTPGICIQLVAVPYSYSFLMALFHTILTFRLSYCHSNIVNHFYCDDMPLRL
 TCSDFRKFQLWIFACAGIMFISSLLIVFVSYMFIIISAILRMHSAEGRQKAFSTCGSHMLAVTIFYG
 TLFMYLQPSSSHALDTDKMASVFYTVIIPMLNPLIYSLQNKEVKEALKKIINKN (SEQ ID NO:
 495)

50 ATGGCCAGAAAAGATATGGCTCACATCAATTGCACCCAGGCGACAGAGTTTATTCTTGTGG
 GCCTCACAGACCATCAGGAGTTGAAGATGCCCTCTTTGTGCTATTCTTATCCATCTACCTC
 TTCACAGTGGTAGGCAACTTGGGTTTGATCCTACTCATTAGAGCGGATACAAGTCTCAACA
 CACCAATGTACTTCTTTCTTAGCAACCTAGCTTTTGTGGATTCTGTTACTCTTCTGTCAAT
 55 ACACCCAAAATGCTTGGGAATTTCTTGTACAAACAAAATGTTATATCCTTTGATGCATGTG
 CTACTCAACTGGGCTGCTTTCTCACCTTCATGATATCAGAATCCTTGCTACTGGCTTCCATG

GCCTATGACCGATATGTGGCCATTTGTAACCCTCTATTGTATATGGTTGTAATGACTCCAG
 GAATCTGCATTCAACTTGTAGCAGTTCCTTATAGCTATAGCTTCCTAATGGCACTATTTAC
 ACCATCCTCACCTTCCGCCTCTCCTATTGCCACTCCAACATTGTCAACCATTTCTATTGTGA
 TGACATGCCTCTCCTCAGGCTAACTTGCTCAGACACTCGCTTCAAACAGCTCTGGATCTTT
 5 GCCTGTGCTGGTATCATGTTCAATTCCTCCCTTCTGATTGTCTTTGTCTCCTACATGTTTCATC
 ATTTCTGCCATCCTGAGGATGCATTCAGCTGAGGGAAGACAGAAGGCTTTCTCGACGTGTG
 GCTCTCACATGCTGGCAGTCACCATATTTCTATGGGACCCTCATTTTTATGTACTTACAGCCT
 AGCTCTAGCCATGCCCTGGACACAGACAAGATGGCCTCTGTCTTCTACACAGTGATCATTC
 CCATGTTGAATCCCTTAATCTATAGCCTCCAGAATAAGGAGGTGAAAGAAGCTCTGAAGA
 10 AAATCATTATCAATAAAAACTAG (SEQ ID NO: 496)

AOLFR171C sequences:

MAEVNIIYVTVFILKGITNRPELQAPCFGVFLVIYLVTVLGNLGLITLIKIDTRLHTPMYYFLSHL
 AFVDLCYSSAITPKMMVNFVVERNTIPFHACATQLGCFLTFMITECFLLASMA YDCYVAICSPL
 15 HYSTLMSRRVCIQLVAVPYYSFLVALFHTVITFRLTYCGPNLNHFYCDLPLFALS CSDTHMK
 EILIFAFAGFDMISSSSIVLTSYIFILAILRIRSTQGQHKAI STCGSHMVTVTIFYGTLIFMYLPKS
 NHSLD TDKMASVFYTVVIPMLNPLIYSLRNKEVKDASKKALDKGCENLQILFLKIRKLY (SEQ
 ID NO: 497)

20 ATGGCTGAAGTTAATATCATTTATGTCACTGTATTCACTGAAAGGAATTACCAACCGGC
 CAGAGCTTCAGGCCCCGTGCTTTGGGGTGTTTTAGTTATCTATCTGGTCACAGTGCTGGG
 CAATCTTGGGTTGATTACTTTAATCAAGATTGATACTCGACTCCACACACCTATGTA TACTATT
 TCCTCAGCCACCTGGCCTTTGTTGACCTTTGTTACTCCTCTGCTATTACACCGAAGATGATG
 GTGAATTTTGTGTTGTGGAACGCAACACCATTCCTTTCCATGCTTGTGCAACCCAACCTGGGTT
 25 GTTTTCTCACCTTCATGATCACTGAGTGTTTCTTCTAGCCTCCATGGCCTACGATTGCTAT
 GTCGCCATCTGTAGTCCCCTGCATTATTCAACACTGATGTCAAGAAGAGTCTGCATTCAAC
 TGGTGGCAGTTCCATATATATACAGCTTCCTGGTTGCCCTCTTCCACACCGTTATCACTTC
 CGTCTGACTTACTGTGGCCCAAACCTTAATTAACCATTTCTATTGTGATGACCTCCCCCTTCTT
 AGCTCTGTCTGCTCAGACACACACATGAAGGAAATCTGATATTTGCCTTTGCTGGCTTT
 30 GATATGATCTCTTCTCTTCCATTGTCCTCACCTCCTACATCTTTATTATTGCCGCTATCCTA
 AGGATCCGCTCTACTCAGGGGCAACACAAAGCCATTTCCACCTGTGGCTCCCATATGGTGA
 CTGCACTATTTTCTATGGCACACTGATCTTTATGTACCTACAGCCCAAATCAAATCACTCC
 TTGGACACAGACAAGATGGCTTCTGTATTTTACACAGTGGTGATCCCCATGTTAAACCCCC
 TAATCTATAGTCTAAGGAACAAAGAAGTGAAAGATGCCTCAAAGAAAGCCTTGATAAAG
 35 GTTGTGAAAACCTTACAGATATTAACATTTTAAAAATAAGAAAACCTTTATTAA (SEQ ID NO:
 498)

AOLFR225B sequences:

MKNRTMFGEFILLGLTNQPELQVMIFLFLTYMLSILGNLTITLTLLDPHLQTPMYFFLRNFSF
 40 LEISFTSIFIPRFLTSMTTGNKVISFAGCLTQYFFAIFLGATEFYLLASMSYDRYVAICKPLHYLTI
 MSSRVCIQLVFCSWLGGFLAILPPIILMTQVDFCVSNILNHYYCDYGPLVELACSDTSLELMVI
 LLAVVTLMVTLVLVTLSTYTYIIRTLRIPSAQRKAFSTCSSHMIVISLSYGSCMFMYNPSAKE
 GGAFNKGI AVLITSVTPLLNPFYTLRNQVQKQAFKDSVKKIVKL (SEQ ID NO: 499)

45 ATGAAAAACAGAACCATGTTTGGTGAGTTTATTCTACTGGGCCTTACAAATCAACCTGAAC
 TCCAAGTGATGATATTCATCTTTCTGTTCTCACCTACATGCTAAGTATCCTAGGAAATCTG
 ACTATTATCACCTCACCTTACTAGACCCCCACCTCCAGACCCCCATGATTTCTTCTCCTCCG
 GAATTTCTCCTTCTTAGAAATTTCTTTCACATCCATTTTTATTCCCAGATTTCTGACCAGCA
 TGACAACAGGAAATAAAGTTATCAGCTTTGCTGGCTGCTTGACTCAGTATTTTTTTGCTAT
 50 ATTTCTTGGAGCTACCGAGTTTTACCTCCTGGCCTCCATGTCTTATGATCGTTATGTGGCCA
 TCTGCAAACCTTGCACTTACCTGACTATTATGAGCAGCAGAGTCTGCATACAACTAGTGTT
 CTGCTCCTGGTTGGGGGATTCTTAGCAATCTTACCACCAATCATCCTGATGACCCAGGTA
 GATTTCTGTGTCTCCAACATTCTGAATCACTATTACTGTGACTATGGGCCTCTCGTGGAGCT
 TGCCTGCTCAGACACAAGCCTCTTAGAACTGATGGTCATCCTCTTGGCCGTTGTGACTCTC
 55 ATGGTTACTCTGGTGCTGGTGACACTTTCTTACACATACATTATCAGGACTATTCTGAGGA
 TCCCTTCTGCCAGCAAAGGACAAAGGCCTTTTCCACTTGTTCTCCCATGATTGTCATC

TCCCTCTCTTATGGCAGCTGCATGTTTATGTACATTAATCCTTCTGCAAAAGAAGGAGGTG
CTTTCAACAAAGGAATAGCTGTACTCATTACTTCGGTTACTCCCTTACTGAATCCCTTCATA
TATACTTTAAGAAATCAGCAAGTGAAACAAGCTTTCAAGGACTCAGTCAAAAAGATTGTG
AAACTTTAA (SEQ ID NO: 500)

5

AOLFR274B sequences:

MEFVFLAYPSCPETHLSFLGVSLVYGLIITGNILIVVSIHTETCLCTSMYYFLGSLSGIEICYTAV
VVPFILANTLQSEKTITLLGCATQMAFFIALGSADCFLLAAMAYDRYVAICHPLQYPLMLTLTL
CVHLVVASVISGLFSLQLVAFIFSLPFCQAQGIEHFFCDVPPVMHVCAQSHIHEQSVLVAAIL
10 AIAVPFLITTSYTFIVAALLKIHSAAGRHRAFSTCSSHLTVVLLQYGCCAFMYLCPSSSYNPKQ
DRFISLVYTLGTPLLNLPLIYALRNSEMKGAVGRVLTRNCLSQNS (SEQ ID NO: 501)

ATGGAATTTGTGTTCTCTGGCCTATCCCTCCTGCCAGAACTGCATATTCTGTCCTTCCTTGG
GGTCAGCCTGGTTTATGGTTTGATCATCACTGGGAACATTCTCATTGTGGTGTCCATTAC
15 ACAGAAACCTGTCTATGCACATCCATGTACTATTTCTGGGCAGCCTTTCTGGGATTGAAA
TATGCTACACTGCAGTGGTGGTGCCCATATCCTGGCCAACACCCTACAGTCAGAGAAGAC
CATCACTCTCCTGGGCTGTGCCACCCAGATGGCTTTCTTCATTGCACTGGGCAGTGTCTGAT
TGCTTCTCTTGGCTGCCATGGCCTATGACCGCTATGTGGCCATTTGCCACCCGTTGCAGTA
CCCTCTCCTCATGACATTGACTCTTTGTGTCCACTTGGTTGTGGCATCAGTCATCAGTGGTC
20 TGTTCTCTGTCCTTAAACTGGTGGCTTCATCTTCTCTCTGCCATTCTGCCAGGCTCAGGGC
ATTGAGCACTTCTTTTGTGATGTGCCACCAGTCATGCATGTTGTTTGTGCTCAGAGTCACAT
TCATGAGCAGTCAGTGTGGTGGCAGCCATACTAGCCATTGCTGTGCCTTTCTTCCTCATC
ACCACCTCCTACACCTTCATAGTGGCTGCTCTGCTCAAGATCCACTCGGCTGCTGGCCGCC
ACCGGGCCTTCTCCACCTGCTCTTCCACCTCACTGTGGTGTGCTGCAGTATGGCTGCTGT
25 GCCTTCATGTACCTGTGCCCCAGTCCAGCTACAACCCCAAGCAAGATCGGTTTCATCTCAC
TGGTGTACACATTGGGAACCCCACTGCTCAACCCCACTTATCTATGCCCTGAGGAACAGTGA
GATGAAAGGGGCCGTAGGGAGAGTTCTTACCAGGAACTGCCTTTCCAGAACAGCTAG
(SEQ ID NO: 502)

30 **AOLFR276B sequences:**

MGGFGTNISSSTSLTGFPEMKGLEHWLAALLLLLYAISFLGNILILFIKEEQSLHQPMYYFLS
LFSVNDLGVSFSTLPTVLAACVCFHAPETTFDACLAQMFFIHFSSWTEFGILLAMSFHDHYAICNP
LRYATVLT DVRVAHNGISIVRSFCMVFPFLPFLKRLPFCKASVVLAHSYCLHADLIRLPWGD
TINSMYGLFVISAFAFVDSLILLISYVLILHSVLAIASRGERLKTNTCVSHIYAVLIFYVPMVSVS
35 MVHRFGRHAPEYVHKFMSLCTSNALPNYLFHQD (SEQ ID NO: 503)

ATGGGGGGCTTTGGGACTAACATCTCAAGTACTACCAGCTTCACTCTAACAGGCTTCCCTG
AGATGAAGGGTCTGGAGCACTGGCTGGCTGCCCTTCTGCTGCTGCTTTATGCTATTTCCCT
CCTGGGCAACATCCTCATCCTCTTTATCATAAAGGAAGAGCAGAGCTTGCACCAGCCAATG
40 TACTACTTCTGTCTCTTTTTCTGTAAATGACCTGGGTGTGTCCTTTTCTACATTGCCCACT
GTACTGGCTGCTGTGTGTTTTCATGCCCCAGAGACAACCTTTGATGCCTGCCTGGCCAGAG
TGTTCTTCATCCACTTTTCTCCTGGACAGAGTTTGGCATCCTACTGGCCATGAGTTTGGAC
CACTATGTGGCCATCTGTAACCCGCTGCGCTATGCCACAGTGCTCACTGATGTCCGTGTGG
CCCACAATGGCATATCCATTGTATCCGCAGCTTCTGCATGGTATTCCCACTTCCCTTCCTC
45 CTGAAGAGACTGCCCTTCTGTAAGGCCAGTGTGGTACTGGCCATTCCCTACTGTCTGCATG
CAGACCTGATTTCGGCTGCCCTGGGGAGACACTACCATCAACAGCATGTATGGCCTGTTTCAT
TGTCATCTCTGCCTTTGGTGTAGATTCACTGCTCATCTCCTCTCCTATGTGCTCATTCTAC
ATTCTGTGCTGGCCATTGCCCTCAGGGGTGAGAGGCTTAAGACACTCAACACATGTGTGTGTC
ACATATCTATGCAGTGTGATCTTCTATGTGGCTATGGTTAGTGTGTCCTATGGTTTCATCGAT
50 TTGGGAGGCATGCTCCTGAATATGTGCACAAGTTCATGTCTCTTTGTACCTCCAATGCTCT
ACCCAATTATCTATTCCATCAAGACTAA (SEQ ID NO: 504)

AOLFR311B sequences:

MDWENCSSLTDFLLGITNNPEMKVTLFAVFLAVYIINFSA NLGMIVLIRMDYQLHTPMYFFLS
55 HLSFCDLCYSTATGPKMLVDLLAKNKSIPFYGCALQFLVFCIFADSECLLSVMAFDYKAIJNP
LLYTVNMSSRVCYLLLTGVYLVGIADALIHMTLAFRLCFCGSNEINHFFCDIPLLLSRSDTQV

NELVLFTVFGFIELSTISGVFISYCYILSVLEIHS AEGRFKALSTCTSHLSAVAIFQGTLLFMYFRP
SSSYSLDQDKMTSLFYTLVVPMLNPLYSLRNKDVKEALKKLNKILF (SEQ ID NO: 505)

5 ATGGACTGGGAAAATTGCTCCTCATTAAGTATTTTTTCTCTTGGGAATTACCAATAACCC
AGAGATGAAAGTGACCCTATTTGCTGTATTCTTGGCTGTTTATATCATTAATTTCTCAGCAA
ATCTTGGGAATGATAGTTTAAATCAGAATGGATTACCAACTTCACACACCAATGTATTTCTT
CCTCAGTCATCTGTCTTTCTGTGATCTCTGCTATTCTACTGCAACTGGGCCCAAGATGCTGG
TAGATCTACTTGCCAAGAACAAGTCAATACCCTTCTATGGCTGTGCTCTGCAATTCTTGGT
CTTCTGTATCTTTGCAGATTCTGAGTGTCTACTGCTGTCACTGATGGCCTTTGATCGGTACA
10 AGGCCATCATCAACCCCTGCTCTATACAGTCAACATGTCTAGCAGAGTGTGCTATCTACT
CTTGACTGGGGTTTATCTGGTGGGAATAGCAGATGCTTTGATACATATGACACTGGCCTTC
CGCCTATGCTTCTGTGGGTCTAATGAGATTAATCATTTCTTCTGTGATATCCCTCCTCTCTT
ATTACTCTCTCGCTCAGATACACAGGTCAATGAGTTAGTGTATTACCCGCTTTTGGTTTA
TTGAAGTGAAGTACCATTTTCAAGAGTTTTTCTTATTGTTATATCATCCTATCAGTCTTG
15 GAGATACACTCTGCTGAGGGGAGGTTCAAAGCTCTCTACATGCACTTCCACTTATCTG
CGGTTGCAATTTTCCAGGGAAGTCTGCTCTTATGTATTTCCGGCCAAGTTCTTCTATTCT
CTAGATCAAGATAAAATGACCTCAATTGTTTTACACCCTTGTGGTCCCATGTTGAACCCCT
GATTTATAGCCTGAGGAACAAGGATGTGAAAGAGGCCCTGAAAAAACTGAAAAATAAAAT
TTTATTTTAA (SEQ ID NO: 506)

20

AOLFR314 sequences:

MEVKNCCMVTEFILLGIPHTEGLEMTLFLVFLPFYACTLLGNVSILVAVMSSARLHTPMYFFLG
NLSVFDMGFSSVTCPKMLLYLMGLSRLISYKDCVCQLFFFHFLGSIECLFTVMAYDRFTAICY
PLRYTVMNPRICVALAVGTWLLGCIHSSILTSLTFTLPYCGPNEVDHFFCDIPALLPLACADTSL
25 AQRVSFTNVGLISLVCFLILLLSYTRITISILSIRTTTEGRRRAFSTCSAHLIALCAYGPIITVYLQPT
PNPMLGTVVQILMNLVGPMLNPLYTLRNKEVKTALKTLHRTGHVPES (SEQ ID NO: 507)

ATGGAGGTGAAGAACTGCTGCATGGTGACAGAGTTCATCCTTTTGGGAATCCACACACA
GAGGGGCTGGAGATGACACTTTTTGTCTTATTCTTGCCCTTCTATGCCTGCACTCTACTGGG
30 AAATGTGTCTATCCTTGTTGCTGTTATGTCTTCTGCTCGCCTTCACACACCTATGTATTTCT
TCCTGGGAAACTTGCTGTGTTGACATGGGTTTCTCCTCAGTGACTTGTCACCAAAATGCT
GCTCTACCTTATGGGGCTGAGCCGACTCATCTCCTACAAAGACTGTGTCTGCCAGCTTTTCT
TCTTCCATTTCCCGGAGCATTGAGTGCTTCTTGTTCGGTGATGGCCTATGACCGCTTC
ACTGCCATCTGTTATCCTCTGCGATACACAGTCATCATGAACCCAAGGATCTGTGTGGCCC
35 TGGCTGTGGGCACATGGCTGTTAGGGTGCATTCAATCCAGTATCTTGACCTCCCTCACCTTC
ACCTTGCCATACTGTGGTCCCAATGAAGTGGATCACTTCTTCTGTGACATTCCAGCACTGTT
GCCCTTGGCCTGTGCTGACACATCCTTAGCCAGAGGGTGAGCTTCACCAACGTTGGCCTC
ATATCTCTGTCTGCTTTCTGCTAATTCTTTATCCTACACTAGAATCACAATATCTATCTT
AAGCATTTCGTACAACTGAGGGCCGTCGCCGTGCTTCTCCACCTGCAGTGCTCACCTCATT
40 GCCATCCTCTGTGCTATGGGCCCATCATCACTGTCTACCTGCAGCCACACCCAACCCCA
TGCTGGGAACCGTGGTACAAATTCTCATGAATCTGGTAGGACCAATGCTGAACCCCTTGAT
CTATACCTTGAGGAATAAGGAAGTAAAAACAGCCCTGAAAACAATATTGCACAGGACAGG
CCATGTTCTGAGAGTTAG (SEQ ID NO: 508)

45 **AOLFR324B sequences:**

MPIANDTQFHTSSFLLGIPGLEDVHIWIGFPFFSVYLIALLGNAAIFFVIQTEQSLHEPMYCYLA
MLDSIDLSTATIPKMLGIFWFNIKEISFGGYLSQMFFIHFVTVMESIVLVAMAFDRYIAICKPL
WYTMILTSKIISLIAGIAVLRSLYMVPLVFLLLRPLFCGHRIPHTYCEHMGARLACASIKVNM
FGLGSISLLLDVLLILSHRILYAVFCLPSWEARLKALNTCGSHIGVILAFSTPAFFSFFTHCFGH
50 DIPQYIHIFLANLYVVPPTLNPVIYGVRTKHIRETVLRIFFKTDH (SEQ ID NO: 509)

ATGCCTATAGCTAACGACACCCAGTTCATCTTCTTCACTTCTACTGCTGGGTATCCCAGG
GCTAGAAGATGTGCACATCTGGATTGGATTCCCTTTTTTCTCTGTGTATCTTATTGCACTCC
TGGGAAATGCTGCTATCTTCTTTGTGATCCAACTGAGCAGAGTCTCCATGAGCCCATGTA
55 CTACTGCCTGGCCATGTTGGATTCCATTGACCTGAGCTTGTCTACGGCCACCATTCCCAAA
ATGCTGGGCATCTTCTGGTTCAATATCAAGGAAATATCTTTGGAGGCTACCTTTCTCAGA

TGTTCCTTCATCCATTTCTTCACTGTCATGGAGAGCATCGTATTGGTGGCCATGGCCTTTGAC
 CGCTACATTGCCATTTGCAAACCTCTTTGGTACACCATGATCCTCACCAGCAAAATCATCA
 GCCTCATTTGCAGGCATTGCTGTCTGAGGAGCTTGATCATGGTCATTCCACTGGTGTCTTCT
 CCTCTTAAGGTTGCCCTTCTGTGGACATCGTATCATCCCTCATACTTACTGTGAGCACATGG
 5 GCATTGCCCCGTCTGGCCTGTGCCAGCATCAAAGTCAACATTATGTTTGGTCTTGGCAGTAT
 TTCTCTCTTGTATTGGATGTGCTCCTTATTATTCTCTCCCATATCAGGATCCTCTATGCTGT
 CTCTGCCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGTGGCTCTCACATT
 GGTGTTATCTTAGCCTTTTCTACACCAGCATTTTTCTCTTTCTTTACACACTGCTTTGGCCAT
 GATATCCCCCAATATATCCACATTTTCTTGGCTAATCTATATGTGGTTGTTCTCTCCACCCT
 10 CAATCCTGTAATCTATGGGGTCAGAACCAACATATTAGGGAGACAGTGCTGAGGATTTTC
 TTCAAGACAGATCACTAA (SEQ ID NO: 510)

AOLFR328 sequences:

15 MALGNHSTITEFLLGLSADPNIRALLFVFLGIYLLTIMENLMLLLVRADSCLHKPMYFFLSH
 LSFVDLCFSSVIVPKMLENLLSQRKTISVEGCLAQVFFVFTAGTEACLLSGMAYDRHAAIRRP
 LLYGQIMGKQLYMHLVWGSWGLGFLDALINVLLAVNMVFCEAKIIHHYSYEMPSLLPLSCSDI
 SRSLIVLLCSTLLHGLGNFLLVFLSYTRIISTILSISSTSGRSKAFSTCSAHLTAVTLYYGSGLLRHL
 MPNSGSPIELIFSVQYTVVTPMLNSLIYSLKNKEVKVALKRTLEKYLQYTRR (SEQ ID NO: 511)

20 ATGGCCTTGGGGAATCACAGCACCATCACCGAGTTCCTCCTCCTTGGGCTGTCTGCCGACC
 CCAACATCCGGGCTCTGCTCTTTGTGCTGTTCTTGGGGATTTACCTCCTGACCATAATGGA
 AAACCTGATGCTGCTGCTCGTGATCAGGGCTGATTCTTGTCTCCATAAGCCCATGTATTTCT
 TCCTGAGTCACCTCTCTTTTGTGATCTCTGCTTCTCTTCAGTCATTGTGCCCAAGATGCTG
 GAGAACCTCCTGTACAGAGGAAAAACATTTAGTAGAGGGCTGCCTGGCTCAGGTCTTCT
 25 TTGTGTTTGTCACTGCAGGGACTGAAGCCTGCCTTCTCTCAGGGATGGCCTATGACCGCCA
 TGCTGCCATCCGCCGCCCACTACTTTATGGACAGATCATGGGTAAACAGCTGTATATGCAC
 CITGTGTGGGGCTCATGGGGACTGGGCTTTCTGGACGCACTCATCAATGTCCTCCTAGCTG
 TAAACATGGTCTTTTGTGAAGCCAAAATCATTACCACTACAGCTATGAGATGCCATCCCT
 CCTCCCTCTGTCTGCTCTGATATCTCCAGAAGCCTCATCGTTTTGCTCTGCTCCACTCTCC
 30 TACATGGGCTGGGAAACTTCCTTTTGGTCTTCTTATCCTACACCCGTATAATCTCTACCATC
 CTAAGCATCAGCTCTACCTCGGGCAGAAGCAAGGCCTTCTCCACCTGCTCTGCCCACCTCA
 CTGCAGTGACACTTTACTATGGCTCAGGTTTGTCTCCGCCATCTCATGCCAAACTCAGGTTT
 CCCCATAGAGTTGATCTTCTCTGTGCAGTATACTGTAGTCACTCCCATGCTGAATTCCCTCA
 TCTATAGCCTGAAAAATAAGGAAGTGAAGGTAGCTCTGAAAAGAACTTTGAAAAAATATT
 35 TGCAATATAACCAGACGTTGA (SEQ ID NO: 512)

CLAIMS

What is Claimed:

1. An isolated nucleic acid sequence selected from the group consisting of:
 - 5 (i) an isolated nucleotide sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID

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 20 SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
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 25 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
 SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
 SEQ ID NO: 508, SEQ ID NO: 510; and SEQ ID NO: 512, or a fragment thereof

which comprises at least 75 nucleotides;

- 30 (ii) an isolated cDNA or an insoluble RNA transcribed therefrom that encodes a
 polypeptide having an amino acid sequence selected from the group consisting of:
 SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ
 ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ

ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ
ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ
ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ
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which encodes at least 25 contiguous amino acids of said polypeptide;

(iii) a nucleic acid sequence that comprises at least 30% sequence identity with an isolated nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, 25 SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, 30 SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92,

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NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
5 SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
10 NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
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SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
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SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
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SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
25 SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID
NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
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SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
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SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID

NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
 SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
 SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
 5 NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
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 NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
 10 SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
 SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
 SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512, or to a fragment thereof

15 which comprises at least 100 contiguous nucleotides thereof;

(iv) a nucleic acid sequence that encodes a polypeptide having at least 40%
 sequence identity at the amino acid level with a polypeptide having an amino acid
 sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ
 ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID
 20 NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID
 NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID
 NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID
 NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID
 NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID
 25 NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID
 NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID
 NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID
 NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ
 ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113,
 30 SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID
 NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131,
 SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID
 NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149,

SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID
NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167,
SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID
NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185,
5 SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID
NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203,
SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID
NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221,
SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID
10 NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239,
SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID
NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257,
SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID
NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,
15 SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID
NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,
SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID
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SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID
20 NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,
SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID
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SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID
NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,
25 SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID
NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,
SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID
NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,
SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID
30 NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,
SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID
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SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID

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 SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID
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 SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID
 5 NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,
 SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID
 NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509
 and SEQ ID NO: 511 or a nucleic acid sequence encoding at least 50 contiguous
 amino acid residues thereof;
- 10 (v) an isolated nucleic acid sequence which encodes an olfactory receptor or a
 fragment thereof that specifically hybridizes and exhibits at least 30% sequence
 identity under stringent conditions to a nucleic acid sequence selected from the group
 consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID
 NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID
 15 NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID
 NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID
 NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID
 NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID
 NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID
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 NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID
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 NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108,
 SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID
 25 NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126,
 SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID
 NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144,
 SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID
 NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162,
 30 SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID
 NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180,
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 NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198,

SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID
NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216,
SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID
NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234,
5 SEQ ID NO: 236, SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242, SEQ ID
NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252,
SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID
NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270,
SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID
10 NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288,
SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID
NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306,
SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID
NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324,
15 SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID
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NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360,
SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID
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SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID
NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396,
SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID
NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414,
25 SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID
NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432,
SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID
NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450,
SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID
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SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID
NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486,
SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID

NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504,
SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512;

(vi) an isolated nucleic acid sequence that specifically hybridizes to (i) or a portion thereof under stringent hybridization conditions that is at least 20-30 nucleotides in

5 length; and

(vii) a naturally occurring allelic or synthetic variant of a nucleic acid sequence according to (i) or (ii), containing at least one substitution, deletion or addition mutation in the coding region.

10 2. The isolated nucleic acid sequence of Claim 1 which is selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214,

SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID
NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232,
SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID
NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250,
5 SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID
NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268,
SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID
NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286,
SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID
10 NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304,
SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID
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SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID
NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340,
15 SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID
NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358,
SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID
NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376,
SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID
20 NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394,
SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID
NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412,
SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID
NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430,
25 SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID
NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448,
SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID
NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466,
SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID
30 NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484,
SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID
NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502,
SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID

NO: 512 or a fragment thereof which comprises at least 75 contiguous nucleotides thereof.

3. The isolated nucleic acid sequence of Claim 1 which encodes a
- 5 polypeptide having an amino acid sequence selected from the group consisting of:
- SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ
ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ
ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ
ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ
10 ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ
ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ
ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ
ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ
ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ
15 ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ
ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109,
SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID
NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127,
SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID
20 NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145,
SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID
NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163,
SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID
NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181,
25 SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID
NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199,
SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID
NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217,
SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID
30 NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235,
SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID
NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253,
SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID

NO.: 263, SEQ ID NO.: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271,
 SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID
 NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289,
 SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID
 5 NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307,
 SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID
 NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325,
 SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID
 NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343,
 10 SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID
 NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361,
 SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID
 NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379,
 SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID
 15 NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397,
 SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID
 NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415,
 SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID
 NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433,
 20 SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID
 NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451,
 SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID
 NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469,
 SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID
 25 NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487,
 SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID
 NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505,
 SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof
 encoding at least 25 contiguous amino acid residues of said polypeptide.

30

4. An isolated nucleic acid sequence having at least 30-60% sequence
 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
 NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID

NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
5 NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
10 ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
15 SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
20 NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
25 SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
30 NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID

NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
 SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
 NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
 SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
 5 NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
 SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
 NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
 SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
 NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
 10 SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
 SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
 NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
 SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
 15 NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
 NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
 SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
 20 SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
 SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512; or a fragment thereof
 comprising at least 100 contiguous nucleotides of any of said sequences.

25 5. An isolated nucleic acid sequence having at least 60-80% sequence
 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
 NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID
 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
 NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
 30 NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
 NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
 NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID

NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
5 SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
10 NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
15 SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
20 NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
25 SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID
NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
30 NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID

NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
5 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
10 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
15 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a fragment thereof
comprising at least 100 contiguous nucleotides of any of said sequences.

6. An isolated nucleic acid sequence having at least 80-90% sequence
20 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID
NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
25 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
30 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,

SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
5 SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
10 NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
15 SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
20 NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID
NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
25 SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
30 NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID

NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
 SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
 NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
 5 NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
 SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
 SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
 10 SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a fragment thereof
 comprising at least 100 contiguous nucleotides of any of said sequences.

7. An isolated nucleic acid sequence having at least 85% sequence
 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
 15 NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID
 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
 NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
 NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
 20 NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
 NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
 NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
 NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
 25 ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
 SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
 NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
 SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
 NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
 30 SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
 NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
 SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
 NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,

SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
5 SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
10 NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
15 SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID
NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
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NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
20 NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
25 SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
30 NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID

NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
 SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
 SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512, or a fragment thereof
 5 comprising at least 100 contiguous nucleotides of any of said sequences.

8. An isolated nucleic acid sequence having at least 90% sequence
 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
 NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID
 10 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
 NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
 NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
 NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
 15 NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
 NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
 NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
 ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
 20 SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
 NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
 SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
 NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
 SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
 25 NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
 SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
 NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
 SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
 NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
 30 SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
 NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
 SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
 NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,

SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, 5 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID 10 NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, 15 SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID 20 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, 25 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID 30 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a fragment thereof comprising at least 100 contiguous nucleotides of any of said sequences.

9. An isolated nucleic acid sequence according to Claim 1 which encodes a polypeptide having at least 40-60% sequence identity with a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID

NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,
 SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID
 NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,
 SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID
 5 NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,
 SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID
 NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,
 SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID
 NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,
 10 SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID
 NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,
 SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID
 NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,
 SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID
 15 NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,
 SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID
 NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,
 SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID
 NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,
 20 SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID
 NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,
 SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID
 NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,
 SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID
 25 NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,
 SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least
 40 contiguous amino acids thereof.

10. An isolated nucleic acid sequence according to Claim 1 which encodes
 30 a polypeptide having at least 60-70% sequence identity with a polypeptide having an
 amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID
 NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID
 NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID

NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID
NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID
NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID
NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID
5 NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID
NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID
NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID
NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ
ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,
10 SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID
NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,
SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID
NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147,
SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID
15 NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,
SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID
NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,
SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID
NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,
20 SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID
NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,
SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID
NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,
SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID
25 NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,
SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID
NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,
SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID
NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,
30 SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID
NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,
SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID
NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,

SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, 5 SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, 10 SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, 15 SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, 20 SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least 40 contiguous amino acids thereof.

11. An isolated nucleic acid sequence according to Claim 1 which encodes 25 a polypeptide having at least 70-80% sequence identity with a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID

NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID
NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID
NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ
ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,
5 SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID
NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,
SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID
NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147,
SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID
10 NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,
SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID
NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,
SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID
NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,
15 SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID
NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,
SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID
NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,
SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID
20 NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,
SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID
NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,
SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID
NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,
25 SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID
NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,
SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID
NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,
SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID
30 NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,
SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID
NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,
SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID

NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,
 SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID
 NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,
 SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID
 5 NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,
 SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID
 NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,
 SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID
 NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,
 10 SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID
 NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,
 SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID
 NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,
 SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID
 15 NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,
 SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least
 40 contiguous amino acids thereof.

12. An isolated nucleic acid sequence according to Claim 1 which encodes
 20 a polypeptide having at least 80-90% sequence identity with a polypeptide having an
 amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID
 NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID
 NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID
 NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID
 25 NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID
 NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID
 NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID
 NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID
 NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID
 30 NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID
 NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ
 ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,
 SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID

NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,
SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID
NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147,
SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID
5 NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,
SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID
NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,
SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID
NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,
10 SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID
NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,
SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID
NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,
SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID
15 NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,
SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID
NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,
SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID
NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,
20 SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID
NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,
SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID
NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,
SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID
25 NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,
SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID
NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,
SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID
NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,
30 SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID
NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,
SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID
NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,

SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, 5 SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, 10 SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least 40 contiguous amino acids thereof.

13. An isolated nucleic acid sequence according to Claim 1 which encodes 15 a polypeptide having about 90-99% sequence identity with a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, 25 SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, 30

SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID
NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,
SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID
NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,
5 SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID
NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,
SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID
NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,
SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID
10 NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,
SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID
NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,
SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID
NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,
15 SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID
NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,
SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID
NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,
SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID
20 NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,
SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID
NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,
SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID
NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,
25 SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID
NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,
SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID
NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,
SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID
30 NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,
SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID
NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,
SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID

NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,
SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID
NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,
SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID
5 NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,
SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least
40 contiguous amino acids thereof.

14. An isolated nucleic acid sequence which exhibits at least 50%
10 sequence identity with a nucleic acid sequence selected from the group consisting of:
SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ
ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ
ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ
ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ
15 ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ
ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ
ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ
ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ
ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ
20 ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100,
SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID
NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118,
SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID
NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136,
25 SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID
NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154,
SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID
NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172,
SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID
30 NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190,
SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID
NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208,
SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID

NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226,
SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID
NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244,
SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID
5 NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262,
SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID
NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280,
SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID
NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298,
10 SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID
NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316,
SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID
NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334,
SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID
15 NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352,
SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID
NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370,
SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID
NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388,
20 SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID
NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406,
SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID
NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424,
SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID
25 NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442,
SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID
NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460,
SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID
NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478,
30 SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID
NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496,
SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID
NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid

sequence which exhibits at least 50% sequence identity to a fragment comprising at least 100 contiguous nucleotides of said nucleic acid sequence.

15. An isolated nucleic acid sequence which exhibits at least 60% sequence identity with a nucleic acid sequence selected from the group consisting of:
- 5 SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262,

SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, 5 SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, 15 SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, 25 SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence which exhibits at least 60% sequence identity to a fragment comprising at 30 least 100 contiguous nucleotides of said nucleic acid sequence.

16. An isolated nucleic acid sequence that exhibits at least 70% sequence identity with a nucleic acid sequence selected from the group consisting of: SEQ ID

NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID
NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
5 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
10 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
15 NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
20 SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
25 NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
30 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,

SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, 5 SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID 10 NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, 15 SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID 20 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence having at least 70% sequence identity with a fragment thereof comprising at least 100 25 contiguous nucleotides thereof.

17. An isolated nucleic acid sequence that exhibits at least 80% sequence identity with a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID 30 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID

NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
5 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
10 NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
15 SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
20 NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
25 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID
30 NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID

NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
 SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
 NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
 SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
 5 NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
 SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
 SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
 NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
 10 SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
 NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
 NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
 SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
 15 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
 SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
 SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence
 having at least 80% sequence identity with a fragment thereof comprising at least 100
 20 contiguous nucleotides thereof.

18. An isolated nucleic acid sequence that exhibits at least 85% sequence
 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
 NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID
 25 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
 NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
 NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
 NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
 30 NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
 NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
 NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ

ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
5 NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
10 SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
15 NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
20 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID
25 NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
30 SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,

SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
 SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
 NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
 5 SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
 NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
 NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
 SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
 10 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
 SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
 SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence
 having at least 85% sequence identity with a fragment thereof comprising at least 100
 15 contiguous nucleotides thereof.

19. An isolated nucleic acid sequence that exhibits at least 90% sequence
 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
 NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID
 20 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
 NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
 NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
 NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
 25 NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
 NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
 NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
 ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
 30 SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
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 NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,

SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
5 SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
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10 NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
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NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
15 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
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SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
25 SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
30 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID

NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
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 NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
 SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
 5 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
 SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
 SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence
 having at least 90% sequence identity with a fragment thereof comprising at least 100
 10 contiguous nucleotides thereof.

20. An isolated nucleic acid sequence that exhibits at least 95% sequence
 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
 NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID
 15 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
 NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
 NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
 NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
 20 NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
 NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
 NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
 ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
 25 SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
 NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
 SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
 NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
 SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
 30 NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
 SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
 NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
 SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID

NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
5 NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
10 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID
15 NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
20 SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
25 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
30 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,

SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence having at least 95% sequence identity with a fragment thereof comprising at least 100
 5 contiguous nucleotides thereof.

21. An isolated nucleic acid sequence that exhibits about 96-99% sequence identity with a nucleic acid sequence encoding an olfactory receptor selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8,
 10 SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58,
 15 SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID
 20 NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152,
 25 SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID
 30 NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID

NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242,
SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID
NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260,
SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID
5 NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278,
SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID
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SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID
NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314,
10 SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID
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SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID
NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350,
SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID
15 NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368,
SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID
NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386,
SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID
NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404,
20 SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID
NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422,
SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID
NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440,
SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID
25 NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458,
SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID
NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476,
SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID
NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494,
30 SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID
NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512
or a fragment having at least 96-99% sequence identity with a fragment thereof
comprising at least 100 contiguous nucleotides thereof.

22. A nucleic acid sequence which encodes for a functional olfactory receptor polypeptide, wherein said nucleic acid sequence comprises a portion which is at least 100 nucleotides in length and exhibits at least 40% sequence identity with at least 100 contiguous nucleotides of a portion of an olfactory receptor encoding a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256,

SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, 5 SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID 10 NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, 15 SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID 20 NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, 25 SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512.

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23. The nucleic acid sequence of Claim 22 which is a chimeric nucleic acid sequence, wherein said nucleic acid sequence is produced by combining portions of at least two different G protein-coupled receptors.

24. The chimeric nucleic acid sequence of Claim 23 wherein said two different G protein-coupled receptors are olfactory receptors.

5 25. The chimeric nucleic acid sequence of Claim 23 wherein said chimeric sequence contains at least 200 contiguous nucleotides that are at least 40% identical to a portion of one of said olfactory receptor encoding nucleic acid sequences.

26. An isolated nucleic acid sequence according to Claim 1, wherein said
10 isolated nucleic acid sequence is directly or indirectly attached to a nucleic acid sequence that encodes a detectable polypeptide.

27. The nucleic acid sequence of Claim 26, wherein said detectable polypeptide is green fluorescent protein, or a fragment or variant thereof.

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28. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 40% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID

20
25
30

NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161,
SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID
NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,
SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID
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20 SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID
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30 SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID
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 NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,
 5 SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID
 NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,
 SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a
 fragment thereof comprising at least 40 contiguous amino acids thereof that optionally
 is directly or indirectly attached to a sequence that facilitates the expression and/or
 10 translocation of said polypeptide on the surface of a cell.

29. An isolated nucleic acid sequence which encodes a polypeptide that
 exhibits at least 50% sequence identity with a polypeptide selected from the group
 consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID
 15 NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID
 NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID
 NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID
 NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID
 NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID
 20 NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID
 NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID
 NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID
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20 SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID
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SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID
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30 SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID
NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467,
SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID
NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,

SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally
5 is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

30. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 60% sequence identity with a polypeptide selected from the group
10 consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID
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20 NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143,
25 SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID
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20 SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID
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SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID
NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467,
SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID
NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,
30 SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID
NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,
SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a
fragment thereof comprising at least 40 contiguous amino acids thereof that optionally

is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

31. An isolated nucleic acid sequence which encodes a polypeptide that
- 5 exhibits at least 70% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID
- 10 NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID
- 15 NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID
- 20 NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,
- 25 SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID
- 30 NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID

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10 SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID
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SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID
25 NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,
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NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,
SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a
fragment thereof comprising at least 40 contiguous amino acids thereof that optionally
30 is directly or indirectly attached to a sequence that facilitates the expression and/or
translocation of said polypeptide on the surface of a cell.

32. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 80% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,

SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, 5 SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, 10 SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, 15 SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, 20 SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, 25 SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

30 33. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 85% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID

NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID
NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID
NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID
NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID
5 NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID
NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID
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NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107,
10 SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID
NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125,
SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID
NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143,
SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID
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SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID
NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,
SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID
NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,
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30 SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID
NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,
SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID
NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,

SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

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34. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 90% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID

NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID
NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID
NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID
NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID
5 NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107,
SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID
NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125,
SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID
NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143,
10 SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID
NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161,
SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID
NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,
SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID
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SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID
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20 SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID
NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,
SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID
NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269,
SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID
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SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID
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SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID
NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,
30 SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID
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SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID
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SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, 5 SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, 10 SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, 15 SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally is directly or indirectly attached to a sequence that facilitates the expression and/or 20 translocation of said polypeptide on the surface of a cell.

35. An isolated nucleic acid sequence which encodes a polypeptide that exhibits about 90-99% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID

NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107,
SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID
NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125,
SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID
5 NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143,
SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID
NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161,
SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID
NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,
10 SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID
NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,
SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID
NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,
SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID
15 NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,
SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID
NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,
SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID
NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269,
20 SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID
NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,
SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID
NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,
SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID
25 NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,
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SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID
NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,
30 SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID
NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377,
SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID
NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,

SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, 5 SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, 10 SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally 15 is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

36. The isolated nucleic acid sequence according to Claim 26, wherein said isolated nucleic acid sequence is operably linked to a constitutive promoter.

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37. The isolated nucleic acid sequence according to Claim 1, wherein said isolated nucleic acid sequence is operably linked to a regulatable promoter.

38. The isolated nucleic acid sequence of Claim 1, wherein said isolated 25 nucleic acid sequence is directly or indirectly attached to a nucleic acid sequence encoding a mammalian rhodopsin polypeptide or a fragment thereof.

39. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes a fragment of at least 60 contiguous amino acids of a polypeptide having 30 an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID

NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID
NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID
NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID
NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID
5 NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID
NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID
NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ
ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,
SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID
10 NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,
SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID
NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147,
SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID
NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,
15 SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID
NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,
SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID
NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,
SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID
20 NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,
SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID
NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,
SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID
NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,
25 SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID
NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,
SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID
NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,
SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID
30 NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,
SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID
NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,
SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID

NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,
SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID
NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,
SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID
5 NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,
SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID
NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,
SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID
NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,
10 SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID
NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,
SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID
NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,
SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID
15 NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,
SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID
NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,
SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID
NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,
20 SEQ ID NO: 509, and SEQ ID NO: 511.

40. The isolated nucleic acid molecule of Claim 39, wherein the nucleotide
sequence encodes at least 100 amino acids.

25 41. The isolated nucleic acid molecule of Claim 39, wherein the nucleotide
sequence encodes at least 150 amino acids.

42. The isolated nucleic acid molecule of Claim 39, wherein the nucleotide
sequence encodes at least 200 amino acids.

30

43. The isolated nucleic acid molecule of Claim 39, wherein the nucleotide
sequence encodes at least 250 amino acids.

44. The isolated nucleic acid molecule of Claim 39, wherein the polypeptide is an olfactory G protein-coupled receptor.

45. The isolated nucleic acid molecule of Claim 39, wherein the expression
5 product binds an odorant.

46. The isolated nucleic acid molecule of Claim 1 comprising a nucleotide sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240.

SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID
NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258,
SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID
NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276,
5 SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID
NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294,
SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID
NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312,
SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID
10 NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330,
SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID
NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348,
SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID
NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366,
15 SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID
NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384,
SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID
NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402,
SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID
20 NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420,
SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID
NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438,
SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID
NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456,
25 SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID
NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474,
SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID
NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492,
SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID
30 NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510
and SEQ ID NO: 512.

47. An expression vector that comprises a nucleic acid sequence according to Claim 1.

48. The expression vector of Claim 47, wherein said vector is a mammalian, yeast, bacterial or insect expression vector.

49. A cell which is transfected or transformed with at least one nucleic acid sequence according to Claim 1.

50. A mammalian cell according to Claim 49.

51. A human cell according to Claim 50.

52. A yeast or insect cell according to Claim 49.

53. The mammalian cell according to Claim 49 which is selected from the group consisting of: an olfactory cell, Chinese hamster ovary cell, baby hamster kidney cell, and a myeloma cell.

54. A solid phase comprising at least one isolated nucleic acid sequence according to Claim 1.

55. A solid phase comprising at least one isolated nucleic acid sequence according to Claim 1, wherein the solid phase is attached to an array comprising at least one additional nucleic acid sequence.

56. The solid phase according to Claim 55 which comprises an array of at least 4 different nucleic acid sequences that encode olfactory receptors or fragments or variants thereof.

57. The solid phase according to Claim 55 which comprises at least 10 different nucleic acid sequences that encode olfactory receptors or fragments or variants thereof.

58. The solid phase according to Claim 55 which comprises at least 50 different nucleic acid sequences that encode olfactory receptors or fragments or variants thereof.

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59. The solid phase according to Claim 55 which comprises at least 100 different sequences that encode olfactory receptors or fragments or variants thereof.

60. An isolated polypeptide that is selected from the group consisting of:

- 10 (i) a polypeptide comprising an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,
- 15
- 20
- 25
- 30

SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID
NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,
SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID
NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,
5 SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID
NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269,
SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID
NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,
SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID
10 NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,
SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID
NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,
SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID
NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341,
15 SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID
NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,
SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID
NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377,
SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID
20 NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,
SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID
NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413,
SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID
NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431,
25 SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID
NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,
SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID
NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467,
SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID
30 NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,
SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID
NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,
SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511;

- (ii) a polypeptide comprising an amino acid sequence that exhibits at least 40% sequence identity with an amino acid sequence selected from the group consisting of:
- SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289,

SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID
 NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307,
 SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID
 NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325,
 5 SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID
 NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343,
 SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID
 NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361,
 SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID
 10 NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379,
 SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID
 NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397,
 SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID
 NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415,
 15 SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID
 NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433,
 SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID
 NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451,
 SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID
 20 NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469,
 SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID
 NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487,
 SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID
 NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505,
 25 SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511;

- (iii) a polypeptide comprising an amino acid sequence that exhibits at least 60% sequence identity with a fragment of a polypeptide according to (i) which fragment is at least 40 amino acids in length;
- (iv) a chimeric polypeptide that comprises a portion of a polypeptide according to
- 30 (i) or (ii) that is at least 40 amino acids in length and a portion of at least one other G protein-coupled receptor; and
- (v) a variant of a polypeptide according to (i) which differs by said polypeptide by at least one substitution, addition or deletion modification.

61. An isolated polypeptide according to Claim 60 wherein such polypeptide exhibits at least 70% sequence identity with a polypeptide having a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,

SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID
NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,
SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID
NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,
5 SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID
NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,
SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID
NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,
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10 NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,
SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID
NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,
SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID
NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,
15 SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID
NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,
SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID
NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437,
SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID
20 NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455,
SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID
NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473,
SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID
NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,
25 SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID
NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509
and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

62. An isolated polypeptide according to Claim 60 wherein said
30 polypeptide exhibits at least 80% sequence identity with a polypeptide having a
sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ
ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID
NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID

NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID
NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID
NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID
NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID
5 NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID
NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID
NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID
NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ
ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113,
10 SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID
NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131,
SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID
NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149,
SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID
15 NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167,
SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID
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SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID
NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203,
20 SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID
NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221,
SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID
NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239,
SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID
25 NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257,
SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID
NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,
SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID
NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,
30 SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID
NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,
SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID
NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,

SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID
 NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,
 SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID
 NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,
 5 SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID
 NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,
 SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID
 NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,
 SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID
 10 NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,
 SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID
 NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437,
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 NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455,
 15 SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID
 NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473,
 SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID
 NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,
 SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID
 20 NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509
 and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

63. An isolated polypeptide according to Claim 60 wherein said
 polypeptide exhibits at least 90% sequence identity with a polypeptide having a
 25 sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ
 ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID
 NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID
 NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID
 NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID
 30 NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID
 NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID
 NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID
 NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID

NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID
NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ
ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113,
SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID
5 NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131,
SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID
NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149,
SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID
NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167,
10 SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID
NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185,
SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID
NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203,
SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID
15 NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221,
SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID
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SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID
NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257,
20 SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID
NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,
SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID
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SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID
NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,
30 SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID
NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,
SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID
NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,

SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

64. An isolated polypeptide according to Claim 60 wherein said polypeptide exhibits about 80-90% sequence identity with a polypeptide having a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID

NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149,
SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID
NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167,
SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID
5 NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185,
SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID
NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203,
SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID
NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221,
10 SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID
NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239,
SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID
NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257,
SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID
15 NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,
SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID
NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,
SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID
NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,
20 SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID
NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,
SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID
NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,
SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID
25 NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,
SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID
NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,
SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID
NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,
30 SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID
NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,
SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID
NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437,

SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, 5 SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

10

65. An isolated polypeptide according to Claim 60 wherein said polypeptide exhibits at least 90-95% sequence identity with a polypeptide having a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, 25 SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, 30 SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID

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SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

5 66. An isolated polypeptide according to Claim 60 wherein said polypeptide exhibits about 95-99% sequence identity with a polypeptide having a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID

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 10 SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID
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 20 SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID
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 25 NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473,
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 SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID
 NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509
 30 and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

67. A variant according to Claim 60(v) which comprises at least 5 conservative amino acid substitutions.

68. A variant according to Claim 60(v) which comprises at most 5 conservative amino acid substitutions.

5 69. A variant according to Claim 60(v) which comprises 5 to 7 conservative substitution modifications.

70. A variant according to Claim 60(v) which comprises 3 to 4 conservative substitution modifications.

10

71. A variant according to Claim 60(v) which comprises 1 or 2 conservative substitution modifications.

72. A solid phase comprising at least one directly or indirectly
15 immobilized isolated polypeptide according to Claim 60, or a cell which expresses said polypeptide on the surface thereof.

73. The solid phase of Claim 72 comprising at least 4 different immobilized polypeptides according to Claim 60, or a cell which expresses said
20 polypeptide on the surface thereof.

74. The solid phase of Claim 72 comprising at least 16 different immobilized polypeptides according to Claim 60, or a cell which expresses said polypeptide on the surface thereof.

25

75. The solid phase of Claim 72 comprising at least 25 different immobilized polypeptides according to Claim 60 or a cell which expresses said polypeptide on the surface thereof.

30 76. A method of detecting expression of an olfactory receptor gene comprising (a) hybridizing at least one sample with a nucleic acid according to Claim 1 and (b) detecting expression of the olfactory receptor gene by a positive hybridization signal.

77. A method of screening a library comprising (a) hybridizing the library with a nucleic acid according to Claim 1 and (b) detecting one or more olfactory receptor clones in the library by a positive hybridization signal.

5

78. A recombinant polynucleotide comprising a nucleic acid according to Claim 1 attached directly or indirectly to a heterologous nucleic acid.

79. An expression vector comprising the nucleic acid of Claim 1 and an operably linked heterologous nucleic acid that drives expression thereof.

10

80. A transfected or transformed cell comprising the recombinant polynucleotide of Claim 78 introduced into a host cell, or a progeny thereof.

81. A transgenic non-human organism comprising the recombinant polynucleotide of Claim 78 introduced into a cell of a host non-human organism, or a progeny thereof.

15

82. A method of making a recombinant polynucleotide comprising ligating the nucleic acid of Claim 1 to a heterologous nucleic acid.

20

83. The method of Claim 82 wherein the heterologous nucleic acid comprises a translational and/or transcriptional regulatory region.

84. A method of making a transfected cell comprising introducing the recombinant polynucleotide of Claim 79 into a host cell, and propagating the host cell in which the recombinant polynucleotide has been introduced.

25

85. A method of detecting specific binding of a putative ligand to an olfactory receptor comprising (a) contacting the putative ligand with a cell in which the expression vector of Claim 79 has been introduced, wherein the olfactory receptor is expressed by the cell thereby, and (b) directly or indirectly detecting specific binding between the putative ligand and the olfactory receptor.

30

86. A method of making transgenic non-human organism comprising introducing the recombinant polynucleotide of Claim 78 into a cell of a host non-human organism, or propagating the host non-human organism in which the
5 recombinant polynucleotide has been introduced.

87. An isolated protein molecule comprising a fragment of at least 60 contiguous amino acids of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID
10 NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID
15 NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ
20 ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151,
25 SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID
30 NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID

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5 NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277,
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10 SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID
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30 SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID
NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO:
511.

88. The isolated protein molecule of Claim 87, wherein the fragment contains at least 100 amino acids.

89. The isolated protein molecule of Claim 87, wherein the fragment
5 contains at least 150 amino acids.

90. The isolated protein molecule of Claim 87, wherein the fragment contains at least 200 amino acids.

10 91. The isolated protein molecule of Claim 87, wherein the fragment contains at least 250 amino acids.

92. The isolated protein molecule of Claim 87, which is a functional olfactory receptor polypeptide.
15

93. The isolated protein molecule of Claim 87, wherein the fragment specifically binds an odorant molecule.

94. A recombinant polypeptide comprising the protein molecule of Claim
20 87 and a heterologous peptide domain.

95. The recombinant polypeptide of Claim 94, wherein the heterologous peptide domain comprises a G protein-coupled receptor transmembrane domain.

25 96. The recombinant polypeptide of Claim 94 comprising a seven-transmembrane receptor with an olfactory receptor ligand-binding domain, wherein the olfactory receptor ligand-binding domain is a chimera of at least two different olfactory receptors.

30 97. A method of detecting specific binding of a ligand to an olfactory receptor comprising (a) contacting the ligand with the protein of Claim 86, and (b) directly or indirectly detecting specific binding between the ligand and the olfactory receptor.

98. An antibody or antibody fragment that specifically binds a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281,

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25 SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID
NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

99. A method of detecting specific binding of the antibody of Claim 98 to
an olfactory receptor comprising (a) contacting the antibody with a sample comprising
30 the olfactory receptor and (b) detecting specific binding therebetween.

100. The method of Claim 99, wherein specific binding of the antibody to a
cell in the sample identifies the cell as an olfactory cell.

101. A method of screening a library of chemical compounds for compounds that are involved in olfactory sensation comprising contacting compounds in said library with at least one polypeptide according to Claim 87 and identifying
5 compounds that specifically bind to at least one of said polypeptides.

102. The method of Claim 101 wherein said library is a combinatorial chemical library.

10 103. The method of Claim 101 wherein said library is a peptide library.

104. The method of Claim 101 wherein said library is a peptide, encoded peptide, benzodiazepine, diversomer, vinylogous polypeptide, nonpeptidal peptidomimetic, or small molecule organic compound library.

15 105. The method of Claim 101 wherein said library is a random combination of compounds.

106. The method of Claim 101 wherein said compounds are screened by
20 high turning point screening.

107. The method of Claim 101 wherein said screening is effected using animal cells or tissues that express at least one of said polypeptides.

25 108. A cell-based assay for identifying molecules that interact with an olfactory receptor comprising:

obtaining a cell that expresses at least one polypeptide according to Claim 60 or a chimeric protein comprising a portion of said protein and that of another G protein-coupled receptor, and which optionally expresses at least one functional G protein;
30 contacting said cell with a molecule to be screened for its ability to modulate an
olfactory receptor; and
detecting whether modulation occurs.

109. The method of Claim 108 wherein modulation is detected based on changes in intracellular calcium.

110. The method of Claim 108 wherein modulation is detected by measuring the transfer of ^{32}P from gamma-labeled GTP to the olfactory receptor polypeptide.

111. The method of Claim 108 wherein modulation is determined based on a comparison to a control compound known to modulate the particular olfactory receptor protein.

112. The method of Claim 108 wherein the G protein is Ga_{15} or Ga_{16} or another promiscuous G protein.

113. The method of Claim 108 wherein modulation is determined by detecting whether a change in the level of intracellular cyclic nucleotides occurs.

114. The method of Claim 108 wherein modulation is determined based on the level of transcription of said olfactory polypeptide after contacting the cell with the screened compound.

115. The method of Claim 108 when said screened compounds are synthesized by computer assisted drug devices based on the predicted or actual three-dimensional structure of the amino acid sequence of the olfactory protein or a fragment thereof.

116. The method of Claim 108 wherein compounds that modulate olfactory receptor are identified based on whether they specifically bind to a olfactory receptor polypeptide.

117. The method of Claim 108 wherein modulation refers to the inhibition of olfactory receptor function.

118. The method of Claim 108 wherein modulation refers to the enhancement of olfactory receptor function.

119. A method for representing the olfactory perception of one or more odors in one or more mammals, comprising:

5 providing values X_1 to X_n representative of the quantitative stimulation of each of n odor receptors of said mammals; and

generating from said values a quantitative representation of odor perception, wherein at least one of said odor receptors is an odor receptor polypeptide having a sequence

10 that is at least about 40% identical to a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39,

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NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

120. The method of claim 119, wherein said representation constitutes a point or a volume in n-dimensional space.

5 121. The method of claim 119, wherein said representation constitutes a graph or a spectrum.

122. The method of claim 119, wherein said representation constitutes a matrix of quantitative representations.

10

123. The method of claim 119, wherein said providing step comprises contacting a plurality of recombinantly produced olfactory receptors with a test composition, and quantitatively measuring the interaction of said composition with said receptors.

15

124. A method for predicting the odor perception in a mammal generated by one or more molecules or combinations of molecules comprising:

providing values X_1 to X_n representative of the quantitative stimulation of each of n odor receptors of said mammal, for one or more molecules or combinations of molecules yielding known odor perception in a mammal,

20

generating from said values a quantitative representation of odor perception in a mammal for the one or more molecules or combinations of molecules yielding known odor perception in a mammal;

25

providing values X_1 to X_n representative of the quantitative stimulation of each of n odor receptors of said mammal, for one or more molecules or combinations of molecules yielding unknown odor perception in a mammal;

generating from said values a quantitative representation of odor perception in a mammal for the one or more molecules or combinations of molecules yielding unknown odor perception in a mammal; and

30

predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown odor perception in a mammal by comparing the quantitative representation of odor perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown odor

perception in a mammal to the quantitative representation of odor perception in a mammal for the one or more molecules or combinations of molecules yielding known odor perception in a mammal, wherein at least one of said odor receptors is a odor receptor polypeptide having a sequence that is at least about 40% identical to a

5 sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO:

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NO: 511.

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AOLFR03.PR : ---LLTDR---NLSMEPTALGFDYDK-LQIPRLVIRL : 35
AOLFR04.PR : ---ENQNN---VTEPTILGHEINLELWKIFSA-VAVIV : 34
AOLFR05.PR : ---GKB---NCTTVABETILGSDVDE-LRVCHIRIRAL : 33
AOLFR06.PR : ---MASER---NQSSTPTETILGFEYPE-IQVPEIRAFPI : 35
AOLFR07.PR : ---SYFYRLKLMKEAVLVKLPT---SLPLLQTLRKSRDMETKNYSSTSCETILGSSNPQ-LQKPRIRAFPI : 70
AOLFR08.PR : ---ATSHSSGAEETILGQORPE-LQUPIRIRAL : 33
AOLFR09.PR : ---LARNNSLVTETILGMDRPE-FWQPPETIRIV : 33
AOLFR10.PR : ---LARNNSLVTETILGMDRPE-FWQPPETIRIV : 33
AOLFR11.PR : ---TIRNSSSVTEETILGQEOPE-LQLP-ELIRIG : 33
AOLFR12.PR : ---ERNHVPDNCNVLNFFADKNKRRNFGQIVSDV---GR-ICYSVSLSGEPTTGMGRNLTNR---PSEETILGSSSRPE-DQKPRIRAFPI : 83
AOLFR13.PR : ---ALPL---DQKNG---SSPTETILGSSDRPE-LELVIRLIRI : 33
AOLFR14.PR : ---FENNO---FASSQSLSRMM-SENITRAVAEAVLGSIRWD-LEVAIRLIRI : 58
AOLFR15.PR : ---SSPTETILGSSDRPE-LELVIRLIRI : 33
AOLFR16.PR : ---RR-NCTLVTEETILGMSRRE-LQILAFIRAFPI : 32
AOLFR17.PR : ---J-NFTDVTETILGMSRRE-WQVLEIRIRIV : 31
AOLFR18.PR : ---SENTNGSAETETILGMDRPE-LQSLIRIRAFPI : 33
AOLFR19.PR : ---ETKNYSSTSCETILGSSNPQ-LQKPRIRAFPI : 34
AOLFR20.PR : ---ENHTMNERETILGMDRPE-LKTLIRIRAFPI : 33
AOLFR21.PR : ---EPKRN---VTDVETILGKONPKQKLVF-NEIL : 31
AOLFR22.PR : ---RXKNN---XTEVETILGSDPVKALFV-NEIL : 31
AOLFR23.PR : ---KNILTRVT---ETILGSDMDHPK-LEIPLEIRAFPI : 33
AOLFR24.PR : ---ETGNLTW---VSDVETILGSDMDHPK-LEIPLEIRAFPI : 33
AOLFR25.PR : ---AAKSS-VTEPTILGTHQPG-LRIPIRIRAFPI : 32
AOLFR26.PR : ---QNVSIISENIRAFPI-SAPQHLLPIRIRAFPI : 34
AOLFR27.PR : ---P-NFTDVTETILGMSRRE-WQVLEIRIRIV : 31
AOLFR28.PR : ---SHSPVETILGMSRRE-WQVLEIRIRIV : 31
AOLFR29.PR : ---GFLSPMPCPCPPQRRMAAGNHSVTETILGMDRPE-LQILIRIRAFPI : 35
AOLFR30.PR : ---GNDTIVETILGSDMDHPK-LEIPLEIRAFPI : 33
AOLFR31.PR : ---GNDTIVETILGSDMDHPK-LEIPLEIRAFPI : 33
AOLFR32.PR : ---NSLK---DGNHTALTETILGMDRPE-LRVIIRIRAFPI : 36
AOLFR33.PR : ---LE---GV-EH-L---LMLLLTDVNSKELQSGNQTSHETILGMDRPE-LQILIRIRAFPI : 54
AOLFR34.PR : ---EP---E-VSEETILGMDRPE-LQILIRIRAFPI : 33
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AOLFR36.PR : ---ANET---SPVNGFVIRIRAFPI-LEKTRVIRAFPI : 1
AOLFR37.PR : ---ANET---SPVNGFVIRIRAFPI-LEKTRVIRAFPI : 1
AOLFR38.PR : ---ANET---SPVNGFVIRIRAFPI-LEKTRVIRAFPI : 1
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AOLFR45.PR : ---ST---H-PAVETILGMDRPE-LQILIRIRAFPI : 35
AOLFR46.PR : ---LT---H-PAVETILGMDRPE-LQILIRIRAFPI : 107
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AOLFR48.PR : ---VDPNGNESSA-T-YETILGMDRPE-LQILIRIRAFPI : 36
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AOLFR50.PR : ---KSLIM---KSLIM---KSLIM---KSLIM : 51
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AOLFR52.PR : ---LGPAVHTMETPASEMIRAFPI : 37

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Figure 1

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AOLFR04.pr	120	140	160	180	200	220
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AOLFR06.pr	120	140	160	180	200	220
AOLFR07.pr	120	140	160	180	200	220
AOLFR08.pr	120	140	160	180	200	220
AOLFR09.pr	120	140	160	180	200	220
AOLFR10.pr	120	140	160	180	200	220
AOLFR11.pr	120	140	160	180	200	220
AOLFR12.pr	120	140	160	180	200	220
AOLFR13.pr	120	140	160	180	200	220
AOLFR14.pr	120	140	160	180	200	220
AOLFR15.pr	120	140	160	180	200	220
AOLFR16.pr	120	140	160	180	200	220
AOLFR17.pr	120	140	160	180	200	220
AOLFR18.pr	120	140	160	180	200	220
AOLFR19.pr	120	140	160	180	200	220
AOLFR20.pr	120	140	160	180	200	220
AOLFR21.pr	120	140	160	180	200	220
AOLFR22.pr	120	140	160	180	200	220
AOLFR23.pr	120	140	160	180	200	220
AOLFR24.pr	120	140	160	180	200	220
AOLFR25.pr	120	140	160	180	200	220
AOLFR26.pr	120	140	160	180	200	220
AOLFR27.pr	120	140	160	180	200	220
AOLFR28.pr	120	140	160	180	200	220
AOLFR29.pr	120	140	160	180	200	220
AOLFR30.pr	120	140	160	180	200	220
AOLFR31.pr	120	140	160	180	200	220
AOLFR32.pr	120	140	160	180	200	220
AOLFR33.pr	120	140	160	180	200	220
AOLFR34.pr	120	140	160	180	200	220
AOLFR35.pr	120	140	160	180	200	220
AOLFR36.pr	120	140	160	180	200	220
AOLFR37.pr	120	140	160	180	200	220
AOLFR38.pr	120	140	160	180	200	220
AOLFR39.pr	120	140	160	180	200	220
AOLFR40.pr	120	140	160	180	200	220
AOLFR41.pr	120	140	160	180	200	220
AOLFR42.pr	120	140	160	180	200	220
AOLFR43.pr	120	140	160	180	200	220
AOLFR44.pr	120	140	160	180	200	220
AOLFR45.pr	120	140	160	180	200	220
AOLFR46.pr	120	140	160	180	200	220
AOLFR47.pr	120	140	160	180	200	220
AOLFR48.pr	120	140	160	180	200	220
AOLFR49.pr	120	140	160	180	200	220
AOLFR50.pr	120	140	160	180	200	220
AOLFR51.pr	120	140	160	180	200	220
AOLFR52.pr	120	140	160	180	200	220

Figure 1

AOLFR01.pr	220	RGILLTVISPLSMLIAI	240	THYLILLOLQCC	260	NHN-TIPPHYC	280	DLAPMKSQSD	300	ELINEVIF-IVGLSVIFPPTISFP	320	SYVCLTRAVLWSS	243
AOLFR02.pr		RGALLVAGSVLWFGPPI		MLCYALRIMS		GNP-VINHEYC		EXTALMKSQSD		ILIPHEIF-SPATFNESCILLIHT		SYVFEVAVLWSS	232
AOLFR03.pr		RGVLLVGSVANGVSCSI		ELCSALKGSH		GNP-TINHEYC		EFSSMLKSCSD		HYINOKLIF-FLATFNESCILLIHT		SYVAFVAVLWSS	231
AOLFR04.pr		RGCLLVGGANVGSVNHAN		QOLLFYQIPEC		GNP-LINHEYC		DLQCLMKSQSD		PHILGHIT-LNNGMWCJAFITLPA		SYVILCS-LEKYS	227
AOLFR05.pr		RVVEVASCXFCVGVCSH		RLHLCALYRIFBY		RSN-VINHEYC		DLQCLMKSQSD		ITVNETLIF-LVATFNESCILLIHT		SYVILCS-LEKYS	230
AOLFR06.pr		RGALLVAGSVLWFGPPI		ELVFLDLHSEC		EST-FINHEYC		DHGVINGASVSD		PYSORLCP-ILAEFNESCILLIHT		SYVLEFVAVLWSS	232
AOLFR07.pr		RGALLVAGSVLWFGPPI		ELVFLDLHSEC		ASH-LINHEYC		DTQPMKKSQSD		ESSORVEM-TEILAFNESCILLIHT		SYVLEFVAVLWSS	267
AOLFR08.pr		RGSLMVAVRSISGFMAT		FVLEMSRLSEC		ASH-LINHEYC		DTQPMKKSQSD		ESSORVEM-TEILAFNESCILLIHT		SYVLEFVAVLWSS	230
AOLFR09.pr		RGSMFFAATWGLAGAT		AHTGCMRLSEC		RSN-TWSEHYC		DIPLMKSQSD		THINEMLIF-IIGGVNTAFITLPA		SYVLEFVAVLWSS	230
AOLFR10.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		SAN-LINHEYC		DIPLMKSQSD		THINEMLIF-IIGGVNTAFITLPA		SYVLEFVAVLWSS	230
AOLFR11.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DVPLMKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	229
AOLFR12.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR13.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR14.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR15.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR16.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR17.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR18.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR19.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR20.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR21.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR22.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR23.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR24.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR25.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR26.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR27.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR28.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR29.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR30.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR31.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR32.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR33.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR34.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR35.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR36.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR37.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR38.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR39.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR40.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR41.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR42.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR43.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR44.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR45.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR46.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR47.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR48.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR49.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR50.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR51.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230
AOLFR52.pr		RGVLLVAGSVLWFGPPI		AHTGCMRLSEC		ASN-VINHEYC		DDQPMKKSQSD		THVSEVVF-IVGVNTLSSLSIS		SYVLEFVAVLWSS	230

Figure 1

AOLFR01.pr	TOGRGA	ESTCASHLAW	340	*	LEFVGL	VCVFFPSST	350	*	HPEDTDKIGAV	AV	TPMHP	ISLNRD	KG	CHLNKISSL	325
AOLFR02.pr	VSSRGA	ESTVASHLTAI			TIEGAIL	CMVNSKNSR			Q-TVKVAS	EV	EMENPP	ISLNRD	KG	DEWHTHTQVFFH	314
AOLFR03.pr	VSSRGA	ESTCASHLTAI			TIEGAIL	CMVNSKNSR			H-TVKVAS	EV	EMENPP	ISLNRD	KG	DAWHTHTQVFFH	313
AOLFR04.pr	SKRGA	ESTCASHLAW			VIEFVP	CHLWVTHPI			DKAV	ES	EMENPP	ISLNRD	KG	SKWKEALAGK	309
AOLFR05.pr	AEGRGA	ESTCASHLTAI			TVRCHVL	SHVNSGNSG			L-LTVAS	EV	EMENPP	ISLNRD	KG	SKWKEALAGK	311
AOLFR06.pr	AEGRGA	ESTCASHLTAI			TVRCHVL	SHVNSGNSG			L-LTVAS	EV	EMENPP	ISLNRD	KG	SKWKEALAGK	314
AOLFR07.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			YVVDRA	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	347
AOLFR08.pr	TEGRGA	ESTCASHLAW			GIFRIT	CMVNSKNSR			E-KERSS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	311
AOLFR09.pr	TEGRGA	ESTCASHLAW			SLEFGAA	CMVNSKNSR			E-KERSS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	313
AOLFR10.pr	TEGRGA	ESTCASHLAW			SLEFGAA	CMVNSKNSR			E-KERSS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	313
AOLFR11.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	309
AOLFR12.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	360
AOLFR13.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	312
AOLFR14.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	341
AOLFR15.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	309
AOLFR16.pr	TEGRGA	ESTCASHLAW			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	311
AOLFR17.pr	TEGRGA	ESTCASHLAW			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	307
AOLFR18.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	305
AOLFR19.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	311
AOLFR20.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	316
AOLFR21.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	299
AOLFR22.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	315
AOLFR23.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	314
AOLFR24.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	307
AOLFR25.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	310
AOLFR26.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	310
AOLFR27.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	316
AOLFR28.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	310
AOLFR29.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	318
AOLFR30.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	326
AOLFR31.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	311
AOLFR32.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	322
AOLFR33.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	332
AOLFR34.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	312
AOLFR35.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	329
AOLFR36.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	319
AOLFR37.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	324
AOLFR38.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	314
AOLFR39.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	323
AOLFR40.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	318
AOLFR41.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	324
AOLFR42.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	311
AOLFR43.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	323
AOLFR44.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	318
AOLFR45.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	324
AOLFR46.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	311
AOLFR47.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	323
AOLFR48.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	318
AOLFR49.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	324
AOLFR50.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	311
AOLFR51.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	323
AOLFR52.pr	AEGRGA	ESTCASHLTAI			ALV	CHLWVTHPI			N-HGRFAS	EV	EMENPP	ISLNRD	KG	CHLWVTHPI	318

Figure 1

440

AOLFR01.pr	:	-----	:	-
AOLFR02.pr	:	-----	:	-
AOLFR03.pr	:	-----	:	-
AOLFR04.pr	:	-----	:	-
AOLFR05.pr	:	-----	:	-
AOLFR06.pr	:	-----	:	-
AOLFR07.pr	:	-----	:	-
AOLFR08.pr	:	-----	:	-
AOLFR09.pr	:	-----	:	-
AOLFR10.pr	:	-----	:	-
AOLFR11.pr	:	-----	:	-
AOLFR12.pr	:	-----	:	-
AOLFR13.pr	:	-----	:	-
AOLFR14.pr	:	-----	:	-
AOLFR15.pr	:	-----	:	-
AOLFR16.pr	:	-----	:	-
AOLFR17.pr	:	-----	:	-
AOLFR18.pr	:	-----	:	-
AOLFR19.pr	:	-----	:	-
AOLFR20.pr	:	-----	:	-
AOLFR21.pr	:	-----	:	-
AOLFR22.pr	:	-----	:	-
AOLFR23.pr	:	-----	:	-
AOLFR25.pr	:	-----	:	-
AOLFR26.pr	:	-----	:	-
AOLFR27.pr	:	-----	:	-
AOLFR28.pr	:	-----	:	-
AOLFR29.pr	:	-----	:	-
AOLFR30.pr	:	-----	:	-
AOLFR31.pr	:	-----	:	-
AOLFR32.pr	:	-----	:	-
AOLFR34.pr	:	-----	:	-
AOLFR35.pr	:	-----	:	-
AOLFR36.pr	:	HSIPTSANPAP	:	305
AOLFR37.pr	:	-----	:	-
AOLFR38.pr	:	EKGQPH	:	300
AOLFR39.pr	:	-----	:	-
AOLFR40.pr	:	-----	:	-
AOLFR41.pr	:	-----	:	-
AOLFR42.pr	:	-----	:	-
AOLFR43.pr	:	-----	:	-
AOLFR44.pr	:	-----	:	-
AOLFR45.pr	:	-----	:	-
AOLFR46.pr	:	-----	:	-
AOLFR47.pr	:	-----	:	-
AOLFR48.pr	:	-----	:	-
AOLFR49.pr	:	-----	:	-
AOLFR50.pr	:	-----	:	-
AOLFR51.pr	:	-----	:	-
AOLFR52.pr	:	-----	:	-

Figure 1

AOLFR54.PT	*	20	*	40	*	60	*	80	*	100	
AOLFR57.PT											50
AOLFR58.PT											59
AOLFR59.PT											99
AOLFR60.PT											49
AOLFR61.PT											49
AOLFR62.PT											49
AOLFR63.PT											49
AOLFR64.PT											49
AOLFR65.PT											53
AOLFR66.PT											49
AOLFR67.PT											49
AOLFR68.PT											51
AOLFR69.PT											86
AOLFR70.PT											77
AOLFR71.PT											47
AOLFR72.PT											47
AOLFR73.PT											47
AOLFR74.PT											47
AOLFR75.PT											47
AOLFR76.PT											45
AOLFR77.PT											47
AOLFR78.PT											49
AOLFR79.PT											54
AOLFR80.PT											47
AOLFR81.PT											65
AOLFR82.PT											45
AOLFR83.PT											46
AOLFR85.PT											45
AOLFR86.PT											72
AOLFR87.PT											101
AOLFR88.PT											47
AOLFR89.PT											72
AOLFR90.PT											99
AOLFR91.PT											45
AOLFR92.PT											45
AOLFR93.PT											46
AOLFR94.PT											48
AOLFR95.PT											72
AOLFR96.PT											47
AOLFR97.PT											98
AOLFR98.PT											48
AOLFR99.PT											47
AOLFR100.PT											47
AOLFR101.PT											51
AOLFR102.PT											47
AOLFR103.PT											47
AOLFR104.PT											47
AOLFR105.PT											47
AOLFR106.PT											47
AOLFR107.PT											47
AOLFR108.PT											63
AOLFR109.PT											47

Figure 2

AOLFR54.pr : * 120 140 160 180 200 * 153
 AOLFR57.pr : * 120 140 160 180 200 * 162
 AOLFR58.pr : * 120 140 160 180 200 * 203
 AOLFR59.pr : * 120 140 160 180 200 * 152
 AOLFR60.pr : * 120 140 160 180 200 * 152
 AOLFR61.pr : * 120 140 160 180 200 * 152
 AOLFR62.pr : * 120 140 160 180 200 * 152
 AOLFR63.pr : * 120 140 160 180 200 * 152
 AOLFR64.pr : * 120 140 160 180 200 * 152
 AOLFR65.pr : * 120 140 160 180 200 * 156
 AOLFR66.pr : * 120 140 160 180 200 * 152
 AOLFR67.pr : * 120 140 160 180 200 * 152
 AOLFR68.pr : * 120 140 160 180 200 * 154
 AOLFR69.pr : * 120 140 160 180 200 * 189
 AOLFR70.pr : * 120 140 160 180 200 * 149
 AOLFR71.pr : * 120 140 160 180 200 * 150
 AOLFR72.pr : * 120 140 160 180 200 * 150
 AOLFR73.pr : * 120 140 160 180 200 * 150
 AOLFR74.pr : * 120 140 160 180 200 * 150
 AOLFR75.pr : * 120 140 160 180 200 * 150
 AOLFR76.pr : * 120 140 160 180 200 * 148
 AOLFR77.pr : * 120 140 160 180 200 * 150
 AOLFR78.pr : * 120 140 160 180 200 * 152
 AOLFR79.pr : * 120 140 160 180 200 * 157
 AOLFR80.pr : * 120 140 160 180 200 * 151
 AOLFR81.pr : * 120 140 160 180 200 * 168
 AOLFR82.pr : * 120 140 160 180 200 * 148
 AOLFR83.pr : * 120 140 160 180 200 * 149
 AOLFR84.pr : * 120 140 160 180 200 * 175
 AOLFR85.pr : * 120 140 160 180 200 * 175
 AOLFR86.pr : * 120 140 160 180 200 * 175
 AOLFR87.pr : * 120 140 160 180 200 * 175
 AOLFR88.pr : * 120 140 160 180 200 * 175
 AOLFR89.pr : * 120 140 160 180 200 * 175
 AOLFR90.pr : * 120 140 160 180 200 * 175
 AOLFR91.pr : * 120 140 160 180 200 * 175
 AOLFR92.pr : * 120 140 160 180 200 * 175
 AOLFR93.pr : * 120 140 160 180 200 * 175
 AOLFR94.pr : * 120 140 160 180 200 * 175
 AOLFR95.pr : * 120 140 160 180 200 * 175
 AOLFR96.pr : * 120 140 160 180 200 * 175
 AOLFR97.pr : * 120 140 160 180 200 * 175
 AOLFR98.pr : * 120 140 160 180 200 * 175
 AOLFR99.pr : * 120 140 160 180 200 * 175
 AOLFR100.pr : * 120 140 160 180 200 * 175
 AOLFR101.pr : * 120 140 160 180 200 * 175
 AOLFR102.pr : * 120 140 160 180 200 * 175
 AOLFR103.pr : * 120 140 160 180 200 * 175
 AOLFR104.pr : * 120 140 160 180 200 * 175
 AOLFR105.pr : * 120 140 160 180 200 * 175
 AOLFR106.pr : * 120 140 160 180 200 * 175
 AOLFR107.pr : * 120 140 160 180 200 * 175
 AOLFR108.pr : * 120 140 160 180 200 * 175
 AOLFR109.pr : * 120 140 160 180 200 * 175

Figure 2

[illegible]

Figure 2

AOLFR54.pr : FRSITVHRFGHEVFKVHIFIPANLVNPPVMPNPDVGNATFGRSRLRTHIGKTSI : 318
 AOLFR57.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 326
 AOLFR58.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 370
 AOLFR59.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 315
 AOLFR60.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 325
 AOLFR61.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 313
 AOLFR62.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 311
 AOLFR63.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 313
 AOLFR64.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 321
 AOLFR65.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 317
 AOLFR66.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 320
 AOLFR67.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 321
 AOLFR68.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 315
 AOLFR69.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 359
 AOLFR70.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 340
 AOLFR71.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 311
 AOLFR72.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 316
 AOLFR73.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 312
 AOLFR74.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 337
 AOLFR75.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 314
 AOLFR76.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 314
 AOLFR77.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 331
 AOLFR78.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 319
 AOLFR79.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 309
 AOLFR80.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 328
 AOLFR81.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 310
 AOLFR82.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 347
 AOLFR83.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 309
 AOLFR84.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 329
 AOLFR85.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 359
 AOLFR86.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 323
 AOLFR87.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 348
 AOLFR88.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 370
 AOLFR89.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 313
 AOLFR90.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 312
 AOLFR91.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 314
 AOLFR92.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 315
 AOLFR93.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 335
 AOLFR94.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 316
 AOLFR95.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 362
 AOLFR96.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 314
 AOLFR97.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 312
 AOLFR98.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 319
 AOLFR99.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 310
 AOLFR100.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 315
 AOLFR101.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 313
 AOLFR102.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 316
 AOLFR103.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 330
 AOLFR104.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 315
 AOLFR105.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 313
 AOLFR106.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 316
 AOLFR107.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 330
 AOLFR108.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 317
 AOLFR109.pr : FRLKIDREV--TFSE--DKPAPFVHTIAFIPNPLVNTFGRSRLRTHIGKTSI : 317

Figure 2

[illegible]

AOLFR110.P : RPEFCGNNQDNFPCGVRQVQKQACQDMVAVHEHNVNSGLMWTLCFCQCLSHVAVTICHVHRAASHENKAVMAGTCHT 320
 AOLFR111.P : SLSCGANNWQHFCQDIPQLMANSSENTANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 266
 AOLFR112.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 293
 AOLFR113.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 292
 AOLFR114.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 268
 AOLFR115.P : RPARCAQALPHFTGCPGSAKIDACSTHNEHNTGGLFLTPVAFHLSVVRFAVWVSSPCGKQWAFKICLP 284
 AOLFR116.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 266
 AOLFR117.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 266
 AOLFR118.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 315
 AOLFR119.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 276
 AOLFR120.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 276
 AOLFR121.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 266
 AOLFR122.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 267
 AOLFR123.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 299
 AOLFR124.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 264
 AOLFR125.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 265
 AOLFR126.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 283
 AOLFR127.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 272
 AOLFR128.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 266
 AOLFR129.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 297
 AOLFR130.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 276
 AOLFR131.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 264
 AOLFR132.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 264
 AOLFR133.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 258
 AOLFR134.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 272
 AOLFR135.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 282
 AOLFR136.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 267
 AOLFR137.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 267
 AOLFR138.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 265
 AOLFR139.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 253
 AOLFR140.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 269
 AOLFR141.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 277
 AOLFR142.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 269
 AOLFR143.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 267
 AOLFR144.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 267
 AOLFR145.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 279
 AOLFR146.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 269
 AOLFR147.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 275
 AOLFR148.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 269
 AOLFR149.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 269
 AOLFR150.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 265
 AOLFR151.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 271
 AOLFR152.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 267
 AOLFR153.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 266
 AOLFR154.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 265
 AOLFR155.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 282
 AOLFR156.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 266
 AOLFR157.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 267
 AOLFR158.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 267
 AOLFR159.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 288
 AOLFR160.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 267
 AOLFR161.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 274
 AOLFR162.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 274
 AOLFR163.P : QLEPCAGNWHQICQDFPMSACQETANLADAILINVLDFCCFVAVTIVWFSVQWPKSTPQSGKAFKICLP 266

Figure 3

AOLFR110.P : A-----DKW/SFTHMPEPAMPVAVLNORSTKRETSRHHVVCQVDFIIRN----- : 340
 AOLFR111.P : L-----SILDVBSMFTMPPETEMPIYSHNFOALVAGMTHKGLTKK----- : 380
 AOLFR113.P : L-----TLDRTANVSVATEWMPHYSLJRKETKATKRTYFGDKASLAHL----- : 316
 AOLFR114.P : V-KDH-----VATNTHSSAMPVTSLENDKOCPEKSKES----- : 338
 AOLFR115.P : TERES-----RAALVWVTEPILNMPVYSLERDSEKSGFVSGKTFYL----- : 342
 AOLFR116.P : L-----DKETAFEDAVTEVLPNPIYVLRNCEWVVRRCQVFNYSKIF----- : 309
 AOLFR117.P : QENM-----KVAATVGTLEPAMPVYSLERKSEAKVZGKILF----- : 330
 AOLFR118.P : A-TLIPV-----HINLHNEPESLNPVYVALOTYCEPAFOVHIFALTKERS----- : 357
 AOLFR119.P : TIPPSLHI-----KVANVLLPEPILNPIYVGVTKGKRSKIRFQGDKGAG----- : 324
 AOLFR120.P : IN-----FNKVSIMVSTPEAMPVYSLANKERKGLGRFSLNFWKQG----- : 317
 AOLFR121.P : IE-----KOLVHSWVTHTEPILNPIYSLERKEKEDACVYGNRIS----- : 309
 AOLFR122.P : LNSDDLATDKLISMPGVTMPMBPIYSLERNDKERAKHFNRRFFSK----- : 312
 AOLFR123.P : NTSDELIGISGVSRMAMPVYSLERKEKAKVLSRHLLKM----- : 346
 AOLFR124.P : FER-----DKWAALVTEPILNPIYSLERKEKEDACVYGNRIS----- : 307
 AOLFR125.P : SILDVBSMFTMPPETEMPIYSHNFOALVAGMTHKGLTKK----- : 315
 AOLFR126.P : DDOD-----WESHSFVTEPILNPIYSLERKEKEDACVYGNRIS----- : 325
 AOLFR127.P : DDOD-----WESHSFVTEPILNPIYSLERKEKEDACVYGNRIS----- : 314
 AOLFR128.P : A-----DKW/SFTHMPEPAMPVAVLNORSTKRETSRHHVVCQVDFIIRN----- : 308
 AOLFR129.P : V-----DKW/SFTHMPEPAMPVAVLNORSTKRETSRHHVVCQVDFIIRN----- : 343
 AOLFR130.P : A-TLIPV-----HINLHNEPESLNPVYVALOTYCEPAFOVHIFALTKERS----- : 324
 AOLFR131.P : E-----DKW/SFTHMPEPAMPVAVLNORSTKRETSRHHVVCQVDFIIRN----- : 309
 AOLFR132.P : I-----DKW/SFTHMPEPAMPVAVLNORSTKRETSRHHVVCQVDFIIRN----- : 303
 AOLFR133.P : YN-----SNKVSIMVSTPEAMPVYSLANKERKGLGRFSLNFWKQG----- : 325
 AOLFR134.P : LERD-----KVAATVGTLEPAMPVYSLERKEKEDACVYGNRIS----- : 327
 AOLFR135.P : LDQE-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 308
 AOLFR136.P : NDKN-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 322
 AOLFR137.P : VEQG-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 307
 AOLFR138.P : LIPPSCHI-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 321
 AOLFR139.P : V-PLIPV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 329
 AOLFR140.P : V-PCVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 314
 AOLFR141.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 312
 AOLFR142.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 326
 AOLFR143.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 317
 AOLFR144.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 320
 AOLFR145.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 318
 AOLFR146.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 311
 AOLFR147.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 308
 AOLFR148.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 315
 AOLFR149.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 311
 AOLFR150.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 311
 AOLFR151.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 311
 AOLFR152.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 311
 AOLFR153.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 311
 AOLFR154.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 311
 AOLFR155.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 311
 AOLFR156.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 311
 AOLFR157.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 311
 AOLFR158.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 311
 AOLFR159.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 311
 AOLFR160.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 311
 AOLFR161.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 311
 AOLFR162.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 311
 AOLFR163.P : A-PPVHV-----KSSVTEVTEPILNPIYSLERKEKEDACVYGNRIS----- : 311

Figure 3



Figure 4

AOLF165.P : * 120 140 160 180 200 * 128
 AOLF166.P : * 120 140 160 180 200 * 127
 AOLF167.P : * 120 140 160 180 200 * 130
 AOLF168.P : * 120 140 160 180 200 * 125
 AOLF169.P : * 120 140 160 180 200 * 123
 AOLF170.P : * 120 140 160 180 200 * 211
 AOLF171.P : * 120 140 160 180 200 * 89
 AOLF172.P : * 120 140 160 180 200 * 132
 AOLF173.P : * 120 140 160 180 200 * 129
 AOLF175.P : * 120 140 160 180 200 * 165
 AOLF176.P : * 120 140 160 180 200 * 145
 AOLF177.P : * 120 140 160 180 200 * 137
 AOLF178.P : * 120 140 160 180 200 * 127
 AOLF179.P : * 120 140 160 180 200 * 127
 AOLF180.P : * 120 140 160 180 200 * 156
 AOLF181.P : * 120 140 160 180 200 * 127
 AOLF182.P : * 120 140 160 180 200 * 132
 AOLF183.P : * 120 140 160 180 200 * 129
 AOLF184.P : * 120 140 160 180 200 * 135
 AOLF185.P : * 120 140 160 180 200 * 209
 AOLF186.P : * 120 140 160 180 200 * 126
 AOLF187.P : * 120 140 160 180 200 * 125
 AOLF188.P : * 120 140 160 180 200 * 125
 AOLF189.P : * 120 140 160 180 200 * 127
 AOLF190.P : * 120 140 160 180 200 * 128
 AOLF191.P : * 120 140 160 180 200 * 125
 AOLF192.P : * 120 140 160 180 200 * 125
 AOLF193.P : * 120 140 160 180 200 * 125
 AOLF194.P : * 120 140 160 180 200 * 127
 AOLF195.P : * 120 140 160 180 200 * 157
 AOLF196.P : * 120 140 160 180 200 * 127
 AOLF197.P : * 120 140 160 180 200 * 127
 AOLF198.P : * 120 140 160 180 200 * 147
 AOLF199.P : * 120 140 160 180 200 * 125
 AOLF200.P : * 120 140 160 180 200 * 127
 AOLF201.P : * 120 140 160 180 200 * 127
 AOLF202.P : * 120 140 160 180 200 * 127
 AOLF203.P : * 120 140 160 180 200 * 127
 AOLF204.P : * 120 140 160 180 200 * 125
 AOLF205.P : * 120 140 160 180 200 * 127
 AOLF206.P : * 120 140 160 180 200 * 127
 AOLF207.P : * 120 140 160 180 200 * 125
 AOLF208.P : * 120 140 160 180 200 * 127
 AOLF209.P : * 120 140 160 180 200 * 127
 AOLF210.P : * 120 140 160 180 200 * 127
 AOLF211.P : * 120 140 160 180 200 * 127
 AOLF212.P : * 120 140 160 180 200 * 127
 AOLF213.P : * 120 140 160 180 200 * 168
 AOLF214.P : * 120 140 160 180 200 * 127
 AOLF215.P : * 120 140 160 180 200 * 127
 AOLF216.P : * 120 140 160 180 200 * 127
 AOLF217.P : * 120 140 160 180 200 * 137

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Figure 4

AOLFR328.P : *ALGNH-----SITTEFFIIGLSADPNIRALLFVLPFCGTYITIMENQIIVIRA : 51

AOLFR24B.P : * 120 140 160 180 200 *
 SHHQ -EMVEIAMSGVDFGLSTSTPRRIUGFWF---NLQESFCEGLLOFFTHMFTGCTVTVVMDRVAIENPILQVTLTNKT-ISTIASVVVGRNML : 157
 AOLFR33B.P : SHHQ -EMVEIAMAGTDGLSTATPKVIGFWF---NLGEMAGGICQVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 157
 AOLFR130B. : HHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 155
 AOLFR142B. : SHHQ -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 160
 AOLFR171C. : RHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 155
 AOLFR218.P : HHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 155
 AOLFR219.P : RHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 179
 AOLFR220.P : AHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 183
 AOLFR221.P : SHHQ -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 155
 AOLFR222.P : HHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 155
 AOLFR223.P : AHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 156
 AOLFR224.P : RHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 155
 AOLFR225B. : HHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 153
 AOLFR227.P : RHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 160
 AOLFR228.P : HHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 155
 AOLFR229.P : RHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 176
 AOLFR230.P : RHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 156
 AOLFR231.P : LHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 155
 AOLFR232.P : HHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 187
 AOLFR233.P : RHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 155
 AOLFR234.P : SHHQ -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 159
 AOLFR235.P : RHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 153
 AOLFR236.P : HHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 155
 AOLFR237.P : RHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 150
 AOLFR238.P : RHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 155
 AOLFR239.P : CHHS -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 155
 AOLFR240.P : AHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 156
 AOLFR241.P : SHHQ -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 155
 AOLFR242.P : SHHQ -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 175
 AOLFR243.P : AHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 154
 AOLFR244.P : RHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 205
 AOLFR245.P : THHS -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 155
 AOLFR246.P : HHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 155
 AOLFR247.P : HHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 155
 AOLFR248.P : HHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 176
 AOLFR249.P : RHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 155
 AOLFR250.P : RHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 195
 AOLFR251.P : KHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 153
 AOLFR252.P : KHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 154
 AOLFR253.P : RHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 173
 AOLFR254.P : RHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 152
 AOLFR255.P : RHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 155
 AOLFR256.P : RHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 154
 AOLFR257.P : RHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 154
 AOLFR259.P : RHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 154
 AOLFR274B. : CCHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 146
 AOLFR276B. : SHHQ -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 157
 AOLFR311B. : CHHH -EMVEIAMALDGLSTATPKVIGFWF---EKKLSGSEVATHTICGLSVMVTVIGIDRIAIONPISNMLTNKV-TAIGIVITRTIAP : 155

Figure 5
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AOLFR314.P : P... 155
 AOLFR324B.P : S... 157
 AOLFR328.P : D... 153
 AOLFR248.P : V... 262
 AOLFR338.P : P... 260
 AOLFR330B.P : S... 261
 AOLFR342B.P : S... 266
 AOLFR371C.P : A... 261
 AOLFR218.P : S... 262
 AOLFR219.P : T... 284
 AOLFR220.P : V... 288
 AOLFR221.P : S... 261
 AOLFR222.P : G... 261
 AOLFR223.P : S... 262
 AOLFR224.P : S... 260
 AOLFR225B.P : T... 259
 AOLFR227.P : C... 261
 AOLFR228.P : A... 261
 AOLFR229.P : G... 282
 AOLFR230.P : S... 262
 AOLFR231.P : S... 260
 AOLFR232.P : G... 293
 AOLFR233.P : A... 265
 AOLFR235.P : S... 261
 AOLFR236.P : A... 296
 AOLFR237.P : S... 260
 AOLFR238.P : A... 261
 AOLFR239.P : S... 261
 AOLFR240.P : A... 262
 AOLFR241.P : S... 281
 AOLFR242.P : V... 259
 AOLFR243.P : G... 261
 AOLFR244.P : G... 311
 AOLFR245.P : S... 260
 AOLFR246.P : S... 261
 AOLFR247.P : A... 261
 AOLFR248.P : S... 282
 AOLFR250.P : A... 301
 AOLFR251.P : A... 259
 AOLFR252.P : G... 261
 AOLFR253.P : G... 279
 AOLFR254.P : G... 268
 AOLFR255.P : G... 251
 AOLFR256.P : A... 261
 AOLFR257.P : A... 260
 AOLFR259.P : A... 260
 AOLFR274B.P : S... 252

Figure 5
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[illegible]

Figure 5
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Figure 5
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